

Table 70: Comparative Sequences relating to SAG 1280

ATACCTTTATTGAGTTGAAAACCTTGGAAATGATTTCTTTGTGGATGAGGCTCATC
 ACTTCAAGAATATCCGTCCAATCACTGGACTTGGGAATGTAGCTGGAAATCACAACAAA
 CTTCTAAAAGAACGTCGGATATGGAGATGAAGGTGAGACAAGTACAGGCAGAGCATGGAG
 ATAGAAATGTCTTTGCGCACAGGAACACCAGTTCTAATCTATTAGTGAACTTTCA
 CCATGATGGATTACATTCAACCTGATGCTTGGAAACGATACTGGTATCAAATTTGACT
 CCTGGGTTGGGCTTGGGAAATATCGAAAACCTGGAACTAGGCGACAGGAGAGATA
 AGTACCAACCCAAAGAACGGTCAAGAAATTGTCACACCTCTGAACITCATGGAACTCT
 ACAAGGAAACTGCCGATATTCAAGACCTCAGACATGCTGATTACCGTAGCCGAAAGCTA
 AGATTATTGGCTGGGAAACGGAGTTAACGCAGACTAGAATTTGGAAAGAGCTGG
 TAAAGCGTTCAAGCCTATCAAGTCAGTAGTTGATCAGAATAGAGATAACATGTTA
 AAAACACAGGAGAAGCCAGAAAACACTGATATTGATATGCCGTTGATGCCCTACT
 CCTTATCGGAAATATCAGAAAATCTCAAGTAGTCTGATAATGTCGAGGCGATTACCGTG
 ATGGAGCTGGAGCAAACGCCATCAGATGATTTCAGATGATTACCGTAGCCGAAAGATA
 AGGAGAAGGGTTTGATGTCACAAATGAACCTAAAGACTTTGTCGATCGAGGGATAC
 CAAAAGAAGAAAATGCCCTTGTCCATGATGCCAATACTGATGAGAAGAAAACCTCTGT
 CACCGAAGGTAAAGTGGAGAAGTACGGATTCCTACGGAAAAAAGGGGAA
 CAGGATTAAACCTCCAATCTGCATGAAAGCTGTCCTACATTAGACCTTCCCTGGAGGC
 CCTCAGACATTGTCAGCGAAATGGACGACTTAATCGACAAGGAAACATGCACCGAGG
 TAGATATTACTAATTAATTAACGGAGCTTGGACAATTACCTCTGGCAGACGCCAGG
 AGAATAAGCTAAAGTATATCACCCAGATAATGACCTCAAAAGATCCTGAGATCAGCTG
 AAGACATTGATGAAACAAACCATGACCCCTCAGACTTAAGGCATTGCCACTGGAAAC
 CTATCTCAAACCTAAAATGGAGTTGGAAAATGAACTGACAGTTTGGAGAATCAAAC
 GAGCCTTTAATCGCTGGGAAACGGAGTATGCCATACCCATTCTGAGGAGAACCC
 TCCCATTATGGAAAAACCGTTGAGTCATGAAATGATAAAGATATTGCCAATTTGGCAA
 CCAAGTCGCAAGATTGTCATGCGATTGACATCAAGGAAATGGATAATCGTGTGAG
 CTGGGACTATCTGCCTGGGAAACCTTACCTACAGGCTCAGAGACCAAGGAAAGTCAGG
 CACTTGCCTAGTTAGAGGATTGATTTAAAGTACACAGGGTCTAGTGAGCCCT
 TACAGAAACCATTTCTTAATGATTGAGGTGATAACCACTATACTGTCGCCCTGATT
 TGAATTCAGAGGAAACCGGATTAGCTGACATTGACCTATTATAGATG
 ACCAGAAAAGCGCAAGCTGGTAAAGGATTAAAAGATAAGCTACAGGAGTAGCCAAG
 TAGAAGTTGATAAAGTCTTCCAAGGAAGGAGACTATCAGCTTGTAAAGGCTAAGTATG
 ATGTTTGTAGCTCCCTGGTIGAAAAGAAGCAGAGATTGAGAGATAGTGAGCTTGG
 CCAAGTTAGTGAGATAACACCCCCAAAAGAACAAACTCGAGATA

SEQ ID. NO. 7002

STRAIN H36B

GGAGGGAAAATGAATCAAGAAGTCCTACTACAAATGAT
 GAGGCCACTATTCTCGTGATAGAGCCTTGTGAGGCATTTATATT
 ACCAACGAGGATTTGATGAGGAGTGGGATGCTTATTCATCAGTT
 ATGACCAACTAGGCAAGAAAATAAGTCTGTCAGTACTTCACCTTG
 GACAGATGTTCACTGTTCTCAGGCTAGTCTTATGATACTGCTCATG
 ATCTATTGACCTATAACACAGTTTCCGCCAAAGTGGTCTTCAAAACCTA
 GATAAAACTATCCCGCTGAAAAAAACCTGGTATAGAGTGGCTTGT
 CAATCTGGCCACTCGTTTCAATTATTGATTCTCAATGGACACTACAAA
 CCATATCGCCGATTCACTCTACAAAGAGTAGGGGAGCTAATTGGTC
 AATGTTGATCTGCTGCTAATTAATTAGCGGATCTATTAGTCGAGATAT
 TGAACAGCTTCTTAACCTACAGGCTGAGCTGAAACTAGAGCTGATG
 AAACITGTTCTAGAAAATGAAGAAACTGTTGATGAGCACAAAACAGTGT
 CATCAAGCAATATCTTTCAGAAGGGCTCTGGTTATTGCTAGTT
 GGATGTTAGATTGCTCTCAACTAGATGTTCAAAAGGAAAACCCAGTCATC
 TGCCAGCTTATGAGAGTTCTTACCGCTTAAATTGAGATTCTAACCA
 TATTTGACCAAATTCGAAATGAACGTTCCAAGTCCCAGTTTACAGC
 AGGTCAGATTGACACAGAGATGAAACCCAGTCTTGTATGGCGAGG
 AATTACTTACTTATCTGAAGCTGATGCCAGTCCCTATGAGCTGAAACGA
 ACGCTGACTACAGTCGAAGAAAAGGAATTAGAAAAATTGGACAAGCCAT
 TAGGATGAAAATCAAGAAAATTGACTCAGCTASGKATTGTTTATCTC
 AGTTGACCCAGACCGAGCTGGTATTTTATTGATGTCAGCAGGAGTCGTT
 CGTTTAWAWAATGCAAGACCTTGTCTCACTAGGTGGTTATCCAAAGCC
 GTTAACCTCAACTAGCCCTGGACAGAAACTACTCCAAATGGACTAAGTC
 ATGAAAAGGGTTCTTCTTGTAGCCAGCTTCCATTGAGAGCTG
 CGACAGGCTGCTTACGCCCTTACACCAAGAAACTCAGCAGAGAAGTC
 GGAGCAATTGAAAAGATAAAGGTAATCAGCCAGATTIAACTCTCAGAG
 ATTGGAAAAGCAAGCTAGAGAAAAGCTGAGGAAAAAGAAGTAGTTGATGAA
 GAATTGGGAAATTCCTACTGGTTCAAGAGTATTGGACATTATCTCT
 GGGGTATTGGTTCTATAAGGGACAGGACTTTGAGGTCTGTCGGTCA
 CGGATGCTGCACTGAACGGTTGATTGGAGCTTAGTCATTGACTT
 TCGGATATCATTGACAAAATTCAGTTCTTATGAGGACTGGGAGA
 AGTCAGTCAGGACTTCATCAGCCAAAGCAGAACCAAACAGAGTTAG
 AAGAAGCGGACAAAGAATTAAACCTATTCTCATTTCTGGAAGAGGAGCTA
 GTTCAGAGTATTGGACTATTGGAAACCGAGTATTGAGAAATGGTCATAA
 CGTACACTGATCTTGAAGAAAACAGATAATCAAACTCTGAAGGAGAGTC
 TCGAAACAATTCCAGAGATTCCAGTAACGGACTTTATTTCAGAAGAT
 TTGACGGACTTTTATCTAAAGACTGCTAGAGATAAGGTTGAGACAAACAT
 TGTGGCCTTCGTTGGTAAAAAAATCTAGAAGTAGAGCACCGCAATGCTT
 CACCAAGTGAACAAAGAACTCTTGCCTAGTATGAGCTGGGGTGGACTA
 GCCTGAAATTCTTGTGACTATAATCCAAAATTTCTAAGGAACGAGA
 AGAAACTGAAAGAGCTAGTCAGATAAAGAGTATTGGATATGAAACAGT
 CCTCCCTGACAGCTTATTACACAGACCCATCCCTGATCCGTAGATGTC
 GATAACTGGAAAGAGATGGCTTACAGGTGCAAATCTAGATCCCTC
 CATGGGAAACAGGAAATTCTTGCCTAGTGCCTAAACACTTAAGGAGAAA
 AGAGTGAGTTGATGGCGTAGAGTTAGATACTATTACAGGAGCTATTGCC
 AACACCTTCATCCCAATGTCATATTGAAATTAGGGATTGAGACGGT
 GGCTTTAACGACAATAGTTGATTGCTGATTCAAATGTCGCCCTTG

Table 70: Comparative Sequences relating to SAG 1280

CCAAATATACGAAITCGGGATAATAGGTACGATAGGCCCTACATGATTCA
 GACTACTTGTCAAAAAGTCAGTCATTGATTTGCTCATGATGGTGGACAAGT
 AGCAGATTATCTCTCCACAGGAACAGTATCGATAAGCGAACAGAAAACATCT
 TACAAGATATTCTGTAGACAACTGAATTCTTGTTGGGTTCTGACTGCCT
 GACTCTGCCCTTAAGGCCATTGCAAGGAACGAGTGTCAACACGGATATGTT
 ATTCTTCCAGAACACTTAGACAAGGGATATGTGGCAGACGATTAGCCT
 TTTCAGGTTCCATTGCTATGACAAGGAGTGTGGCATTTGGCTCAATCCT
 TATTTGATGGAAATAACATAGCCAGGTGCTAGGAACCTACGAGGTCA
 GAATTTAACGGAGGAACACTTCTGTTAAGGGACTAGTGACTTG
 TTGCAAGTGTGAAACAGCTTAACTGTTAAGGCCAACAGAGGATT
 GATAGAAATAGGGTCATCAATTACCCAGATGTGTTGACCAAACAGTC
 TGATACCTCCATTCCAGCTGAAATGAGGGAAAATCTAGGTCACTACAGTT
 TTGGTTATCAGGGTCTACAGTTACTATCGAGATAACAAAGGCATTCCA
 GTCGGAACCAAGACGGAAGAAATCAGTTACTATGTCGATGAAGAG

SEQ ID. NO. 7003

STRAIN 18RS21

GrAGGGAAAATGAATCAAGAAGTCTTAACAAATGATGAGA
 GCCACTATTCTCGTGTAGAGCCTTGTGTTAGGCATTTTTATTACCA
 AGCAGAGCATTGATGAGGAGTGGGATAGTCCTTATTTCATCAGTTTATGA
 CCAATAGGCAAGAAATAAAATAGTCAGTCAACTTCACTTGGAGACA
 GATGTTTCAGCTTTGTCCAGGCTAGTCCTTATGATAGTGTCTATGATCT
 ATTGACCTATAACACAAGTTTCCGGCCAAAGTGGTCCTCAAAACTAGATA
 AACATAGCCTGCTGAAAAAAACCTGGTGTAGAAGCTGGCCTTGTTCAAT
 CTGGCCACTCGTTCAATTATGGATTCCAATGGACACTACAAACCAT
 ATCGCCGATTCACTCTTACAAAGAGTAGGGAGCTAATTGGTCAATG
 TGATCTGTGCTAATAATTAGCGGATCTGTTAGTCGAGATATTGAA
 CAGTTCTTAACTTACAGGCTGAGCTGAAACTAGAGCTGATGAAAC
 TGGTCTAGAAAATGAGAAACCTGTTGATGAGCACAACAAAGTGGTCAATC
 AAGCAATATCTTTGAGAAGAGGCTCTCTGGTTATTGCTAGTTGGAT
 GTAGATTGTCAGTCAACTAGATGTTCAATAGGAAAACAGTCATCTGCC
 AGCTTATGAGAGTTACTCTTACGACGTAATTGAGATTCTAACATATT
 TTGACCAAAATTGCAATGAACTTCCAAAGTCCAAAGTTAGACGAGGT
 GATTTGACACAGAGATGGAATGACCCAGTCCTTGTAGGGGAGGAATT
 ACTTACTTATCTCGAAGCTGATGGCAGTCCTATGAGCTGAAACGAACGC
 TGAATCACAGTcGAAGAAAAGGAATTAGAAAAAAATTGGACAAGCATTAGG
 ATAGAAAATGAGAAAATTGACTCAGCTAGGGATTGATTTATCTCAGTT
 TGACCCAGACCGACTCGGTTTTATTGGATGTCAGCAGGTGCTTTGTT
 TAAAAAAATGAGACCTTGTCTTACTAGGTGTTATCCAAAGCCTCGGT
 ACTCAACTAGCCCTTGCAGAACTACTCCAAATGGGACTAAGTCATGA
 AAAGGTTGAAATTCTTGGTAGCCAGCTTCCATTGAAGAGCTGCG
 AAGTTGCCCTACGCCCTTTAACCCAAGAACCTCAGCAGAGATGCGGAG
 CAATTTGAAAAGATAAAGGTATCAGCCAGATTAACTCTCAGAGAATTG
 GAAAGGCAAGCTAGAGAAAAGCTGAGAGAAAAGAAGTGTGAGAAGAAAT
 TCGCGGAAATTCAGGTTAGAGAGTATTGGACACTTATCTCTGGGG
 TCATTGGTTCTATAAGGGACAGGACTTGGAGGTATGTCGGTCAGCGA
 TGCTCGATTGACCGGTTGATTCGGATTGAGTTAGTCATGACTTTTCCG
 ATATCATGAAACAAATCCAGCTCTTATGTGAGGACCTGGAAAGAGTC
 AGTCAGGCACTTCATCAGCCAAAGGAGAACACCACAGAGTTAGAAGA
 AGCGGACCAAGAATTAAACCTATTCTCATTTCAGGCTATGTCGGTCAGCG
 AGAGTATTGGACTATTGGACACAGAGTCATTGAGAAATGGTCATAACGAT
 ACTGATCTGAAGAACACAGATAATCAAACTCTGAAGAGGAAGTGTG
 AACAACTCCAGAGATTCCAGTAACGGACTTTATTCTCAGAGATTG
 CGGACTTTATCCTAACACTGCTAGAGATAAGGGTGGAGACAAACATTGT
 GCCTTCTGGTGTGAAAATCTAGAGTGAAGGACCCGAATCTTCA
 AAGTGAACAAGAACTCTTGCAGTATGTAAGGCTGGGTGGACTAGCCA
 ATGAATTCTTGTGACTATAATCCAAAATTTCTAAGGAAACCGAGAACGAA
 CTGAAGAGCCTAGTCACAGATAAAAGAGTATTCGGATATGAAACAGTC
 CCTGACAGCCTATTACACAGACCCATCCCTGATCGTCAGATGTGGGATA
 AGTTGAAAAGAGATGGCTTACAGGTGGCAAATCTAGATCCTTCCATG
 GGAACAGGGAAATTCTTGGCTATGCCAAAACACTTAAGGAAAAGAG
 TGAGTTGATGGCTAGAGTGTAGATACTTACAGGAGCTATTGCCAAC
 ACCTTCATCCAAATAGTCATAATTGAAATTAGGGATTGAGACGGTGGCT
 TTAACGGACAAATAGTTGATTTGAGTTCAAATGTGCCCTTGGCAA
 TATACGAAATTGGGATAATAGCTACGAGTAGGCCATTACATGATTGACT
 ACTTGTCAAAAGTCACTTGTATTGCTCATGATGGTGACAAGTAGGG
 ATTATCTCTTACAGGAACCTATGGATAAGCGAACAGAAAACATCTTACA
 AGATAATTGAGACAACTGAATTCTTGTGGGGTTGCACTGCGCTGACT
 CTGCCCTTAAGGCCATTGCAAGGAACGAGTGTCAACACGGATATGTTATC
 TTCCGAAACACTTAGACAACGGATATGTCAGACGAGCTTACGGCTTTC
 AGGTTCCATTGCTATGACAAGGGATATGTCAGACGAGCTTACGGCTTTC
 TTGATGAGGAATAACATAGCCAGGTGCTAGGAACCTACGAGGTCA
 TTAAACGGGAAACACTTCTGTTAGGGACTAGTGATGACTTGATTG
 AAGTGTGAAACAGCTAAATCACGTTAACGGCTTAAAGGCCAACAGGAGATTGATA
 GAAATGAGGTCACTATTACCCAGATGTGTTGACCAAACAAAGTC
 ACCTCCATTCCAGCTGAAATGAGGGAAAATCTAGGTCACTACAGTTTGG
 TTATCAGGGGTCTACAGTTACTATCGAGATAACAAAGGCATTGAGTC
 GAACCAAGACGGAAGAAATCAGTTACTATGTCGATGAAGAG

MSA Alignment Results: Pretty output
PRETTY of: /biotmp/msa31161.2{*} June 20, 2002 10:41 ..

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNt_2603}	GgAGGGAAAA TGAATCAAGA AGTCTTACTA CAAATGATGA GAGCCACTAT
msa31161.2{327d_18RS21}	GnAGGGAAAA TGAATCAAGA AGTCTTACTA CAAATGATGA GAGCCACTAT
msa31161.2{327dNT_H36B}	GgAGGGAAAA TGAATCAAGA AGTCTTACTA CAAATGATGA GAGCCACTAT
Consensus	***** * ***** * ***** * ***** * ***** * *****
	51
msa31161.2{327dNt_2603}	TCCTCGTGAT AGAGCCTTGC TTGAGGCATT TTTATATTAC CAAGCAGAGC
msa31161.2{327d_18RS21}	TCCTCGTGAT AGAGCCTTGC TTGAGGCATT TTTATATTAC CAAGCAGAGC
msa31161.2{327dNT_H36B}	TCCTCGTGAT AGAGCCTTGC TTGAGGCATT TTTATATTAC CAAGCAGAGC
Consensus	***** * ***** * ***** * ***** * ***** * *****
	100
msa31161.2{327dNt_2603}	ATTTTGATGA GGAGTGGGAT AGTCTTATTTC ATCAGTTTAT GACCAATAGG
msa31161.2{327d_18RS21}	ATTTTGATGA GGAGTGGGAT AGTCTTATTTC ATCAGTTTAT GACCAATAGG
msa31161.2{327dNT_H36B}	ATTTTGATGA GGAGTGGGAT AGTCTTATTTC ATCAGTTTAT GACCAATAGG
Consensus	***** * ***** * ***** * ***** * ***** * *****
	150
msa31161.2{327dNt_2603}	CAAGAAATAA ATAAGTCIGT TCAAGTACTT CACTTTGAGA CAGATGTTTC
msa31161.2{327d_18RS21}	CAAGAAATAA ATAAGTCIGT TCAAGTACTT CACTTTGAGA CAGATGTTTC
msa31161.2{327dNT_H36B}	CAAGAAATAA ATAAGTCIGT TCAAGTACTT CACTTTGAGA CAGATGTTTC
Consensus	***** * ***** * ***** * ***** * ***** * *****
	200
msa31161.2{327dNt_2603}	AGCTTTGTC CAGGCTAGTC CTTATGATAC TGCTCATGAT CTATTGACCT
msa31161.2{327d_18RS21}	AGCTTTGTC CAGGCTAGTC CTTATGATAC TGCTCATGAT CTATTGACCT
msa31161.2{327dNT_H36B}	AGCTTTGTC CAGGCTAGTC CTTATGATAC TGCTCATGAT CTATTGACCT
Consensus	***** * ***** * ***** * ***** * ***** * *****
	250
msa31161.2{327dNt_2603}	ATACACAAAGT TTTCGGCCAA AGTGGTCTTC AAAAACTAGA TAAACTATCG
msa31161.2{327d_18RS21}	ATACACAAAGT TTTCGGCCAA AGTGGTCTTC AAAAACTAGA TAAACTATCG
msa31161.2{327dNT_H36B}	ATACACAAAGT TTTCGGCCAA AGTGGTCTTC AAAAACTAGA TAAACTATCG
Consensus	***** * ***** * ***** * ***** * ***** * *****
	300
msa31161.2{327dNt_2603}	CCGTCTGAAA AAAACTTGGT GATAGAAGTG GCCTTGTCA ATCTGGCAC
msa31161.2{327d_18RS21}	CCGTCTGAAA AAAACTTGGT GATAGAAGTG GCCTTGTCA ATCTGGCAC
msa31161.2{327dNT_H36B}	CCGTCTGAAA AAAACTTGGT GATAGAAGTG GCCTTGTCA ATCTGGCAC
Consensus	***** * ***** * ***** * ***** * ***** * *****
	350
msa31161.2{327dNt_2603}	TCGTTTCAA TTATTGGATT CCAATGGACA CTACCAAACC ATATGCCGG
msa31161.2{327d_18RS21}	TCGTTTCAA TTATTGGATT CCAATGGACA CTACCAAACC ATATGCCGG
msa31161.2{327dNT_H36B}	TCGTTTCAA TTATTGGATT CCAATGGACA CTACCAAACC ATATGCCGG
Consensus	***** * ***** * ***** * ***** * ***** * *****
	400
msa31161.2{327dNt_2603}	ATTCACTCTT ACAAAAGAGT AGGGGAGCTA ATTGGTCAA TGTGTATCGT
msa31161.2{327d_18RS21}	ATTCACTCTT ACAAAAGAGT AGGGGAGCTA ATTGGTCAA TGTGTATCGT
msa31161.2{327dNT_H36B}	ATTCACTCTT ACAAAAGAGT AGGGGAGCTA ATTGGTCAA TGTGTATCGT
Consensus	***** * ***** * ***** * ***** * ***** * *****
	450
msa31161.2{327dNt_2603}	GTGGCTAATA ATTTAGCGGA TCGTATTAGT CGAGATAATTG AACAGTTCT
msa31161.2{327d_18RS21}	GTGGCTAATA ATTTAGCGGA TCGTATTAGT CGAGATAATTG AACAGTTCT
msa31161.2{327dNT_H36B}	GTGGCTAATA ATTTAGCGGA TCGTATTAGT CGAGATAATTG AACAGTTCT
Consensus	***** * ***** * ***** * ***** * ***** * *****
	500
msa31161.2{327dNt_2603}	CTTAACCTAC GAGCCTGAGC TTGAAACTAG AGCTGATGAA ACTGTTCTAG
msa31161.2{327d_18RS21}	CTTAACCTAC GAGCCTGAGC TTGAAACTAG AGCTGATGAA ACTGTTCTAG
msa31161.2{327dNT_H36B}	CTTAACCTAC GAGCCTGAGC TTGAAACTAG AGCTGATGAA ACTGTTCTAG
Consensus	***** * ***** * ***** * ***** * ***** * *****
	550
msa31161.2{327dNt_2603}	AAAAATGAAGA AACTGTTGAT GAGCACAAAA CAAGTGTCA TCAAGCAATA
msa31161.2{327d_18RS21}	AAAAATGAAGA AACTGTTGAT GAGCACAAAA CAAGTGTCA TCAAGCAATA
msa31161.2{327dNT_H36B}	AAAAATGAAGA AACTGTTGAT GAGCACAAAA CAAGTGTCA TCAAGCAATA
Consensus	***** * ***** * ***** * ***** * ***** * *****
	600
msa31161.2{327dNt_2603}	TCTTTTCGAG AAGAGGGCTC TCTGGTTATT GCTAGTTTG ATGTAGATTT
msa31161.2{327d_18RS21}	TCTTTTCGAG AAGAGGGCTC TCTGGTTATT GCTAGTTTG ATGTAGATTT
msa31161.2{327dNT_H36B}	TCTTTTCGAG AAGAGGGCTC TCTGGTTATT GCTAGTTTG ATGTAGATTT
Consensus	***** * ***** * ***** * ***** * ***** * *****
	650
msa31161.2{327dNt_2603}	GTCTCAACTA GATGTTCAAA TAGGAAAAAC CAGTCATCTG CCAGCTTATG
msa31161.2{327d_18RS21}	GTCTCAACTA GATGTTCAAA TAGGAAAAAC CAGTCATCTG CCAGCTTATG
msa31161.2{327dNT_H36B}	GTCTCAACTA GATGTTCAAA TAGGAAAAAC CAGTCATCTG CCAGCTTATG
Consensus	***** * ***** * ***** * ***** * ***** * *****
	700

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNt_2603}	701	AAGAGTTATC CTTACGACGT AAATTTGAGA TTCTAACATA TTTTGACCAA	750
msa31161.2{327d_18RS21}		AAGAGTTATC CTTACGACGT AAATTTGAGA TTCTAACATA TTTTGACCAA	
msa31161.2{327dNT_H36B}		AAGAGTTATC CTTACGACGT AAATTTGAGA TTCTAACATA TTTTGACCAA	
Consensus	*****	*****	*****
msa31161.2{327dNt_2603}	751	ATTCGAAATG AACGTTCCAA AGTCCCAAGT TTTAGACGAG GTGATTGTA	800
msa31161.2{327d_18RS21}		ATTCGAAATG AACGTTCCAA AGTCCCAAGT TTTAGACGAG GTGATTGTA	
msa31161.2{327dNT_H36B}		ATTCGAAATG AACGTTCCAA AGTCCCAAGT TTTAGACGAG GTGATTGTA	
Consensus	*****	*****	*****
msa31161.2{327dNt_2603}	801	CACAGAGATG GAAATGACAC CAGTCTTGA TGCGGAGGAA TTACTTACTT	850
msa31161.2{327d_18RS21}		CACAGAGATG GAAATGACAC CAGTCTTGA TGCGGAGGAA TTACTTACTT	
msa31161.2{327dNT_H36B}		CACAGAGATG GAAATGACAC CAGTCTTGA TGCGGAGGAA TTACTTACTT	
Consensus	*****	*****	*****
msa31161.2{327dNt_2603}	851	ATCTCGAACG TGATGGCAGT CCCTATGAGC TGAAACGAAC GCTGACTACA	900
msa31161.2{327d_18RS21}		ATCTCGAACG TGATGGCAGT CCCTATGAGC TGAAACGAAC GCTGACTACA	
msa31161.2{327dNT_H36B}		ATCTCGAACG TGATGGCAGT CCCTATGAGC TGAAACGAAC GCTGACTACA	
Consensus	*****	*****	*****
msa31161.2{327dNt_2603}	901	GTCGAAGAAA AGGAATTAGA AAAAATTGGA CAAGCCATTA GGATAGAAAA	950
msa31161.2{327d_18RS21}		GTCGAAGAAA AGGAATTAGA AAAAATTGGA CAAGCCATTA GGATAGAAAA	
msa31161.2{327dNT_H36B}		GTCGAAGAAA AGGAATTAGA AAAAATTGGA CAAGCCATTA GGATAGAAAA	
Consensus	*****	*****	*****
msa31161.2{327dNt_2603}	951	TCAAGAAAAA TTGACTCAGC TAGGgATTGa TTTATCTCAG TTTGACCCAG	1000
msa31161.2{327d_18RS21}		TCAAGAAAAA TTGACTCAGC TAGGgATTGa TTTATCTCAG TTTGACCCAG	
msa31161.2{327dNT_H36B}		TCAAGAAAAA TTGACTCAGC TasGkATTGr TTTATCTCAG TTTGACCCAG	
Consensus	*****	*****	*****
msa31161.2{327dNt_2603}	1001	ACCGAGTCGG TATTTTATTG gATGCAGCAG GTCGTTTCG TTTAaAaAAT	1050
msa31161.2{327d_18RS21}		ACCGAGTCGG TATTTTATTG gATGCAGCAG GTCGTTTCG TTTAaAaAAT	
msa31161.2{327dNT_H36B}		ACCGAGTCGG TATTTTATTG KATGCAGCAG GTCGTTTCG TTTAaAaAAT	
Consensus	*****	*****	*****
msa31161.2{327dNt_2603}	1051	GCAGACCTTG CTTACTAGG TGGTTATCCC AAAGCCTCGG TAACTCAACT	1100
msa31161.2{327d_18RS21}		GCAGACCTTG CTTACTAGG TGGTTATCCC AAAGCCTCGG TAACTCAACT	
msa31161.2{327dNT_H36B}		GCAGACCTTG CTTACTAGG TGGTTATCCC AAAGCCTCGG TAACTCAACT	
Consensus	*****	*****	*****
msa31161.2{327dNt_2603}	1101	AGCCCTTGCG ACAGAACTAC TCCAAATGGG ACTAAAGTCAT GAAAAGGTG	1150
msa31161.2{327d_18RS21}		AGCCCTTGCG ACAGAACTAC TCCAAATGGG ACTAAAGTCAT GAAAAGGTG	
msa31161.2{327dNT_H36B}		AGCCCTTGCG ACAGAACTAC TCCAAATGGG ACTAAAGTCAT GAAAAGGTG	
Consensus	*****	*****	*****
msa31161.2{327dNt_2603}	1151	AATTTTTCTT TGGTAGCCAG CTITCCATTG AAGAGCTGCC ACAAGTTGCC	1200
msa31161.2{327d_18RS21}		AATTTTTCTT TGGTAGCCAG CTITCCATTG AAGAGCTGCC ACAAGTTGCC	
msa31161.2{327dNT_H36B}		AATTTTTCTT TGGTAGCCAG CTITCCATTG AAGAGCTGCC ACAAGTTGCC	
Consensus	*****	*****	*****
msa31161.2{327dNt_2603}	1201	TACGCCTTT TAACCAAGA ACTCAGCAGA GAAGATGCC AGCAATTGTA	1250
msa31161.2{327d_18RS21}		TACGCCTTT TAACCAAGA ACTCAGCAGA GAAGATGCC AGCAATTGTA	
msa31161.2{327dNT_H36B}		TACGCCTTT TAACCAAGA ACTCAGCAGA GAAGATGCC AGCAATTGTA	
Consensus	*****	*****	*****
msa31161.2{327dNt_2603}	1251	AAAAGATAAA GGTAAATCAGC CAGATTTAAC TCTCAGAGAT TGGAAAAGCA	1300
msa31161.2{327d_18RS21}		AAAAGATAAA GGTAAATCAGC CAGATTTAAC TCTCAGAGAT TGGAAAAGCA	
msa31161.2{327dNT_H36B}		AAAAGATAAA GGTAAATCAGC CAGATTTAAC TCTCAGAGAT TGGAAAAGCA	
Consensus	*****	*****	*****
msa31161.2{327dNt_2603}	1301	AGCTAGAGAA AGCTGAGGGA AAAGAAGTAG TTGATGAAGA ATTGCGGGA	1350
msa31161.2{327d_18RS21}		AGCTAGAGAA AGCTGAGGGA AAAGAAGTAG TTGATGAAGA ATTGCGGGA	
msa31161.2{327dNT_H36B}		AGCTAGAGAA AGCTGAGGGA AAAGAAGTAG TTGATGAAGA ATTGCGGGA	
Consensus	*****	*****	*****
msa31161.2{327dNt_2603}	1351	AATCCACTGG TTCAAGAGAT ATTGGACACT TATCCCTCTGG GGTCAATTGGT	1400
msa31161.2{327d_18RS21}		AATCCACTGG TTCAAGAGAT ATTGGACACT TATCCCTCTGG GGTCAATTGGT	
msa31161.2{327dNT_H36B}		AATCCACTGG TTCAAGAGAT ATTGGACACT TATCCCTCTGG GGTCAATTGGT	
Consensus	*****	*****	*****

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNt_2603}	1401	1450
msa31161.2{327d_18RS21}	TTCCTATAAG GGACAGGACT TTGAGGTCA GTCGGTCAGC GATGCTCGAT	
msa31161.2{327dNT_H36B}	TTCCTATAAG GGACAGGACT TTGAGGTCA GTCGGTCAGC GATGCTCGAT	
Consensus	*****	*****
msa31161.2{327dNt_2603}	1451	1500
msa31161.2{327d_18RS21}	TGAACGGTTT GATTGGATT GAGTTAGTCA ATGACTTTTC GGATATCATT	
msa31161.2{327dNT_H36B}	TGAACGGTTT GATTGGATT GAGTTAGTCA ATGACTTTTC GGATATCATT	
Consensus	*****	*****
msa31161.2{327dNt_2603}	1501	1550
msa31161.2{327d_18RS21}	GAACAAAATC CAGTCTTTA TGTGAGGACC TGGGAAGAAC TCAGTCAGGC	
msa31161.2{327dNT_H36B}	GAACAAAATC CAGTCTTTA TGTGAGGACC TGGGAAGAAC TCAGTCAGGC	
Consensus	*****	*****
msa31161.2{327dNt_2603}	1551	1600
msa31161.2{327d_18RS21}	ACTTCATCAG CCAAAGGCAG AACCACAAAC AGAGTTAGAA GAAGCGGACC	
msa31161.2{327dNT_H36B}	ACTTCATCAG CCAAAGGCAG AACCACAAAC AGAGTTAGAA GAAGCGGACC	
Consensus	*****	*****
msa31161.2{327dNt_2603}	1601	1650
msa31161.2{327d_18RS21}	AAGAATTAAA CCTTATTCTCA TTCTGGAAG AGGAGCcAGT TCAGAGTATT	
msa31161.2{327dNT_H36B}	AAGAATTAAA CCTTATTCTCA TTCTGGAAG AGGAGCcAGT TCAGAGTATT	
Consensus	*****	*****
msa31161.2{327dNt_2603}	1651	1700
msa31161.2{327d_18RS21}	GGACTATTGG AACCAAGATGA TTCAGAAAAAT GGTCTAAACG ATACTGATCT	
msa31161.2{327dNT_H36B}	GGACTATTGG AACCAAGATGA TTCAGAAAAAT GGTCTAAACG ATACTGATCT	
Consensus	*****	*****
msa31161.2{327dNt_2603}	1701	1750
msa31161.2{327d_18RS21}	TGAAGAAAACA GATAATCAA TTCCCTGAAGA GGAAAGTCGTC GAAACAAATC	
msa31161.2{327dNT_H36B}	TGAAGAAAACA GATAATCAA TTCCCTGAAGA GGAAAGTCGTC GAAACAAATC	
Consensus	*****	*****
msa31161.2{327dNt_2603}	1751	1800
msa31161.2{327d_18RS21}	CAGAGATTCC AGTAACGGAC TTITATTTTC CAGAAGATTTC GACGGACTTT	
msa31161.2{327dNT_H36B}	CAGAGATTCC AGTAACGGAC TTITATTTTC CAGAAGATTTC GACGGACTTT	
Consensus	*****	*****
msa31161.2{327dNt_2603}	1801	1850
msa31161.2{327d_18RS21}	TATCCTAAGA CTGCTAGAGA TAAGGTTGAG ACAAACATTG TGGCCATTG	
msa31161.2{327dNT_H36B}	TATCCTAAGA CTGCTAGAGA TAAGGTTGAG ACAAACATTG TGGCCATTG	
Consensus	*****	*****
msa31161.2{327dNt_2603}	1851	1900
msa31161.2{327d_18RS21}	TTTGGTAAAA AATCTAGAAG TAGAGCACCG CAATGTTCA CCAAGTGAAAC	
msa31161.2{327dNT_H36B}	TTTGGTAAAA AATCTAGAAG TAGAGCACCG CAATGTTCA CCAAGTGAAAC	
Consensus	*****	*****
msa31161.2{327dNt_2603}	1901	1950
msa31161.2{327d_18RS21}	AAGAACCTCT TGCCAAGTAT GTAGGCTGGG GTGGACTAGC CAATGAATT	
msa31161.2{327dNT_H36B}	AAGAACCTCT TGCCAAGTAT GTAGGCTGGG GTGGACTAGC CAATGAATT	
Consensus	*****	*****
msa31161.2{327dNt_2603}	1951	2000
msa31161.2{327d_18RS21}	TTTGATGACT ATAATCCAA ATTCTAAG GAACGAGAAC AACTGAAGAG	
msa31161.2{327dNT_H36B}	TTTGATGACT ATAATCCAA ATTCTAAG GAACGAGAAC AACTGAAGAG	
Consensus	*****	*****
msa31161.2{327dNt_2603}	2001	2050
msa31161.2{327d_18RS21}	CCTAGTCACA GATAAAGAGT ATTGGATAT GAAACAGTCC TCCCTGACAG	
msa31161.2{327dNT_H36B}	CCTAGTCACA GATAAAGAGT ATTGGATAT GAAACAGTCC TCCCTGACAG	
Consensus	*****	*****
msa31161.2{327dNt_2603}	2051	2100
msa31161.2{327d_18RS21}	CCTATTACAC AGACCCATCC CTGATCCGTC AGATGTGGGA TAAGTTGGAA	
msa31161.2{327dNT_H36B}	CCTATTACAC AGACCCATCC CTGATCCGTC AGATGTGGGA TAAGTTGGAA	
Consensus	*****	*****

Table 70: Comparative Sequences relating to SAG 1280

Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2101	AGAGATGGCT	TTACAGGTGG	CAAAATCCTA	GATCCTTCCA	TGGGAACAGG
msa31161.2{327d_18RS21}		AGAGATGGCT	TTACAGGTGG	CAAAATCCTA	GATCCTTCCA	TGGGAACAGG
msa31161.2{327dNT_H36B}		AGAGATGGCT	TTACAGGTGG	CAAAATCCTA	GATCCTTCCA	TGGGAACAGG
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2150					
msa31161.2{327d_18RS21}						
msa31161.2{327dNT_H36B}						
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2151	GAATTCTTT	GCGGCTATGC	CAAAACACTT	AAGAGAAAAG	AGTGAGTTGT
msa31161.2{327d_18RS21}		GAATTCTTT	GCGGCTATGC	CAAAACACTT	AAGAGAAAAG	AGTGAGTTGT
msa31161.2{327dNT_H36B}		GAATTCTTT	GCGGCTATGC	CAAAACACTT	AAGAGAAAAG	AGTGAGTTGT
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2200					
msa31161.2{327d_18RS21}						
msa31161.2{327dNT_H36B}						
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2201	ATGGCGTAGA	GTIAGATACT	ATTACAGGAG	CTATTGCCAA	ACACCTTCAT
msa31161.2{327d_18RS21}		ATGGCGTAGA	GTIAGATACT	ATTACAGGAG	CTATTGCCAA	ACACCTTCAT
msa31161.2{327dNT_H36B}		ATGGCGTAGA	GTIAGATACT	ATTACAGGAG	CTATTGCCAA	ACACCTTCAT
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2250	CCCATAAGTC	ATATTGAAT	TAAGGGATT	GAGACGGTGG	CTTTTAACGA
msa31161.2{327d_18RS21}		CCCATAAGTC	ATATTGAAT	TAAGGGATT	GAGACGGTGG	CTTTTAACGA
msa31161.2{327dNT_H36B}		CCCATAAGTC	ATATTGAAT	TAAGGGATT	GAGACGGTGG	CTTTTAACGA
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2251	CAATAGTTT	GATTGGTGA	TTCAAATGT	GCCCTTTGCC	AATATACGAA
msa31161.2{327d_18RS21}		CAATAGTTT	GATTGGTGA	TTCAAATGT	GCCCTTTGCC	AATATACGAA
msa31161.2{327dNT_H36B}		CAATAGTTT	GATTGGTGA	TTCAAATGT	GCCCTTTGCC	AATATACGAA
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2300					
msa31161.2{327d_18RS21}						
msa31161.2{327dNT_H36B}						
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2301	CAATAGTTT	GATTGGTGA	TTCAAATGT	GCCCTTTGCC	AATATACGAA
msa31161.2{327d_18RS21}		CAATAGTTT	GATTGGTGA	TTCAAATGT	GCCCTTTGCC	AATATACGAA
msa31161.2{327dNT_H36B}		CAATAGTTT	GATTGGTGA	TTCAAATGT	GCCCTTTGCC	AATATACGAA
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2350	TTGCGGATAA	TAGGTACGAT	AGGCCTTACA	TGATTCATGA	CTACTTTGTC
msa31161.2{327d_18RS21}		TTGCGGATAA	TAGGTACGAT	AGGCCTTACA	TGATTCATGA	CTACTTTGTC
msa31161.2{327dNT_H36B}		TTGCGGATAA	TAGGTACGAT	AGGCCTTACA	TGATTCATGA	CTACTTTGTC
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2351	AAAAAGTCAC	TTGATTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
msa31161.2{327d_18RS21}		AAAAAGTCAC	TTGATTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
msa31161.2{327dNT_H36B}		AAAAAGTCAC	TTGATTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2400					
msa31161.2{327d_18RS21}						
msa31161.2{327dNT_H36B}						
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2401	AAAAGTCAC	TTGATTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
msa31161.2{327d_18RS21}		AAAAGTCAC	TTGATTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
msa31161.2{327dNT_H36B}		AAAAGTCAC	TTGATTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2450	TTCCACAGGA	ACTATGGATA	AGCGAACAGA	AAACATCTTA	CAAGATATTC
msa31161.2{327d_18RS21}		TTCCACAGGA	ACTATGGATA	AGCGAACAGA	AAACATCTTA	CAAGATATTC
msa31161.2{327dNT_H36B}		TTCCACAGGA	ACTATGGATA	AGCGAACAGA	AAACATCTTA	CAAGATATTC
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2500	GTGAGACAAAC	TGAATTCTT	GGTGGGGTTC	GACTGCCCTGA	CTCTGCCCTT
msa31161.2{327d_18RS21}		GTGAGACAAAC	TGAATTCTT	GGTGGGGTTC	GACTGCCCTGA	CTCTGCCCTT
msa31161.2{327dNT_H36B}		GTGAGACAAAC	TGAATTCTT	GGTGGGGTTC	GACTGCCCTGA	CTCTGCCCTT
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2550					
msa31161.2{327d_18RS21}						
msa31161.2{327dNT_H36B}						
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2551	AAGGCCATTG	CAGGAACGAG	TGTCACAACG	GATATGTTAT	TCTTCCAGAA
msa31161.2{327d_18RS21}		AAGGCCATTG	CAGGAACGAG	TGTCACAACG	GATATGTTAT	TCTTCCAGAA
msa31161.2{327dNT_H36B}		AAGGCCATTG	CAGGAACGAG	TGTCACAACG	GATATGTTAT	TCTTCCAGAA
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2600	ACACTTAGAC	AAGGGATATG	TGGCAGACGA	TTTAGCCTTT	TCAGGTTCCA
msa31161.2{327d_18RS21}		ACACTTAGAC	AAGGGATATG	TGGCAGACGA	TTTAGCCTTT	TCAGGTTCCA
msa31161.2{327dNT_H36B}		ACACTTAGAC	AAGGGATATG	TGGCAGACGA	TTTAGCCTTT	TCAGGTTCCA
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2650	TTCGCTATGA	CAAGGATAGT	CGCATTGGC	TCAATCCCTTA	TTTTGATGGA
msa31161.2{327d_18RS21}		TTCGCTATGA	CAAGGATAGT	CGCATTGGC	TCAATCCCTTA	TTTTGATGGA
msa31161.2{327dNT_H36B}		TTCGCTATGA	CAAGGATAGT	CGCATTGGC	TCAATCCCTTA	TTTTGATGGA
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2700					
msa31161.2{327d_18RS21}						
msa31161.2{327dNT_H36B}						
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2750	GAATACAATA	GCCAGGTGCT	AGGAACCTAC	GAGGTCAGGA	ATTTTAACGG
msa31161.2{327d_18RS21}		GAATACAATA	GCCAGGTGCT	AGGAACCTAC	GAGGTCAGGA	ATTTTAACGG
msa31161.2{327dNT_H36B}		GAATACAATA	GCCAGGTGCT	AGGAACCTAC	GAGGTCAGGA	ATTTTAACGG
Consensus	*****	*****	*****	*****	*****	*****
msa31161.2{327dNt_2603}	2800	AGGAACACTT	TCTGTTAAGG	GGACTAGTGA	TGACTTGATT	GCAAGTGTG
msa31161.2{327d_18RS21}		AGGAACACTT	TCTGTTAAGG	GGACTAGTGA	TGACTTGATT	GCAAGTGTG

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNT_H36B}	AGGAACACTT	TCTGTTAAGG	GGACTAGTGA	TGACTTGATT	GCAAGTGTG
Consensus *****					
	2801				2850
msa31161.2{327dNT_2603}	AAACAGCTCT	AAATCACGTT	AAGGCCCAA	GAGAGATTGA	TAGAAATGAG
msa31161.2{327d_18RS21}	AAACAGCTCT	AAATCACGTT	AAGGCCCAA	GAGAGATTGA	TAGAAATGAG
msa31161.2{327dNT_H36B}	AAACAGCTCT	AAATCACGTT	AAGGCCCAA	GAGAGATTGA	TAGAAATGAG
Consensus *****					
	2851				2900
msa31161.2{327dNT_2603}	GTCATCATTA	ACCCAGATGT	GTGACCAAA	CAAGTCATG	ATACCTCCAT
msa31161.2{327d_18RS21}	GTCATCATTA	ACCCAGATGT	GTGACCAAA	CAAGTCATG	ATACCTCCAT
msa31161.2{327dNT_H36B}	GTCATCATTA	ACCCAGATGT	GTGACCAAA	CAAGTCATG	ATACCTCCAT
Consensus *****					
	2901				2950
msa31161.2{327dNT_2603}	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTT	GGTTATCAGG
msa31161.2{327d_18RS21}	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTT	GGTTATCAGG
msa31161.2{327dNT_H36B}	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTT	GGTTATCAGG
Consensus *****					
	2951				3000
msa31161.2{327dNT_2603}	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTCGAGT	CGGAACCAAG
msa31161.2{327d_18RS21}	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTCGAGT	CGGAACCAAG
msa31161.2{327dNT_H36B}	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTCGAGT	CGGAACCAAG
Consensus *****					
	3001				3033
msa31161.2{327dNT_2603}	ACCGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG	
msa31161.2{327d_18RS21}	ACCGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG	
msa31161.2{327dNT_H36B}	ACCGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG	
Consensus *****					

SEQ ID. NO. 7004

STRAIN H36B frame: 1

GGKMNQEVLQMMRATI PRDRALLEAFLYYQAEHFDEEWDSL I HQFMTNRQEINKSVQL
 HFETDVSASFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPSEKNLVIEVALFNLATRFQ
 LLDSNGHYQTISPDSSLQKSRGANLVNVYRVANNLADRISRDIEQFLLTYEPELETRADE
 TVILLEETVDEHKTSHVQAISFREEGLVIASLDVDSLSQLDVQIGKTSHLPAYEELSRR
 KFEILTYFDQIRNERSKVPSPRRGDFDTEMEMTPVFDGEELLTYLEADGSPYELKRTLTT
 VEEKELEKIGQAIARIENQEKLTLQXIXLSQFDPDRVGILXAAGRXLXNADLASLGGYP
 KASVTQLALATELLQMGSLSHKEVFFFFGSQSLSIIEELRQVAYAFLHQELSREDAEQFEKDK
 GNQPDLTLDWKSKLEAKGVDEEFAENPLVQRVLDTYPLGSLVSYKGQDFEVMSVS
 DARLNGLIRIELVNDFSDIEQNPVLYVRTWEEVSQALHQPKAEPQTELEADQELNLF
 FLEEEELVQSISGLLEPDDSENGHNDTDLTETDNQIPEEEVVEIPEIPVTDFYFPEDLTDF
 YPKTARDKVETNIVAIRLVKNLEVEHRNASPSEQELLAKYVGWGGLANEFFDDYNPKFSK
 EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMDKLERDGFTGGKILDPSTMGTGNFF
 AAMPKHLREKSELYGVELDTITGAIAKHLHPNSHIEIKGFETVAFNDNSFDLVISNVPA
 NIRIADNRYDREPMIHDYFVKSLSDLHHGQVAIISSTGTMMDKRTENIQDIRETTEFL
 GGVRLPDASFKAIAAGTSVTTDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNPYFDG
 EYNSQVLGTYEVRFNGGTLSVKGTSDDLIAASVETALNHVKAPREIDRNVEIINPDVLTK
 QVNDTSIPAEMRENLGQYSFGYQGSTVYYRDNKGI RVGTTKEEISYYVDEE

SEQ ID. NO. 7005

STRAIN 18RS21 frame: 1

XGKMNQEVLQMMRATI PRDRALLEAFLYYQAEHFDEEWDSL I HQFMTNRQEINKSVQL
 HFETDVSASFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPSEKNLVIEVALFNLATRFQ
 LLDSNGHYQTISPDSSLQKSRGANLVNVYRVANNLADRISRDIEQFLLTYEPELETRADE
 TVILLEETVDEHKTSHVQAISFREEGLVIASLDVDSLSQLDVQIGKTSHLPAYEELSRR
 KFEILTYFDQIRNERSKVPSPRRGDFDTEMEMTPVFDGEELLTYLEADGSPYELKRTLTT
 VEEKELEKIGQAIARIENQEKLTLQGIDLSQLFDPDRVGILDAAGRFRLKNAIDLALLGGYP
 KASVTQLALATELLQMGSLSHKEVFFFFGSQSLSIIEELRQVAYAFLHQELSREDAEQFEKDK
 GNQPDLTLDWKSKLEAKGVDEEFAENPLVQRVLDTYPLGSLVSYKGQDFEVMSVS
 DARLNGLIRIELVNDFSDIEQNPVLYVRTWEEVSQALHQPKAEPQTELEADQELNLF
 FLEEEEPVQSISGLLEPDDSENGHNDTDLTETDNQIPEEEVVEIPEIPVTDFYFPEDLTDF
 YPKTARDKVETNIVAIRLVKNLEVEHRNASPSEQELLAKYVGWGGLANEFFDDYNPKFSK
 EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMDKLERDGFTGGKILDPSTMGTGNFF
 AAMPKHLREKSELYGVELDTITGAIAKHLHPNSHIEIKGFETVAFNDNSFDLVISNVPA
 NIRIADNRYDREPMIHDYFVKSLSDLHHGQVAIISSTGTMMDKRTENIQDIRETTEFL
 GGVRLPDASFKAIAAGTSVTTDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNPYFDG
 EYNSQVLGTYEVRFNGGTLSVKGTSDDLIAASVETALNHVKAPREIDRNVEIINPDVLTK
 QVNDTSIPAEMRENLGQYSFGYQGSTVYYRDNKGI RVGTTKEEISYYVDEE

SEQ ID. NO. 7006

STRAIN 2603 frame: 1

GGKMNQEVLQMMRATI PRDRALLEAFLYYQAEHFDEEWDSL I HQFMTNRQEINKSVQL
 HFETDVSASFVQASPYDTAHDLLTYTQVFGQSGLQKLDKLSPSEKNLVIEVALFNLATRFQ
 LLDSNGHYQTISPDSSLQKSRGANLVNVYRVANNLADRISRDIEQFLLTYEPELETRADE
 TVILLEETVDEHKTSHVQAISFREEGLVIASLDVDSLSQLDVQIGKTSHLPAYEELSRR
 KFEILTYFDQIRNERSKVPSPRRGDFDTEMEMTPVFDGEELLTYLEADGSPYELKRTLTT
 VEEKELEKIGQAIARIENQEKLTLQGIDLSQLFDPDRVGILDAAGRFRLKNAIDLALLGGYP
 KASVTQLALATELLQMGSLSHKEVFFFFGSQSLSIIEELRQVAYAFLHQELSREDAEQFEKDK
 GNQPDLTLDWKSKLEAKGVDEEFAENPLVQRVLDTYPLGSLVSYKGQDFEVMSVS

Table 70: Comparative Sequences relating to SAG 1280

DARLNGLIRIELVNDFSDIIEQNPVLYVRTWEEVSQALHQPKAEPQTELEADQELNLF
 FLEEEPVQSIGLEPDDSENGHNDTDLLEETDNQIPEIPVTDFYFPEDLTDF
 YPKTARDKVETNIAIRLVKNLEVEHRNASPSEQELLAKYVGWGGILANEFFDDYNPKFSK
 EREELKSLVTDKEYSDMKSSTAYTDPSSLRQMWDKLERDGFTEGGKILDPSMTGNFF
 AAMPKHLREKSELYGVELDTITGAIAKHLHPNSHIEIKGFTVAFNDNSFDLVI SNVPFA
 NRIADNRYDRPYMIHDGQVAIISSTGTMDKRTENIQDIRETTEFL
 GGVRLPDGSAFKAIAGTSVTIDMFFKHLDKGVADDLAFSGSIRYDKDSRIWLNPYFDG
 EYNSQVLGTYEVRFNGGTLSKGTSDDLIASVETALNHVKAPREIDRNNEVIINPDVLTK
 QVNDTSI PAEMRENLGQYSFGYQGSTVYYRDNKGIRVGKTEEISYYVDEE

PRETTY OF: /biotmp/msa23816.2{*} June 20, 2002 11:04 ..

msa23816.2{327dNT_H36B}	gGKMNQEVLL	QMMRATIPRD	RALLEAFLYY	QAEHFDEEW	SLIHQFMTR	50
msa23816.2{327dNT_2603}	gGKMNQEVLL	QMMRATIPRD	RALLEAFLYY	QAEHFDEEW	SLIHQFMTR	
msa23816.2{327d_18RS21}	xGKMNQEVLL	QMMRATIPRD	RALLEAFLYY	QAEHFDEEW	SLIHQFMTR	
Consensus	*****	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	QEINKSVQL	HFETDVSAFV	QASPYDTAHD	LLTYTQVFGQ	SGLQKLKLS	100
msa23816.2{327dNT_2603}	QEINKSVQL	HFETDVSAFV	QASPYDTAHD	LLTYTQVFGQ	SGLQKLKLS	
msa23816.2{327d_18RS21}	QEINKSVQL	HFETDVSAFV	QASPYDTAHD	LLTYTQVFGQ	SGLQKLKLS	
Consensus	*****	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	PSEKNLVIEV	ALFNLATRFQ	LLDSNGHYQT	ISPDSLLQKS	RGANLVNVYR	150
msa23816.2{327dNT_2603}	PSEKNLVIEV	ALFNLATRFQ	LLDSNGHYQT	ISPDSLLQKS	RGANLVNVYR	
msa23816.2{327d_18RS21}	PSEKNLVIEV	ALFNLATRFQ	LLDSNGHYQT	ISPDSLLQKS	RGANLVNVYR	
Consensus	*****	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	VANNLADRIS	RDIEQFLITY	EPELETRADE	TVLENEETVD	EHKTSVHQAI	200
msa23816.2{327dNT_2603}	VANNLADRIS	RDIEQFLITY	EPELETRADE	TVLENEETVD	EHKTSVHQAI	
msa23816.2{327d_18RS21}	VANNLADRIS	RDIEQFLITY	EPELETRADE	TVLENEETVD	EHKTSVHQAI	
Consensus	*****	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	SFREEGSLVI	ASLDVDSLSQL	DVQIGKTSHL	PAYEELSLRR	KFEILTYFDQ	250
msa23816.2{327dNT_2603}	SFREEGSLVI	ASLDVDSLSQL	DVQIGKTSHL	PAYEELSLRR	KFEILTYFDQ	
msa23816.2{327d_18RS21}	SFREEGSLVI	ASLDVDSLSQL	DVQIGKTSHL	PAYEELSLRR	KFEILTYFDQ	
Consensus	*****	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	IRNERSKVPS	FRRGDFDTEM	EMTPVFDGEE	LLTYLEADGS	PYELKRTLT	300
msa23816.2{327dNT_2603}	IRNERSKVPS	FRRGDFDTEM	EMTPVFDGEE	LLTYLEADGS	PYELKRTLT	
msa23816.2{327d_18RS21}	IRNERSKVPS	FRRGDFDTEM	EMTPVFDGEE	LLTYLEADGS	PYELKRTLT	
Consensus	*****	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	VEEKELEKIG	QAIRIENQEK	LTOIxIxLSQ	FDPDRVGI	xAAGRxRlxN	350
msa23816.2{327dNT_2603}	VEEKELEKIG	QAIRIENQEK	LTOlgIdLSQ	FDPDRVGI	AAAGRFRlxN	
msa23816.2{327d_18RS21}	VEEKELEKIG	QAIRIENQEK	LTOlgIdLSQ	FDPDRVGI	AAAGRFRlxN	
Consensus	*****	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	ADLASLGGYP	KASVTQLALA	TELLQMG	EKVEFFF	LSIEELRQVA	400
msa23816.2{327dNT_2603}	ADLASLGGYP	KASVTQLALA	TELLQMG	EKVEFFF	LSIEELRQVA	
msa23816.2{327d_18RS21}	ADLASLGGYP	KASVTQLALA	TELLQMG	EKVEFFF	LSIEELRQVA	
Consensus	*****	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	YAFLhQELSR	EDAEQFEKDK	GNQPD	WKS	KLEKAEG	450
msa23816.2{327dNT_2603}	YAFLhQELSR	EDAEQFEKDK	GNQPD	WKS	KLEKAEG	
msa23816.2{327d_18RS21}	YAFLhQELSR	EDAEQFEKDK	GNQPD	WKS	KLEKAEG	
Consensus	*****	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	NPLVQRVLDT	YPLGSLVSYK	GQDFEVMSVS	DARLNGLIRI	ELVNDFS	500
msa23816.2{327dNT_2603}	NPLVQRVLDT	YPLGSLVSYK	GQDFEVMSVS	DARLNGLIRI	ELVNDFS	
msa23816.2{327d_18RS21}	NPLVQRVLDT	YPLGSLVSYK	GQDFEVMSVS	DARLNGLIRI	ELVNDFS	
Consensus	*****	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	EQN	PVLYV	WEEVSQALHQ	PKAEPQTELE	EADQELNLFS	550
msa23816.2{327dNT_2603}	EQN	PVLYV	WEEVSQALHQ	PKAEPQTELE	EADQELNLFS	
msa23816.2{327d_18RS21}	EQN	PVLYV	WEEVSQALHQ	PKAEPQTELE	EADQELNLFS	
Consensus	*****	*****	*****	*****	*****	*****
msa23816.2{327dNT_H36B}	GLLEPDDSEN	GHNDTDLEET	DNQIPEEEVV	ETIPEIPVTD	FYFPEDLTDF	600
msa23816.2{327dNT_2603}	GLLEPDDSEN	GHNDTDLEET	DNQIPEEEVV	ETIPEIPVTD	FYFPEDLTDF	
msa23816.2{327d_18RS21}	GLLEPDDSEN	GHNDTDLEET	DNQIPEEEVV	ETIPEIPVTD	FYFPEDLTDF	
Consensus	*****	*****	*****	*****	*****	*****

Table 70: Comparative Sequences relating to SAG 1280

msa23816.2{327dNT_H36B}	601	YPKTARDKVE TNIVAIRLVK NLEVEHRNAS PSEQELLAKY VGWGGLANEF	650
msa23816.2{327dNT_2603}		YPKTARDKVE TNIVAIRLVK NLEVEHRNAS PSEQELLAKY VGWGGLANEF	
msa23816.2{327d_18RS21}		YPKTARDKVE TNIVAIRLVK NLEVEHRNAS PSEQELLAKY VGWGGLANEF	
Consensus	*****	*****	*****
msa23816.2{327dNT_H36B}	651	FDDYNPKFSK EREELKSLVT DKEYSDMKQS SLTAYYTDPS LIRQMWDKLE	700
msa23816.2{327dNT_2603}		FDDYNPKFSK EREELKSLVT DKEYSDMKQS SLTAYYTDPS LIRQMWDKLE	
msa23816.2{327d_18RS21}		FDDYNPKFSK EREELKSLVT DKEYSDMKQS SLTAYYTDPS LIRQMWDKLE	
Consensus	*****	*****	*****
msa23816.2{327dNT_H36B}	701	RDGFTGGKIL DPSMGTGNFF AAMPKHLREK SELYGVELDT ITGAIAKHLH	750
msa23816.2{327dNT_2603}		RDGFTGGKIL DPSMGTGNFF AAMPKHLREK SELYGVELDT ITGAIAKHLH	
msa23816.2{327d_18RS21}		RDGFTGGKIL DPSMGTGNFF AAMPKHLREK SELYGVELDT ITGAIAKHLH	
Consensus	*****	*****	*****
msa23816.2{327dNT_H36B}	751	PNSHIEIKGF ETVAFNDNSF DLVISNPFA NIRIADNRYD RPYMIHDYFV	800
msa23816.2{327dNT_2603}		PNSHIEIKGF ETVAFNDNSF DLVISNPFA NIRIADNRYD RPYMIHDYFV	
msa23816.2{327d_18RS21}		PNSHIEIKGF ETVAFNDNSF DLVISNPFA NIRIADNRYD RPYMIHDYFV	
Consensus	*****	*****	*****
msa23816.2{327dNT_H36B}	801	KKSLDLLHDG GOVAIISSTG TMDKRTENIL QDIRETTEFL GGVRLPDSAF	850
msa23816.2{327dNT_2603}		KKSLDLLHDG GQVAIISSTG TMDKRTENIL QDIRETTEFL GGVRLPDSAF	
msa23816.2{327d_18RS21}		KKSLDLLHDG GQVAIISSTG TMDKRTENIL QDIRETTEFL GGVRLPDSAF	
Consensus	*****	*****	*****
msa23816.2{327dNT_H36B}	851	KAIAGTSVITI DMLFFQKHLD KGYYVADDLAF SGSIRYDKDS RIWLNPYFDG	900
msa23816.2{327dNT_2603}		KAIAGTSVITI DMLFFQKHLD KGYYVADDLAF SGSIRYDKDS RIWLNPYFDG	
msa23816.2{327d_18RS21}		KAIAGTSVITI DMLFFQKHLD KGYYVADDLAF SGSIRYDKDS RIWLNPYFDG	
Consensus	*****	*****	*****
msa23816.2{327dNT_H36B}	901	EYNSQVLGTY EVRNFNGGTL SVKGTSDDL I ASVETALNHV KAPREIDRNE	950
msa23816.2{327dNT_2603}		EYNSQVLGTY EVRNFNGGTL SVKGTSDDL I ASVETALNHV KAPREIDRNE	
msa23816.2{327d_18RS21}		EYNSQVLGTY EVRNFNGGTL SVKGTSDDL I ASVETALNHV KAPREIDRNE	
Consensus	*****	*****	*****
msa23816.2{327dNT_H36B}	951	VIINPDVLTK QVNNTSIPAE MRENLGQYSF GYQGSTVYYR DNKGIRVGTK	1000
msa23816.2{327dNT_2603}		VIINPDVLTK QVNNTSIPAE MRENLGQYSF GYQGSTVYYR DNKGIRVGTK	
msa23816.2{327d_18RS21}		VIINPDVLTK QVNNTSIPAE MRENLGQYSF GYQGSTVYYR DNKGIRVGTK	
Consensus	*****	*****	*****
msa23816.2{327dNT_H36B}	1001	TEEISYYVDE E	1011
msa23816.2{327dNT_2603}		TEEISYYVDE E	
msa23816.2{327d_18RS21}		TEEISYYVDE E	
Consensus	*****	*	

Table 71: Comparative Sequences relating to SAG1333**SEQ ID NO. 7101****STRAIN 2603**

ATGAAAAAGAAAATTATTTGAAAAGTAGTGTCTTGTTAGTCGCTGGGACTTCTATT
 ATGTTCTCAAGCGTGTGCGGCCAAGTCGGTGTCCAAGTTATAGCGTCAATGACTTT
 CATGGTGACTTGAACAATACTGGAACAGAAATATGCTGATGAAAAGTTGCTAATGCT
 GGACTGCTGCTCAATTAGATGCTTATATGGATGACGCTCAAAAAGATTCAAACAAAACT
 AACCTTAATGGTGAAGCATTAGGGTCAAGCAGGGCATATGGTTGGAGCAAGTCAGCC
 AACTCTGGGCTTCTCAAGATGAAACCACACTGCAAAATTITAATGCAATGAATGTTGAG
 TATGGCACATTGGTAACCATGAAATTGATGAAAGGGTTGGCAGAAATATAATCGTATCGTT
 ACTGGTAAGGCCCTGTCAGCAATTCTAATTAATATAATACAGAAATCATACCCACAT
 GAAGCTGAAAACAAGAAATTGATGTCAGCAATGTTATGATAAAGTTAACACAAATT
 CCTTACAATTGGAAAGGCCATTACGCTTAAATGCTGAAATAACAAAAGTTGTAAC
 GTTGGCTTATCGGGATGTCACCAAGACATCCCACACCTTGTCTTACGTAAGGAAATTAT
 GAACAATATGAATTAGATGAACTGTAAGCTTAATACCCAAAGAAATTACAA
 GCTAAAATGTCAGGACTATTGATGTTCTCCACATGACTGCAACAGTAAAGATGAT
 ATTGCTGAAGGCTGAAAGCAGAACATGTAAGAAAAGTCATCAACTCTCCCTGAAAAT
 AGCGTAGATAATTGCTTGTGTCAGCAATCATCAATACAACATGCTTGTGGTAA
 ACTCGTATGTCAGCGCTCTCAAGGAAAAGCCTATGCTGATGTCAGCTGGTGTCTT
 GATACTGATACACAAGATTCTTGTGAGACCCCTTCAGCTTAAGTAATTGCACTGCTCCT
 GTTGGAAAACAGGTTAGTGGCAGATTCAGCAGGCTTAAGCTTAATGCTTAC
 AAACAAGTAAACAGCTAAATTGTACTGCGCAGGTAAGTGTATGCTGAGCTT
 GTTGGATCAAGATAATGTTAGTCCGTAGGCAGCCTCATCACAGAGGCTCAACTAGCAATT
 GCICGAAAAGCTGGCAGATTCAGCTTAAGCTGCAACAGCAGTTCAACCT
 TTGCTTAATCTACAGTGTGAAATTCTTCTTCATTAAGCTGGTCTGCGATAACCTTAC
 GAACAATACCGCAAAACACATTTCAGGCTTAAGCTGAGGAAATTAC
 ACAGATAATAAAGAGGGCGGGAGAAAACACATTAAAGTTGTAAGGCTTATAAATCA
 AATGGTGAGGAATCAATCCTGATGCAAATACAAATTAGTTATCAATGACTTTTATTC
 GTTGGTGGTGGATGGCTTGGCAGAACTTCAGGCTTCAAGGACATTAAACCC
 GATACTAGGGTTTATGCTCTATATGCTACTGTTAGAGCTGTTAAAGCTGAGC
 GTTCCAAATAATAACCTTAAACCTATGTCAGTGAAGATGGTAAATGAAACTATTACA
 CAAATGATGTTACACATGCAATTAAAGAACCTTAAAGATGACCAAGGAAATT
 GTAGCACAAGGATTGATGAGCATTAAACCAAACAAATTACACCAATTACAGTATTAAACCTATG
 AACCTGTAACTACAATTCCACAAAACACATTACACCAATTACAGTATTAAACCTATG
 AGAAAATTATGGCAACCATCAAAACTCCACTACTGTAAAATCAAAACAAATTACCAAAAACA
 AACCTGAAATATGGACAATCATTCTTATGTCGTTGGACTTATAGGAATT
 GCTTTAAACAAAGAAAACATATGAA

SEQ ID NO. 7102**STRAIN 090**

AACTCGGTGTCCAAGTTATAGGGTCAATGACTTCTATGGTGCACITGAC
 AATACTGGAAACGCAAATGCTGAGGGAAAAGTTACTAATGCTGGCAC
 TGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTCAAAC
 AAACTAACCCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTATATGGTT
 GGAGCAAGTCAGCTAACTCAGGGCTTCTCAAGATGAAACCAACCGTTAA
 AACATTAAATGCAATGAAATGTTGAGTATGGCACATTAGGTAAACCATGAAAT
 TTGATGAAGGTTGGCAGAAATACAATCGTATGTTACTGGAAAGGCCCT
 GCTCCAGATTCTAATATAAAATATATTACGAAATCATACCCACACGAAGC
 TGCAAAACAGAATTGTTAGTGGCAAACGTTATTGATAAAGTTAACAAAC
 AAATCCCTTACACATTGGCAACATTGCTTAAAGCTTAAACAAATTCTGTAAT
 AACAAAAGTGTGAACGTTGGCTTATCGGAATCGTTACCAAAAGACATCCC
 AAACCTTGTCTACGTTAAATGAAACAAATGAAATTTTAGATGAAG
 CTGAAACAAATACCGCTTAAACCGCAAAAGAAATTACAAGCTAAAATGTCAG
 GCTATTGTTAGTCCCTGCTCATGTTACCTGCAACAAAGCAAGGATGATAATTG
 TGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCATCAACTCTCCCTG
 AAAATAGCGTGTGATATTGCTTGTGACACATCATCAATATACAAAT
 GGTCTTGTGGTAAAGCTCGCATTGTCAGCGCTCTCAAGGAAAAGC
 CTATGCTGACGTACGGTGTCTAGATACTGATACACAAGATTCTG
 AAACCCCTTCAGCTAAAGTACTGTTGAGGCTAAACTATCGTTAAACCA
 AGTGGCGATATTCAAGCCATTGTTGACCAAGCTAAACTATCGTTAAACCA
 AGTAAAGCAAGGTTAAAGTGTACTGCGAGGTAAGTGGCATATTACGC
 GTTCTGTTGATCAAGATAATTGTTAGTCCAGTAGGCAGCCTCATCACAGAG
 GCTCAACTGCAATTGCTGAAAAGCTGGCCAGATATCGATTGGCCAT
 GACAATAATGGTGGCAATTGCTGACTTACTCATCAAACAGATGGAA
 CAATCACCTGGGAGCTGCACAAGCAGTTCAACCTTTGTTAATATCTTA
 CAAGTCGTCGAAATTACTGTTAGAGATCTTATAAGCACTCAACGAACA
 ATACGACCAAAAACAAATTCTTCTTCAAAATAGCTGGTCTGCGATAACA
 CTTACACAGATAATAAGAGGGGGAGAGAAAACACATTAAAGTTGTA
 AAAGCTTATAAAATCAAATGGTGAAGAAATCAATCTGATGCAAATACAA
 ATTGTTATCAATGACTTTTATTGCTGGTGTGATGCTTGTGCAAGCT
 TCAGAAATGCGCAAACCTCTAGGGAGCCATTATCCCGATACAGAGTATT
 ATGGCCTATATCACTGATTAGAAAAGCTGGTAAAGAAAGTGTGAGCGTTCC
 AAATAATAACCTAAAATCTATGTCACATGAAAGATGGTTAAATGAAACCA
 TTACACAAAATGATGTTACACATAGCATTATAAGAAACTTTATTAGAT
 CGACAAGGAAATATTGTTAGCACAAGAGATTGATCAGACACTTAAACCA
 AACAAAATCAAAATCTACAAAATCAACCCCTGTAACCTACAAATTCCACAAA
 AACAAATTACACCAATTACAGCTTAAACCTTATGAGAAATTATGGCAAA
 CCATCAAACCTCACTACTGTTAAATCAAACAA

SEQ ID NO. 7103**STRAIN A909**

GGTCAATGACTTCTGGTGCATGGACAATTGGAACAGCAAATATG
 CCTGACGAAAAGTTACTAATGCTGGCAGCTGCTCAATTAGATGCTT

Table 71: Comparative Sequences relating to SAG1333

TATGGATGATGCTAAAAAGATTCAAACAAACTAACCTAATGGTGA
 GCATTAGAGTTCAGCTGGTATGGTGGAGCAAGTCAGCTAACTCA
 GGCTCTCAAGATGAAACCAACCGTTAAAACATTAAATGCAATGAATGT
 TGAGTATGGCACATTAGGTAAACCATGAATTGATGAAGGTTGGCAGAAT
 ACAATCGTATCGTTACTGGAAGGCCCTGCCTCAGATTCTAATATAAT
 AATATTACGAATCATACCCACAGCAAGCTGCAAACAAAGAAATTGTAGT
 GGCACACGTTATTGATAAAAGTTAACAAACAAATCCCTACAATTGAAAC
 CTACACTATTAAATAATTCTCTGTAATAAACAAAAGTGTGAACGTTGGC
 TTATCGGAATCGTACCAAAGACATCCCCAACCTTGTCTTACGTA
 TTATGAAACATATAATTGATGAAGCTGAAACAATCGTAAATACG
 CCAAAGAATTACAAGCTAAAATGTCAGGCTATTGTAGTCCCTGCTCAT
 GTACCTGCAACAAAGCAAGGATGATATTGCTGAAGGTGAAGCAGCAGAAAT
 GATGAAAAAAAGTCATCACTCTCCCTGAAAATACGCTAGATATTGCTCT
 TTGCTGGACACAATCATCAATATAACAAATGGCTTGTTGTA
 AAAACTCGTATTGCAAGGAAAGCTATGCTGATGTTACCGTGGTGT
 ATTGCTAACAGCTCTCAAGGAAAGCTATGCTGATGTTACCGTGGTGT
 CCTAGATACTGATAACAAAGATTCTGAAACCCCTCAGCTAAAGTAA
 TTGCACTGCTCTGGTAAAAACAGTAGTGCCTGATATTCAAGCCATT
 GTTGCAAGCTAATACTATGTTAAACAGTAACAGAAGCTAAAATTGG
 TACTGCGAGGTAAAGTGGCATGATTACGCTCTGTTGATCAAGATAATG
 TTAGTCGGTAGGCAGCCTCATCACAGGCTCAACTGCAATTGCTCGA
 AAAAGCTGGCCAGATATGCAATTGCAACAAATAATGGTGGCATTG
 TGCTGACTTACATCAAACCCAGATGAAACATCACCTGGGAGCTGCA
 AACAGCTTCAACCTTTGGTAAATCTACAGTCTGCAAATTACTGGT
 AGAGATCTTATAAAGCACTCAACGAACAATACGACAAAAACAAAATT
 CTCTCCAAATAGCTGGTCTGGATACCTTACACAGATAATAAAGAGG
 GCGGGGAAGAAACCATTTAAAGTTGTAAGCTTATAAATCAAATGGT
 GAGGAATCAAATCTGATGCAAATACAAATTAGTTATCAATGACTTTT
 ATTGCGTGGTGGTATGGCTTGCAGGCTCAGAAATGCAAACTTCTAG
 GAGCCATTAACTCCGATACAGGTTATTGCTGCTTATATCAGTATT
 GAAAAGCTGGTAAAAAAAGTGAGCTTCAAAATAATAACCTAAAATCTA
 TGCACTATGAAAGTGGTAAATGAAACTTACACAAAATGATGGTACAT
 ATAGCATTATAAAGAAACTTATTAGTGTGACAAGGAAATAATTGTTAGCA
 CAAGAGATTGATCACAGACACTTAAACAAACAAATCAAATCTACAAA
 AATCAACCCCTGTAACACAAACAAATTACACCAATTACAG
 CTAAATACCCATGAGAAATTGCAACACCATAACTCCACTACTGTA
 AAATCAAACAA

SEQ ID NO. 7104

STRAIN H36B

CCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTCACTTG
 ACAAACTGGAAACGCAAATATGCTGACGAAAAGTTACTAATGCTGGC
 ACTGCTGCAAACTGCTTATGATGGTGTGCTCAAAGGATTCAA
 ACAAAACTACCCCTAATGGTGAAGCAATTAGAGTTCAAGCTGGTATATGG
 TTGGAGCAAGTCCAGCTAACCTCAGGGCTTCTCAAGATGAACCAACCGTT
 AAAACATTAACTCAATGAATGTTGAGTGGCACATTAGGTAAACATGA
 ATTGATGAAGGTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCC
 CTGCTCCAGATTCTAATATAAATATAACGAAATCATACCCACAGGAA
 GCTGAAACAAAGAAATTGTTAGTGGCAACGTTATTGATAAAAGTTAA
 ACAAACTTCAACATTGAAACCTTACACTTAAACCTTATCTGTA
 ATAACAAAAGTGTGACGTTGGCTTATGGAATCTTACCAAAAGACATC
 CCAAACCTTGTCTTACGTAACAAATTATGAAACATATGAATTAGTGA
 AGCTGAAACAACTGTTAAATCGCCAAGGAAATTACAAGGTTAAAATGTC
 AGGCTATTGTTAGTCTTGTCTCATGTTACCTGCAACAGCAAGGATGATATT
 GCTGAAGGTGAAGCAGCAGAAATGATGAAAAAAAGTCATCAACTCTTCCC
 TGAAATAGCTGAGATATTGCTTGTGACACAATCATCAATATAACAA
 ATGGTCTTGTGGTAAACCTGGTATTGCAAGGCTCTCTCAAGGAAA
 GCCTATGCTGATGTAAGTGGCTCTAGATACTGATACACAAAGATT
 TGAAACCCCTTCACTAAAGTAATTGCAAGTGTCTGGTAAAAACAG
 GTAGTGGCATATTCAAGGCTTGTGACACAATCATCAATCTGTTAAA
 CAAGTAACAGAACGTTAACTGGTACTGCGAGGTAAGTGGCATGATTAAC
 GGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAG
 AGGCTAACACTGCAATTGCTGAAAAAGCTGGCAGGATATGCAATTG
 ATGACAACAAATGTTGGCATTGCTGCTGACTTACTCATCAAACCCAGATGG
 AACAAATCACCTGGGAGCTGCAACAGCAGTTCAACCTTTGGTAAATATCT
 TACAATGCTGCGAAATTACTGGTAGAGATCTTATAAAGGCACTCAACGAA
 CAATACGACAAAAACAAATTCTCTTCAAATAGCTGGTCTGCGATA
 CACTACACAGATAATAAAGGGGGGGAGAACACCAATTAAAGTTG
 TAAAAGCTTATAAATCAAATGCTGAGGAAATCAATCTGATGCAAAATAC
 AAAATTAGTTATACTGACTTTTATCGGGGGGGTGTGAGGCTTGCAG
 CTTCAGAAATGCCAAACTTCTAGGAGCCATTAAATCCCGATAACAGAGGTAT
 TTATGGCTTATCACTGATTAGAAAAGCTGGTAAAAAAAGTGAGCGTT
 CCAAATAATAAACTTAACTGACTATGAAAGATGGTTAATGAAAC
 TAATTACACAAAATGATGGTACATATGCAATTAAAGAAACTTTATTAG
 ATCGACAAGGAAATATTGTTAGCACAAGGATTGATCAGACACTTAAAC
 CAAACAAAATCACCAAAATCTACACCAATTACCCCTGTAACACAAATTCA
 AACCAATTACACCAATTACAGCTTAAACCCCTATGAGAAATTATGGCA
 AACCATCAAACACTTCACTACTGTTAAATCAAA

SEQ ID NO. 7105

STRAIN 18RS21

GACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTT
 ATGGTGCCTGACAATACTGGAAACGCAAATATGCTGACGAAAAGTT
 AnTAATGCTGGCACTGCTCAATTAGTGTCTTATGATGATGCTCA

Table 71: Comparative Sequences relating to SAG1333

AAAAGATTTCAAACAACTAACCTTAATGGTGAAGCATTAGACTTCAGCTGGTGATATTGCGGAAAGCCTGCAAGCTGGTGTATGGTGGACCAAGTCAGCTAACCTAGCCATTCTTCAGATGAACCAACCGTTAAACCATTTAATGCAATGAATGTTGAGTATGGCAGAACATTAGTAAACCATGATTTGATGAAGGTTGGCAGAAATACAATCGTATCGTTAATGGAAAGGCCCTGCTCCAGATTCTTAATAATAAATATTAGCAAATACATACCAACAGGCTGCAAAAAGAATTGTAATGTCAGTGGCAAACAGTATTGTAAGGTAAACAAACAAATCTTCAAACTTGAACAGGAACTTGGAAACCTTACACTATTAAAAATATTCTGTAAATAACAAAAGTGTGAACGTTGGCTTATCGGAATCGTTACCAAAAGACATCCAAAACCTTGTCTTCACTGAAACATATGATATTTTAGATGAAGGCTGAAACAACTGTAAATACGCAGAAAGAATTACAAGCTAAAAAATGTCAGGGTATTGTAGTCCTGCTCATGTACTGCAACAAAGCAAGGATGATATTGTGAGAGGTGAACGCAGAAATGATGAAAAAAAGTCAACTCAACTCTTCGTTGAAATAGCGTAGATTATTGCTTCTGCGACACAACTATCAATATAACAAATGGCTTCTGGTGTAAACACTGTATTGTCACAGGCTCTCTCAAGGAAAAGCCTATGCTGATGTACGTGGTGTCTAGATACTGATACAAAGATTCTATTGAAACCCCTTCAGCTTAAAGTATTGCGATTGTCCTGCTGTAAAAAAACAGGTAGTCGGATATTCAAGGCCATTGTCAGGAACTTAATACTATCGTTAACAAAGTAACAGAAGCTAAATIGGTACTGCGGAGGTAAAGTGGCATGATTACCGCTTCTGTTGATCAAGATAATTGTTAGTCCTGGTAGGCA GGCTCATCACAGAGGCTCAACTGACCAATTGCTGAAAGCTGGCCAGATATCGATTTCGCTGACATTACTCATCAAACCCAGATGGAACAATCACCTGGGGAGCTGCACAAGCAGTTAACCTT TTGGTAAATATCTTACAATGCTGCGAAATTACTGTAAGAGATCTTATAAAAGCCTCAACCGAACAAATACCGACCAAAAACAAAATTCTCTTCAATAGCTGGTCTGAGATAACTTACAGATAATAAAGAGGGGGGGGAGAAACACCATTTAAAGTTGTTAAAGCTTATAAATCCTAAATGCTGGAGGAAATACCTTGTGCAAAATACAAATTGTTGATTAATGACTTTTATTCTGGTGGTGTGATGGCTTGTGCAAGCTTCAAGGAAATGCCAAACTCTAGGAGGCTTAAATCCGATACAGAGGTTATTATGGCTTATATCAGTGAATTAGAAAAGCTGTTAAAAGTGGCTTGTCAAAATTTAATAAAACCCCTAAATGCTTCAACTGAGATGGTTATAAGGAAACTTACACAAAATGATGTTACATATGCTGGAGGTTAAAGAACTTTATTAGATGCAAGGAAATATTGTAGCACAAGAGATTGTATCAGACATTTAAACAAAACAAATCCTAAACAAATGCTTAAACCCCTTCAACATACATTCAACAAAACAAATTACACCAATTTCAGCTTAAACCTTGTAAAGAATTATGGCAACCCATCAACTCTAGGAGGCTTAAACCTTGTAAAGA

SEQ ID NO. 7106

STRAIN M732

ACCAAGTCGGTGTCCAAGTTATAGCGCTCAATGACTTTCATGGTGCACTT
GACAATCTGGAAACAGCAGAACATATTGCCGTACGGAAAAGTTACTAATGCTGG
CATCTGCTGCTCAATTAGCTTATATGGATGATGCTCAAAAGATTTC
AACAAACTAACCTTAATGGTGAAGCATTAGAGTTCAGCTGGTGATATG
GTGGAGCACTGCAGCTAATCAGGCTCTTCTCAAGATGACCAACCGT
TAAACATTTAATGCCATGATGTGACTATGGCATAATGGGACATACATGG
AATTGTAGAACGGTTGGCGAAATACATCGTATCTGGTACTGGAAAGGCC
CCTGCTCCAGATTCTAATATAAATAATTACGAAATCATACCCACAGA
AGCTGCAAAAACAGAAAATTGTAGTGGCAACAGCTTATGATAAAGTTAAC
AACAAATCCCTTACAAATTGGAAACCTTACACTTAAATAATTCCTGTA
AATAACAAAAGTGTGAACGGTGGCTTATCGGAATCGTACCAAAGACAT
CCCCAACCTTGTCTITACCTAAAAATTGTAAACATATTGAAATTTTAGATG
AAGCTGAAACATCGTTAAATACGCCAAAGAATACAGCTTAAATGTC
AAGGCTATTGTTAGCTCTGCTCATGTCACCTGCAACAGAACGGATGATAT
TGTGAGGTGAAGCAGCAGAAATGTAAGGAAAGTCAATCTCAACTCTCC
CTGAGATTAGCGTAGATTGTGCTTGTGGCACACATCATCAATATA
AATGCTTGTGGTAAACTCGTATTGTCACAGCGCTCTCAAGGAAA
AGCTTATGCTGATGTAACGGTGTCTTACGATACACAAAGATTTC
TTGAAACCCCTTCAGCTTAAAGTAATTGCGAGTCTCTGTAACAAAC
GGTAGTGCCTGATTCTAACGACATTGTTGACCAGCTAATACTCTGTTAA
ACAAGTAACAGAACGCTAAATTGGTACTGCCGAGGTAAAGTGGCATGATTA
CGCTTCTGTTGATCAAGATAATTGTTAGTCCGGTAGGCACCTCATCACA
GAGGCTCAACTAGCAATTGCTCGAACAAAGCTGCGGAGATATGATTG
CATGACAAATAATGGCGATTCTGCTGACTTACTCATCAAACAGATG
GAACAATCACCTGGGAGCTGCACAAAGCAGTTCAACCTTTGGTAATATC
TTCAAGTCGGCAAAATTACTGGTAGAGATCTTATAAGGACTCAACAG
ACAATACAGACAAAACAAAATTCTCTTCAATAGTGGTCTGGAT
ACACTTACACAGATAATAAGAGGGGGGGAGAACACCATTTAAAGTT
GTAAAAGCTTATAATCAATGGTGGAAAATCAATCTGATGCAAAATA
CAAATTAGTTATCAATGACTTTTATCTGGTGTGGTATGCTTTC
GCTTCAGAAATCCTTCAACTCTAGGACCCATTATCCTGATCAAGGGTA
TTTATGGCTTATATCACTGATTAGAAAAGCTGGTAAAGGACT
TCCAATAATAACCTAAATCTATGTCACATGAAAGATGGTTAATGAAA
CTTATACACAAATGATGGTACATATAGCAATTAAAGAACACTT
GATGCGACAAGGAATATTGTAGCACAAGAGATTGATCAGACACTTAAA
CCAAACAAATCCTAAACATTACAAAAATCAACCTGTTAATCAACATTACA
AAAACAAATTACCCAATTACAGCTTAAACCTTATGAGAAAATTATGGC
AAACCATCAACTCCTACTGTAAATCAAACAA

SEQ ID NO. 7107

STRAIN COHESION

ACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTCACCT
GACAATACTGGAACAGCAAATATGCCGTGACGGAAAGTTACTAATGCTGG
CACTGTGCTCAATTAGTAGCTTATATGGATGATGCTCAAAAAGATTTC
AACAACAACTAACCTTAATGTGAAAGCTTATTAGAGTTCAAGCTGGTATATG

Table 71: Comparative Sequences relating to SAG1333

GTTGGAGCAAGTCCAGCTAACCTAGGGCTCTTCAGAGATGAACCAACCGT
 TAAAACATTAAATGCAATGAAATGTTGAGTATGGCACATTAGGTAAACCATG
 AATTGATGAAGGTTGGCAGAATACAATCGTATCGTACTGGAAAGGCC
 CCTGCTCAGATTCTAATATAAAATATTACGAAATCATACCCACAGA
 AGCTGAAAACAAGAAATTGTAAGTGGCAACCGTTATGATAAAGTTAAC
 AACAAATCCCTACAATTGGAACCTTACACTATTAAAATATTCCCTGTA
 AATAACAAAAGTGTAAACGTTGGCTTATCGGAATCGTACCAAAGACAT
 CCCAAACCTTGtCTTAGCTAAATTATGAAACAATATGAAATTITTAGATG
 AAAGCTGAAACAACTTACGTTAAATACGCCAAGAAATTACAGCTAAAATGTC
 AAGGCTATTGTAGTCCTGCTCATGTACCTGCAACAGCAAGGATGATAT
 TGCTGAGGTGAAGCAGCAGAAATGATGAAAAAAAGTCAATCAACTCTCC
 CTGAAAATAGCTGAGATATTGCTTGGCAGACAAATCATCAATPATACA
 AATGGTCITGGTAAAGACTGTTATGTAACAGCGCTCTCAAGGAAA
 AGCCTATGCTGATGTAAGTGGCTCTAGATACTGATAACACAAGATTC
 TTGAAACCCCTACGCTAAAGTAATTGCAAGGATTGCTCTGGTAAAAAAACA
 GTAGTGGCGATATTCAAGCCATTGtTGACCAAGCTAAACTATCGTTAA
 ACAAGTAACAGAAGCTAAATTCGTAAGTGGCAGGAGTAAGTGGCATGATTA
 CGCGITCTGTTGATCAAGATAATGTTAGTGGCTGGTAGGCAGGCCATCACA
 GAGGCTCAACTAGCAATTGCTCGAAAAGCTGGCCAGATATCGATTGTC
 CATGACAAATAATGGTGGCATCTGCTGACTTACTCATCAAACCGATG
 GAACAATCACCTGGGAGCTGCACAAGCAGTCAACCTTTGGTAAATATC
 TTACAAGTCGAAATTACTGTAAGAGATCTTTAAAGCACTCAACGA
 ACATACTGGAACACCCAAATTCCTCTTCAAAATAGCTGGCTCGAT
 ACACITACACAGATAATAAGAGGGGGGAGAAACACCATTTAAAGIT
 GTAAAAGCTTATAATCAAATGGTGGAGAAATCAATCTGATGCAA
 CAAATAGTATTAATGACTTTTATTGGTGGTGGTAGTGGCTTGGCAA
 GCTTCAGAAATGCAAATCTTCAAGGAGCTTATCCGATACAGAGGT
 TTATGGCTTATTAATGATGTTAGAAAAGCTGGTAAAAAGTGAGCAT
 TCCAATAATAACCTTAAATCTATGCTACTATGAAAGTGGTAAATGAAA
 CTATTACACAAAATGATGGTACATATAGCATTATAAGAAACTTTTTTA
 GATCGACAAGGAAATATTGAGCACAAGAGATTGATCAGACACTTTAA
 CCAAACAAAATCAAACCTACACAAAATCACCCCTGTAACCAATTCA
 AAAACAAATTACACCAATTACAGCTTAAACCCCTATGAGAAATTATGGC
 AAACCATCAAACCTCCACTACTGTTAAATCAA

SEQ ID NO. 7108

STRAIN M781

CAAGTCGGTGTCCAAGTTATAGCGTCAATGACTTTCATGGTCACTTGA
 CAATACTGGAACACCCAAATATGCCCTGACGGAAAAGTTACTAATGCTGGCA
 CTGCTGCTCAATTAGCTTATATGGATGATGCTAAAAGATTTCAA
 CAAACTAACCTTAACTGGTAAAGCATTAGAGTCAAGCTGGTATATGGT
 TGAGAGCTGCAAGCTAACCTCAGGGCTTCTCAAGATGAACCAACCGTTA
 AACATTTAAATGCAATGAAATGTTGAGGACATTAGGTAAACCCTGAA
 TTGATGAAGGTTGGCAGAATACAATCTTATGTTACTGGAAAGGCC
 TGCTCAGATTCTAAATATAAAATAATGAAATCATACCCACAGAAG
 CTGAAACCAAGAAAGTGTAGTGGCAAACCTTATGGATAAAGTTAACAAA
 CAATACCCCTACAATTGGAAACCTTACACTTTAAATATCCGTA
 TAACAAAAGTGTGAACGTTGGCTTATGGATCGTACCAAAGACATCC
 CAAACCTGTCTTACGTTAAATGAAACCAATATGAAATTAGATGAA
 GCTGAAACATCGTAAATACGCCAAAGGATTACAAGCTAAAATGTC
 GGCTATTGTTGCTCATGTAACCTGCAACAAGCAAGGATGATATTG
 CTGAAGGTGAAGCAGCAGAAATGATGAAAAGTCAATCAACTCTTCC
 GAAATAGCTGAGATATTGCTTGGCAGACAAATCATCAATATACAAA
 TGGCTTCTGGTAAAAGCTGTTATGTAACAGCGCTCTCTCAAGGAAAAG
 CCTATGCTGATGTAAGTGGCTCTAGATACTGATAACACAAGATTTCATT
 GAAACCCCTGCTTACGTTAAAGTAAATTGCACTTGTCTGGTAAAAAACAGG
 TAGTGCCGATATTCAAGCCATTGtTGACCAAGCTAAACTATCGTTAAC
 AAGTAACAGAAGCTAAATTGGTACTGCCAGGTAAGTGGCATGATTACG
 CGCTCTGTGATCAAGATAATGTTAGTCCCGTAGGCAGCCTCATCACAGA
 GGCTCAACTAGCAATTGCTCGAAAAGCTGGCCAGATATCGATTGGCCA
 TGACAAATAATGGTGGCATCTGCTGACTTACTCATCAAACCGATGGA
 ACAATCACCTGGGAGCTGCACAAGCAGTTCAACCTTTGGTAAATATCTT
 ACAAGTCGAAATTACTGGTAGAGATCTTATAAAGCACTCAACGAAAC
 ATACGACAAAACAAAATTCCTCTCAAAATGCTGCTCGGATAC
 ACTTACACAGATAATAAGAGGGGGGGAGAAACACCAATTAAAGTTG
 AAAAGCTTATAAAATCAAATGGTGGAGGAATCAATCTGATGCAA
 AATTAGTTCAATGACTTTTATTGGTGGTGGTAGTGGCTTGGCAAGC
 TTACGAAATGCAAACCTCTAGGAGCCATTATCCGATACAGAGGTATT
 TATGGCTTATTAATGCTGTTAGAAAAGCTGGTAAAAAGTGAGCATTC
 CAAATAAAACCTTAAATCTGTCATTGTAACATGAAAGATGGTTAAATGAA
 ATTACACAAAATGATGGTACATATAGCATTATAAGAAACCTTTTTAGA
 TCGACAAGGAAATATTGAGCACAAGAGATTGATCAGACACTTTAAACC
 AAACAAAATCAAACCAATTACAGCTTAAACCCCTATGAGAAATTATGGCA
 ACCATCAAACCTCCACTACTGTTAAATCAA

SEQ ID NO. 7109

STRAIN CJB110

GACCAAGTCGGTGTCCAAGTTATAGCGTCAATGACTTTCATGGTCA
 ACTTGACAATACGGAAACAGCAAATATGCCCTGACGGAAAAGTTACTAATG
 CTGGCACTGCTGCTCAATTAGATGCTTATATGGATGATGCTAAAAGAT
 TTCAAAACAAACTAACCTTAACTGGTGAAGGATTAGAGTCAAGCTGGTGA
 TATGGTTGGAGCAAGTCCAGCTAACCTGTAACCAATTCA
 AAACAAATTACACCAATTACAGCTTAAACCCCTATGAGAAATTATGGCA
 ACCATCAAACCTCCACTACTGTTAAATCAA

Table 71: Comparative Sequences relating to SAG1333

CCGTTAAAACATTAATGCAATGAATGTTGAGTATGGCACATTAGGTAAAC
 CATGAATTGATGAAGGTTGGCAGAATACAATCGTATCGTTACTGGAAA
 GGGCCCTGCTCCAGATTcTAATATAAAATAATTACGAAATCATACCCAC
 ACGAAGCTGAAACAAAGAAATTGTAAGTGGCAAACGTTATTGATAAAGTT
 AACAAACAAATCCCTAACATTGGAAACCTTACGCTATTAAAAATATTCC
 TGTAATAACAAAAGTGTGAACGTTGGCTTATCGGAATCGTTACCCAAG
 ACATCCCAACCCCTGTCTTACGTTAAATTATGAAACAATATGAATTTTTA
 GATGAAGCTGAAACAAATCGTTAAATACGCCAAGAATTACAAGCTAAAAA
 TGTAAGGCTATTGTAAGTGTCTTGCTCATGACCTGCCAACAGCAAGGATG
 ATATTGCTGAAGGTGAAGCAGCAAATGTGAAAAAGTCATCAACTC
 TTCCCTGAAAATAGCTAGATATTGTCCTTGCTGACACAATCATCAATA
 TACAATGGCTTGTGGTAAACTCGCATTGTCAGTACAAGCGCTCTCAAG
 GAAAAGCCTATGCTGACGTACGGTGGCTAGATACTGATAACACAAGAT
 TTCAATTGAAACCCCTCAGCTAAAGTAGTTGCAATTGCTCTGGTAAAAA
 AACAGGTAGTGGCGATTCAGCCATTGTCAGCAAGCTAACTATATCG
 TTAACACAAGTAAAGCTAAATGGTACTGCTGAGCTGAGCTGAGCTG
 ATTACCGGTTCTGTGATCAAGATAATTGTTAGTCCAGTAGGCAGCCTCAT
 CACAGAGGCTCAACTAGCAATTGCTGAAAAGCTGGCCAGATATCGATT
 TTGCGCATGACAATTAATGGTGGCATTGCTGACTTACTCATCAAACCA
 GATGCAACATCACCTGGGGAGCTGCAACAGCAGTTCAACCTTTGGTAA
 TATCTTACAAGTCGCAAATTACTGGTAGAGATCTTATAAAGCACTCA
 ACCGAACAATGACCCAAAACAAAATTTCTTCAAATAGCTGGTCTG
 CGATCACACTACACAGATAATAAGAGGGCGGAGAAGAACACCCATTAA
 AGTTCTAAAGCTTATAAATCAATGGTGAAGAAATCAATCTGATGCAA
 AATACAAATTAGTTATCAATGACTTTTATTCGGTGGTGTATGGCTTT
 GCAAGCTTACAGGAAATGCCAACATTCTAGGAGCCATTAAATCCCATA
 GGTATTATGGCTTATATCACTGATTAGAAAAGCTGGTAAAAAGTGA
 GCGTTCAAATAATAACCTAAAATCTATGCACTATGAAGATGGTTAAT
 GAAACTTACAGGAAATGGTACACATAGCATTATAAGAAAACCTTTA
 TTAGATGACAAAGGAAATATGTTAGCACAGAGATTGATCAGACACTT
 TAAACCAAACAAAATCTACAAAATCAACCCCTGTAACACTACAATT
 CACAAAAACAAATTACACCAATTACAGCTATTAAACCCATTAGGAAATT
 TGGCAACCATAACCTCAACTACTGTAAAATCA

SEQ ID NO. 7110

STRAIN 1169NT

CAAGTCGGTGTCCAAGTTATAGGCGTCATGACTTTCATGGTCACITGA
 CAATACTGGAACAGCAAATATGCCATGAGGGAAAGTTGCTATGCTGGT
 CTGCTGCTCAATTAGATGCTTATATGGATGACGCTAAAAAGATTTCAAA
 CAAACTAACCTTAATGGTGAAGCATTAGGGTTCAAGCAGGGCATATGGT
 TGGAGCAAGTCAGCCAACTCTGGGCTTCITCAAGATGAAACACTGTC
 AAAATTAAATGCAATGAATGTTGAGTATGGCACATTGGTAACCATGAA
 TTGATGAGGGTTGGCAGAATATACTGATCGTTACTGGTAAGGCCCC
 TGCTCCAGATTCTAATAATTAAATATTAGCAAATCATACCCACATGAAG
 CTGCAAACAAAGAAATTGTAAGTGGCAAATGTTATTGATAAAGTTAACAA
 CAAATTCTTACATTGGAAACCTTACGCTTAAATTAAAGATTCTCTGTA
 TAACAAAAGTGTGAACGTTGGCTTATCGGGATTCTCACCAAGACATCC
 CAAACCTGTCTTACGTTAAATTATGAACAAATATGAATTTTAGATGAA
 GCTGAAACAACTCGTTAAATCGGCAAAGAAATTACAAGCTAAAATGTC
 AGCTATTGTAAGCTCGCACATGTAACCTGCAACAAAGTAAAATGATATTG
 CTGAACGCTGAAGCAGCAGAAATGATGAAAAAGTCATCAACTCTTCCCT
 GAAAATAGCTGTAAGTATTGCTTTGCTGACACAATCATCAATATAACAA
 TGCTCTTGTGGTAAACCTCGTATTGTCAGCAAGCGCTCTCTCAAGGAAAAG
 CCTATGCTGATGTAAGTGGTGTCTTAGATACTGATAACACAAGATTCA
 GAGACCCCTTCAGCTAAAGTAATTGCAATTGCTCTGGTAAAAAACAGG
 TAGTGGCATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAC
 AAGTAAACAGAAGCTAAATTGCTACTGCGGAGGTAAAGTGTATGATTACG
 CGTTCTGTTGATCAAGATAATTGTTAGTCCGGTAGGCAGCTCATCACAGA
 GGCTCAACTAGCAATTGCTGCAAAAGCTGGCCAGATATCGATTGGCCA
 TGCAAAATAATGGGCAATTGCTGCTGACTTACTCATCAAACCGAGATGGA
 ACAATCACCTGGGAGCTGCAACAGCTTCAACCTTTGGTAAATATCTT
 ACAAGTGTGAAATTACTGGTAGAGATCTTATAAAGCACTCAACGAAAC
 AATACGACCAAAACAAAATTCTTCTTCAAAATAGCTGGTCTGCGATAC
 ACTTACACAGATAATAAGAGGGCGGGGAGAAACACCCATTAAAGTTG
 AAAAGCTTATAAATCAAATGGTGGAGGAATCACTCTGATGCAAATACA
 ATTAGTTATCAATGACTTTTATTGCTGTTGCTGATGGCTTTGCAAGC
 TTGAGAATGCAACATTCTAGGAGCATTAAACCCGATAACAGAGGTATT
 TATGGCTTATATCACTGATTAGAAAAGCTGGTAAAAAGTGTGAGCGTTC
 CAAATAATAAAACCTAAATCTGTCATGAAAGATGGTAAATGAAACT
 ATTACACAGATAATAAGAGGGCGGGGAGAAACACCCATTAAAGAAA
 TCGCAAGGAAATTGTAAGGACAAAGAGATTGATCAGACACTTTAAAC
 AAACAAAATCTACAAAATCAACCCCTGTAACACTACAATTACAA
 AACAAATTACACCAATTACAGCTATTAAACCCATTAGGAAATTATGGCA
 ACCATCAAACCTCAACTACTGTAAAATCA

SEQ ID NO. 7111

STRAIN JM9130013

CGGTGTCAGCTTATAGGCGTCATGACTTTCATGGTCACCTGACAATA
 CTGGAACAGCAAATATGCCATGAGGGAAAGTTACTAATGCTGGCACTGCT
 GCTCAATTAGATGCTTATATGGATGATECTCAAAAGATTTCAAACAAAC
 TAACCCCTAATGGTGAAGCATTAGAGTTCAAGCTGCTGATATGTTGGAG
 CAAGTCCAGCTAACTCAGGGCTTCTCAAGATGAAACCAACGTTAAAAC
 TTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAAATTG

Table 71: Comparative Sequences relating to SAG1333

TGAAGGTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCCTGCTC
 CAGATTCTAATATAAATATTACGAAATCATACCCACACGAAAGCTGCA
 AAACAAGAAAATTGTAGTGGCAAACGTTATTGATAAAGTTAACAAACAAAT
 CCTTACAATTGGAACCTTACACTTAAATTCCTGAAATAACAA
 AAAGTGTGAACGTTGGCTTATCGGAATCCTTACCAAAGACATCCAAAC
 CTGTCTTACGTAAAAATTATGAACAATATGAATTTTAGATGAAGCTGA
 AACAAATCGTTAAATACGCCAAAGAAATTACAAGCTAAAATGTCAGGCTA
 TTGAGTCTTGCTCATGTACCTGCAACAAGCAAGGATGATAATTGCTGAA
 GTGAGCAGCAGAAGAAATGATGAAAAAGTCATCAACTCTTCCCTGAAA
 TAGCGTAGATTGTCTTGCGACAAATCATCAATATAACAAATGGTC
 TTGTTGGTAAACTCGTATTGAGTACAAGGCCTCTCTAAGGAAAAGCTAT
 GCTGATGAGTGTGGCTCTAGATACTGATACACAAGATTGAAAC
 CCCTCAGCTAAAGTAATTGAGTGTGGCTCTGGTAAAAAAACAGGTAGTG
 CGGATATTCAAGCCATTGAGCCAAGCTAATACATCGTTAAACAGTA
 ACAGAAGCTAAATGGTACTGCGAGGTAGTGGCATGATTACCGCTTC
 TGTGATCAAGATAATTGAGTGTGGCTGGTAGCAGCCTCATCACAGAGGCTC
 AACTAGCAATTGCTCGAAAAGCTGGCCAGATATCGATTGCGATGACA
 AATAATGGTGGCAATTGCTGCTGACTTACTCATCAAACCAAGATGAAACAAAT
 CACCTGGGGAGCTGACAAGCAGTTAACCTTTGGTAATATCTTACAAG
 TCGTCAAGTACTGGTAGAGATCTTATAAGCACTCAACGAAACAAATAC
 GACCAAAACAAATTTCTCTTCAAAATAGCTGGTCTGGGATACACTTA
 CACAGATAATAAAGAGGGGGAGAAACACCATTAAAGTTGCTAAAAG
 CTATAAATCAATGTTAGGAGAAAATCAATCTGATGCAAATACAAATTAA
 GTTATCAATGACTTTTATTCCGTGGTGTGATGGCTTGCAAGCTTCAG
 AAATGCCAAACTTCTAGGAGGCTTAATCCGATACAGAGGTATTATGG
 CCTATATCACTGTTAGGAGGCTTAATGGTAAAGACTGAGGCTTCCAAAT
 AATAACCTAAATCTPATGCACTATGAAGATGGTTATGAAACTTATTAC
 ACAAAATGATGGTACATATAGCATTATTGAGAAACTTTATTTAGATGAC
 AAGGAATATTGAGCACAAGAGATTGATCAGACACTTTAAACCAAAACA
 AAATCAAAATCTACAAAATCAACCCCTGTAACTACAAATTACACAAAAACA
 ATTACACCAATTACAGCTATTACCCCTATGAGAAATTATGGCAACCAT
 CAAACTCCACTACTGTAACAAATCAAAA

PRETTY of: /biotmp/msa237456.2{*} May 14, 2003 03:20 ..

	1	50
msa237456.2{328_1169NT}	-----	
msa237456.2{328_2603}	atggaaaaaga aaattatTTT gaaaagtagt gttcttggtt tagtcgtgg	
msa237456.2{328_18RS21}	-----	
msa237456.2{328_H36B}	-----	
msa237456.2{328_COH1}	-----	
msa237456.2{328_M732}	-----	
msa237456.2{328_M781}	-----	
msa237456.2{328_JM9130013}	-----	
msa237456.2{328_A909}	-----	
msa237456.2{328_090}	-----	
msa237456.2{328_CJB110}	-----	
Consensus	*****	*****
	51	100
msa237456.2{328_1169NT}	-----	caagtc ggtgtccaag
msa237456.2{328_2603}	gacttctatt atgttctcaa gcgtgttgcgc gGACcaagtC ggtgtccaag	
msa237456.2{328_18RS21}	-----	GACcaagtC ggtgtccaag
msa237456.2{328_H36B}	-----	CcaagtC ggtgtccaag
msa237456.2{328_COH1}	-----	--ACcaagtC ggtgtccaag
msa237456.2{328_M732}	-----	--ACcaagtC ggtgtccaag
msa237456.2{328_M781}	-----	--caagtC ggtgtccaag
msa237456.2{328_JM9130013}	-----	--C ggtgtccaag
msa237456.2{328_A909}	-----	
msa237456.2{328_090}	-----	aagtC ggtgtccaag
msa237456.2{328_CJB110}	-----	GACcaagtC ggtgtccaag
Consensus	*****	*****
	101	150
msa237456.2{328_1169NT}	ttatagGCGT CAATGACTTT CATGGTGACAC TTGACAATAC TGGAACAGCA	
msa237456.2{328_2603}	ttatagGCGT CAATGACTTT CATGGTGACAC TTGACAATAC TGGAACAGCA	
msa237456.2{328_18RS21}	ttatagGCGT CAATGACTTT CATGGTGACAC TTGACAATAC TGGAACAGCA	
msa237456.2{328_H36B}	ttatagGCGT CAATGACTTT CATGGTGACAC TTGACAATAC TGGAACAGCA	
msa237456.2{328_COH1}	ttatagGCGT CAATGACTTT CATGGTGACAC TTGACAATAC TGGAACAGCA	
msa237456.2{328_M732}	ttatagGCGT CAATGACTTT CATGGTGACAC TTGACAATAC TGGAACAGCA	
msa237456.2{328_M781}	ttatagGCGT CAATGACTTT CATGGTGACAC TTGACAATAC TGGAACAGCA	
msa237456.2{328_JM9130013}	ttatagGCGT CAATGACTTT CATGGTGACAC TTGACAATAC TGGAACAGCA	
msa237456.2{328_A909}	----CCGT CAATGACTTT CATGGTGACAC TTGACAATAC TGGAACAGCA	
msa237456.2{328_090}	ttatagGCGT CAATGACTTT CATGGTGACAC TTGACAATAC TGGAACAGCA	
msa237456.2{328_CJB110}	ttatagGCGT CAATGACTTT CATGGTGACAC TTGACAATAC TGGAACAGCA	
Consensus	-----	*****
	151	200
msa237456.2{328_1169NT}	ATGGAAAAGT TgcTAATGCT GGtACTGCTG CTCAATTAGA	
msa237456.2{328_2603}	ATATGCCCTG AtGGAAAAGT TgcTAATGCT GGtACTGCTG CTCAATTAGA	
msa237456.2{328_18RS21}	ATATGCCCTG AcGGAAAAGT TanTAATGCT GGtACTGCTG CTCAATTAGA	
msa237456.2{328_H36B}	ATATGCCCTG AcGGAAAAGT TactTAATGCT GGtACTGCTG CTCAATTAGA	
msa237456.2{328_COH1}	ATATGCCCTG AcGGAAAAGT TactTAATGCT GGtACTGCTG CTCAATTAGA	

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_M732}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_M781}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_JM9130013}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_A909}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_090}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_CJB110}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
Consensus	*****	*****	*****	*****	*****
	201				250
msa237456.2{328_1169NT}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAAACT	AACCTTAATG
msa237456.2{328_2603}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAAACT	AACCTTAATG
msa237456.2{328_18RS21}	TGCTTATATG	GATGATGCTC	AAAAAGATT	CAAACAAACT	AACCTTAATG
msa237456.2{328_H36B}	TGCTTATATG	GATGATGCTC	AAAAAGATT	CAAACAAACT	AACCTTAATG
msa237456.2{328_COH1}	TGCTTATATG	GATGATGCTC	AAAAAGATT	CAAACAAACT	AACCTTAATG
msa237456.2{328_M732}	TGCTTATATG	GATGATGCTC	AAAAAGATT	CAAACAAACT	AACCTTAATG
msa237456.2{328_M781}	TGCTTATATG	GATGATGCTC	AAAAAGATT	CAAACAAACT	AACCTTAATG
msa237456.2{328_JM9130013}	TGCTTATATG	GATGATGCTC	AAAAAGATT	CAAACAAACT	AACCTTAATG
msa237456.2{328_A909}	TGCTTATATG	GATGATGCTC	AAAAAGATT	CAAACAAACT	AACCTTAATG
msa237456.2{328_090}	TGCTTATATG	GATGATGCTC	AAAAAGATT	CAAACAAACT	AACCTTAATG
msa237456.2{328_CJB110}	TGCTTATATG	GATGATGCTC	AAAAAGATT	CAAACAAACT	AACCTTAATG
Consensus	*****	*****	*****	*****	*****
	251				300
msa237456.2{328_1169NT}	GTGAAAGCAT	TAGgGTTCAA	GCAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_2603}	GTGAAAGCAT	TAGgGTTCAA	GCAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_18RS21}	GTGAAAGCAT	TAGAgTTCAA	GctGGtGATA	TGGTTGGAGC	AAGTCCAGCt
msa237456.2{328_H36B}	GTGAAAGCAT	TAGAgTTCAA	GctGGtGATA	TGGTTGGAGC	AAGTCCAGCt
msa237456.2{328_COH1}	GTGAAAGCAT	TAGAgTTCAA	GctGGtGATA	TGGTTGGAGC	AAGTCCAGCt
msa237456.2{328_M732}	GTGAAAGCAT	TAGAgTTCAA	GctGGtGATA	TGGTTGGAGC	AAGTCCAGCt
msa237456.2{328_M781}	GTGAAAGCAT	TAGAgTTCAA	GctGGtGATA	TGGTTGGAGC	AAGTCCAGCt
msa237456.2{328_JM9130013}	GTGAAAGCAT	TAGAgTTCAA	GctGGtGATA	TGGTTGGAGC	AAGTCCAGCt
msa237456.2{328_A909}	GTGAAAGCAT	TAGAgTTCAA	GctGGtGATA	TGGTTGGAGC	AAGTCCAGCt
msa237456.2{328_090}	GTGAAAGCAT	TAGAgTTCAA	GctGGtGATA	TGGTTGGAGC	AAGTCCAGCt
msa237456.2{328_CJB110}	GTGAAAGCAT	TAGAgTTCAA	GctGGtGATA	TGGTTGGAGC	AAGTCCAGCt
Consensus	*****	*****	*****	*****	*****
	301				350
msa237456.2{328_1169NT}	AACTCtGGGC	TTCTTCAGA	TGAACCAA	GtcaAAAtT	TTAATGCAAT
msa237456.2{328_2603}	AACTCtGGGC	TTCTTCAGA	TGAACCAA	GtcaAAAtT	TTAATGCAAT
msa237456.2{328_18RS21}	AACTCaGGGC	TTCTTCAGA	TGAACCAA	GttaAAACaT	TTAATGCAAT
msa237456.2{328_H36B}	AACTCaGGGC	TTCTTCAGA	TGAACCAA	GttaAAACaT	TTAATGCAAT
msa237456.2{328_COH1}	AACTCaGGGC	TTCTTCAGA	TGAACCAA	GttaAAACaT	TTAATGCAAT
msa237456.2{328_M732}	AACTCaGGGC	TTCTTCAGA	TGAACCAA	GttaAAACaT	TTAATGCAAT
msa237456.2{328_M781}	AACTCaGGGC	TTCTTCAGA	TGAACCAA	GttaAAACaT	TTAATGCAAT
msa237456.2{328_JM9130013}	AACTCaGGGC	TTCTTCAGA	TGAACCAA	GttaAAACaT	TTAATGCAAT
msa237456.2{328_A909}	AACTCaGGGC	TTCTTCAGA	TGAACCAA	GttaAAACaT	TTAATGCAAT
msa237456.2{328_090}	AACTCaGGGC	TTCTTCAGA	TGAACCAA	GttaAAACaT	TTAATGCAAT
msa237456.2{328_CJB110}	AACTCaGGGC	TTCTTCAGA	TGAACCAA	GttaAAACaT	TTAATGCAAT
Consensus	*****	*****	*****	*****	*****
	351				400
msa237456.2{328_1169NT}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTGAT	GAAGGgTTGG
msa237456.2{328_2603}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTGAT	GAAGGgTTGG
msa237456.2{328_18RS21}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTGAT	GAAGGgTTGG
msa237456.2{328_H36B}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTGAT	GAAGGgTTGG
msa237456.2{328_COH1}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTGAT	GAAGGgTTGG
msa237456.2{328_M732}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTGAT	GAAGGgTTGG
msa237456.2{328_M781}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTGAT	GAAGGgTTGG
msa237456.2{328_JM9130013}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTGAT	GAAGGgTTGG
msa237456.2{328_A909}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTGAT	GAAGGgTTGG
msa237456.2{328_090}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTGAT	GAAGGgTTGG
msa237456.2{328_CJB110}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTGAT	GAAGGgTTGG
Consensus	*****	*****	*****	*****	*****
	401				450
msa237456.2{328_1169NT}	CAGAATAtAA	TCGTATCGTT	ACTGGtAAAG	CCCCCTGCTCC	AGATTCTAAT
msa237456.2{328_2603}	CAGAATAtAA	TCGTATCGTT	ACTGGtAAAG	CCCCCTGCTCC	AGATTCTAAT
msa237456.2{328_18RS21}	CAGAATACAA	TCGTATCGTT	ACTGGtAAAG	CCCCCTGCTCC	AGATTCTAAT
msa237456.2{328_H36B}	CAGAATACAA	TCGTATCGTT	ACTGGtAAAG	CCCCCTGCTCC	AGATTCTAAT
msa237456.2{328_COH1}	CAGAATACAA	TCGTATCGTT	ACTGGtAAAG	CCCCCTGCTCC	AGATTCTAAT
msa237456.2{328_M732}	CAGAATACAA	TCGTATCGTT	ACTGGtAAAG	CCCCCTGCTCC	AGATTCTAAT
msa237456.2{328_M781}	CAGAATACAA	TCGTATCGTT	ACTGGtAAAG	CCCCCTGCTCC	AGATTCTAAT
msa237456.2{328_JM9130013}	CAGAATACAA	TCGTATCGTT	ACTGGtAAAG	CCCCCTGCTCC	AGATTCTAAT
msa237456.2{328_A909}	CAGAATACAA	TCGTATCGTT	ACTGGtAAAG	CCCCCTGCTCC	AGATTCTAAT
msa237456.2{328_090}	CAGAATACAA	TCGTATCGTT	ACTGGtAAAG	CCCCCTGCTCC	AGATTCTAAT
msa237456.2{328_CJB110}	CAGAATACAA	TCGTATCGTT	ACTGGtAAAG	CCCCCTGCTCC	AGATTCTAAT
Consensus	*****	*****	*****	*****	*****
	451				500
msa237456.2{328_1169NT}	ATtaATAATA	TTACGAAATC	ATACCCACAt	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_2603}	ATtaATAATA	TTACGAAATC	ATACCCACAt	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_18RS21}	ATtaATAATA	TTACGAAATC	ATACCCACAc	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_H36B}	ATtaATAATA	TTACGAAATC	ATACCCACAc	GAAGCTGCAA	AACAAGAAAT

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_COH1}	AtaAATAATA	TTACGAAATC	ATACCCACAC	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_M732}	AtaAATAATA	TTACGAAATC	ATACCCACAC	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_M781}	AtaAATAATA	TTACGAAATC	ATACCCACAC	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_JM9130013}	AtaAATAATA	TTACGAAATC	ATACCCACAC	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_A909}	AtaAATAATA	TTACGAAATC	ATACCCACAC	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_090}	AtaAATAATA	TTACGAAATC	ATACCCACAC	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_CJB110}	AtaAATAATA	TTACGAAATC	ATACCCACAC	GAAGCTGCAA	AACAAGAAAT
Consensus	*****	*****	*****	*****	*****
	501				550
msa237456.2{328_1169NT}	TGTAGTGGCA	AATGTTATTG	ATAAAGTTAA	CAAACAAATt	CCTTACAATT
msa237456.2{328_2603}	TGTAGTGGCA	AATGTTATTG	ATAAAGTTAA	CAAACAAATt	CCTTACAATT
msa237456.2{328_18RS21}	TGTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_H36B}	TGTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_COH1}	TGTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_M732}	TGTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_M781}	TGTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_JM9130013}	TGTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_A909}	TGTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_090}	TGTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_CJB110}	TGTAGTGGCA	AACGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
Consensus	*****	*****	*****	*****	*****
	551				600
msa237456.2{328_1169NT}	GGAAgCCTTA	CgCTATTAAA	AATATTCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_2603}	GGAAgCCTTA	CgCTATTAAA	AATATTCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_18RS21}	GGAAaCCTTA	CaCTATTAAA	AATATTCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_H36B}	GGAAaCCTTA	CaCTATTAAA	AATATTCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_COH1}	GGAAaCCTTA	CaCTATTAAA	AATATTCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_M732}	GGAAaCCTTA	CaCTATTAAA	AATATTCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_M781}	GGAAaCCTTA	CaCTATTAAA	AATATTCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_JM9130013}	GGAAaCCTTA	CaCTATTAAA	AATATTCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_A909}	GGAAaCCTTA	CaCTATTAAA	AATATTCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_090}	GGAAaCCTTA	CgCTATTAAA	AATATTCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_CJB110}	GGAAaCCTTA	CgCTATTAAA	AATATTCTG	TAAATAACAA	AAGTGTGAAC
Consensus	*****	*****	*****	*****	*****
	601				650
msa237456.2{328_1169NT}	GTGGCTTTA	TCGGgATTGT	CACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_2603}	GTGGCTTTA	TCGGgATTGT	CACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_18RS21}	GTGGCTTTA	TCGGgATC GT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_H36B}	GTGGCTTTA	TCGGgATC GT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_COH1}	GTGGCTTTA	TCGGgATC GT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_M732}	GTGGCTTTA	TCGGgATC GT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_M781}	GTGGCTTTA	TCGGgATC GT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_JM9130013}	GTGGCTTTA	TCGGgATC GT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_A909}	GTGGCTTTA	TCGGgATC GT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_090}	GTGGCTTTA	TCGGgATC GT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_CJB110}	GTGGCTTTA	TCGGgATC GT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
Consensus	*****	*****	*****	*****	*****
	651				700
msa237456.2{328_1169NT}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_2603}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_18RS21}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_H36B}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_COH1}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_M732}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_M781}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_JM9130013}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_A909}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_090}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_CJB110}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
Consensus	*****	*****	*****	*****	*****
	701				750
msa237456.2{328_1169NT}	ATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAAgCTAT	TGTAGTtCTC
msa237456.2{328_2603}	ATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAAgCTAT	TGTAGTtCTC
msa237456.2{328_18RS21}	ATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt
msa237456.2{328_H36B}	ATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt
msa237456.2{328_COH1}	ATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt
msa237456.2{328_M732}	ATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt
msa237456.2{328_M781}	ATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt
msa237456.2{328_JM9130013}	ATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt
msa237456.2{328_A909}	ATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt
msa237456.2{328_090}	ATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt
msa237456.2{328_CJB110}	ATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAgGCTAT	TGTAGTcCTt
Consensus	*****	*****	*****	*****	*****
	751				800
msa237456.2{328_1169NT}	GCACATGTAC	CTGCAACAAG	tAAaaATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_2603}	GCACATGTAC	CTGCAACAAG	tAAaaATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_18RS21}	GCTCATGTAC	CTGCAACAAG	cAAggATGAT	ATTGCTGAAG	GTGAAGCAGC

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_H36B}	GCTCATGTAC	CTGCAACAAG	cAAggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_COH1}	GCTCATGTAC	CTGCAACAAG	cAAggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_M732}	GCTCATGTAC	CTGCAACAAG	cAAggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_M781}	GCTCATGTAC	CTGCAACAAG	cAAggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_JM9130013}	GCTCATGTAC	CTGCAACAAG	cAAggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_A909}	GCTCATGTAC	CTGCAACAAG	cAAggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_090}	GCTCATGTAC	CTGCAACAAG	cAAggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_CJB110}	GCTCATGTAC	CTGCAACAAG	cAAggATGAT	ATTGCTGAAG	GTGAAGCAGC
Consensus	*****	*****	-*****	*****	*****
					850
msa237456.2{328_1169NT}	AGAAAATGATG	AAAAAAAGTC	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_2603}	AGAAAATGATG	AAAAAAAGTC	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_18RS21}	AGAAAATGATG	AAAAAAAGTC	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_H36B}	AGAAAATGATG	AAAAAAAGTC	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_COH1}	AGAAAATGATG	AAAAAAAGTC	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_M732}	AGAAAATGATG	AAAAAAAGTC	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_M781}	AGAAAATGATG	AAAAAAAGTC	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_JM9130013}	AGAAAATGATG	AAAAAAAGTC	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_A909}	AGAAAATGATG	AAAAAAAGTC	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_090}	AGAAAATGATG	AAAAAAAGTC	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_CJB110}	AGAAAATGATG	AAAAAAAGTC	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
Consensus	*****	*****	*****	*****	*****
					900
msa237456.2{328_1169NT}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_2603}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_18RS21}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_H36B}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_COH1}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_M732}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_M781}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_JM9130013}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_A909}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_090}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_CJB110}	TTGTCTTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
Consensus	*****	*****	*****	*****	*****
					950
msa237456.2{328_1169NT}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_2603}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_18RS21}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_H36B}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_COH1}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_M732}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_M781}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_JM9130013}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_A909}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAtGTACG
msa237456.2{328_090}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAcGTACG
msa237456.2{328_CJB110}	ACTCGtATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGAcGTACG
Consensus	*****	*****	*****	*****	*****
					1000
msa237456.2{328_1169NT}	TGGTGTcTA	GATACTGATA	CACAAGATTT	CATTGAGACC	CCTTCAGCTA
msa237456.2{328_2603}	TGGTGTcTA	GATACTGATA	CACAAGATTT	CATTGAGACC	CCTTCAGCTA
msa237456.2{328_18RS21}	TGGTGTcTA	GATACTGATA	CACAAGATTT	CATTGAAACC	CCTTCAGCTA
msa237456.2{328_H36B}	TGGTGTcTA	GATACTGATA	CACAAGATTT	CATTGAAACC	CCTTCAGCTA
msa237456.2{328_COH1}	TGGTGTcTA	GATACTGATA	CACAAGATTT	CATTGAAACC	CCTTCAGCTA
msa237456.2{328_M732}	TGGTGTcTA	GATACTGATA	CACAAGATTT	CATTGAAACC	CCTTCAGCTA
msa237456.2{328_M781}	TGGTGTcTA	GATACTGATA	CACAAGATTT	CATTGAAACC	CCTTCAGCTA
msa237456.2{328_JM9130013}	TGGTGTcTA	GATACTGATA	CACAAGATTT	CATTGAAACC	CCTTCAGCTA
msa237456.2{328_A909}	TGGTGTcTA	GATACTGATA	CACAAGATTT	CATTGAAACC	CCTTCAGCTA
msa237456.2{328_090}	TGGTGTcTA	GATACTGATA	CACAAGATTT	CATTGAAACC	CCTTCAGCTA
msa237456.2{328_CJB110}	TGGTGTcTA	GATACTGATA	CACAAGATTT	CATTGAAACC	CCTTCAGCTA
Consensus	*****	*****	*****	*****	*****
					1050
msa237456.2{328_1169NT}	AAGTAatTTGC	AGTTGCTCC	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_2603}	AAGTAatTTGC	AGTTGCTCC	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_18RS21}	AAGTAatTTGC	AGTTGCTCC	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_H36B}	AAGTAatTTGC	AGTTGCTCC	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_COH1}	AAGTAatTTGC	AGTTGCTCC	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_M732}	AAGTAatTTGC	AGTTGCTCC	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_M781}	AAGTAatTTGC	AGTTGCTCC	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_JM9130013}	AAGTAatTTGC	AGTTGCTCC	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_A909}	AAGTAatTTGC	AGTTGCTCC	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_090}	AAGTAatTTGC	AGTTGCTCC	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_CJB110}	AAGTAatTTGC	AGTTGCTCC	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
Consensus	*****	*****	*****	*****	*****
					1100
msa237456.2{328_1169NT}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_2603}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_18RS21}	GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA				
msa237456.2{328_H36B}	GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA				
msa237456.2{328_COH1}	GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA				
msa237456.2{328_M732}	GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA				
msa237456.2{328_M781}	GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA				
msa237456.2{328_JM9130013}	GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA				
msa237456.2{328_A909}	GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA				
msa237456.2{328_090}	GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA				
msa237456.2{328_CJB110}	GCCATTGTTG ACCAAGCTAA TACTATCGTT AAACAAGTAA CAGAAGCTAA				
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	1101	GCCGAGGTAA GTGtCATGAT TACCGCTTCT GTTGATCAAG			1150
msa237456.2{328_2603}	AATTGGTACT	GCCGAGGTAA GTGtCATGAT TACCGCTTCT GTTGATCAAG			
msa237456.2{328_18RS21}	AATTGGTACT	GCCGAGGTAA GTGgCATGAT TACCGCTTCT GTTGATCAAG			
msa237456.2{328_H36B}	AATTGGTACT	GCCGAGGTAA GTGgCATGAT TACCGCTTCT GTTGATCAAG			
msa237456.2{328_COH1}	AATTGGTACT	GCCGAGGTAA GTGgCATGAT TACCGCTTCT GTTGATCAAG			
msa237456.2{328_M732}	AATTGGTACT	GCCGAGGTAA GTGgCATGAT TACCGCTTCT GTTGATCAAG			
msa237456.2{328_M781}	AATTGGTACT	GCCGAGGTAA GTGgCATGAT TACCGCTTCT GTTGATCAAG			
msa237456.2{328_JM9130013}	AATTGGTACT	GCCGAGGTAA GTGgCATGAT TACCGCTTCT GTTGATCAAG			
msa237456.2{328_A909}	AATTGGTACT	GCCGAGGTAA GTGgCATGAT TACCGCTTCT GTTGATCAAG			
msa237456.2{328_090}	AATTGGTACT	GCCGAGGTAA GTGgCATGAT TACCGCTTCT GTTGATCAAG			
msa237456.2{328_CJB110}	AATTGGTACT	GCCGAGGTAA GTGgCATGAT TACCGCTTCT GTTGATCAAG			
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	1151	TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT			1200
msa237456.2{328_2603}	ATAATGTTAG	TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT			
msa237456.2{328_18RS21}	ATAATGTTAG	TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT			
msa237456.2{328_H36B}	ATAATGTTAG	TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT			
msa237456.2{328_COH1}	ATAATGTTAG	TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT			
msa237456.2{328_M732}	ATAATGTTAG	TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT			
msa237456.2{328_M781}	ATAATGTTAG	TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT			
msa237456.2{328_JM9130013}	ATAATGTTAG	TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT			
msa237456.2{328_A909}	ATAATGTTAG	TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT			
msa237456.2{328_090}	ATAATGTTAG	TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT			
msa237456.2{328_CJB110}	ATAATGTTAG	TCCgGTAGGC AGCCTCATCA CAGAGGCTCA ACTAGCAATT			
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	1201	GCTGCCAGA TATCGATTT GCCATGACAA ATAATGGTGG			1250
msa237456.2{328_2603}	GCTGCCAGA TATCGATTT GCCATGACAA ATAATGGTGG				
msa237456.2{328_18RS21}	GCTGCCAGA TATCGATTT GCCATGACAA ATAATGGTGG				
msa237456.2{328_H36B}	GCTGCCAGA TATCGATTT GCCATGACAA ATAATGGTGG				
msa237456.2{328_COH1}	GCTGCCAGA TATCGATTT GCCATGACAA ATAATGGTGG				
msa237456.2{328_M732}	GCTGCCAGA TATCGATTT GCCATGACAA ATAATGGTGG				
msa237456.2{328_M781}	GCTGCCAGA TATCGATTT GCCATGACAA ATAATGGTGG				
msa237456.2{328_JM9130013}	GCTGCCAGA TATCGATTT GCCATGACAA ATAATGGTGG				
msa237456.2{328_A909}	GCTGCCAGA TATCGATTT GCCATGACAA ATAATGGTGG				
msa237456.2{328_090}	GCTGCCAGA TATCGATTT GCCATGACAA ATAATGGTGG				
msa237456.2{328_CJB110}	GCTGCCAGA TATCGATTT GCCATGACAA ATAATGGTGG				
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	1251	CATTCTGTGCT GACTTACTCA TCAAACCAGA TGGAACAAATC ACCTGGGGAG			1300
msa237456.2{328_2603}	CATTCTGTGCT GACTTACTCA TCAAACCAGA TGGAACAAATC ACCTGGGGAG				
msa237456.2{328_18RS21}	CATTCTGTGCT GACTTACTCA TCAAACCAGA TGGAACAAATC ACCTGGGGAG				
msa237456.2{328_H36B}	CATTCTGTGCT GACTTACTCA TCAAACCAGA TGGAACAAATC ACCTGGGGAG				
msa237456.2{328_COH1}	CATTCTGTGCT GACTTACTCA TCAAACCAGA TGGAACAAATC ACCTGGGGAG				
msa237456.2{328_M732}	CATTCTGTGCT GACTTACTCA TCAAACCAGA TGGAACAAATC ACCTGGGGAG				
msa237456.2{328_M781}	CATTCTGTGCT GACTTACTCA TCAAACCAGA TGGAACAAATC ACCTGGGGAG				
msa237456.2{328_JM9130013}	CATTCTGTGCT GACTTACTCA TCAAACCAGA TGGAACAAATC ACCTGGGGAG				
msa237456.2{328_A909}	CATTCTGTGCT GACTTACTCA TCAAACCAGA TGGAACAAATC ACCTGGGGAG				
msa237456.2{328_090}	CATTCTGTGCT GACTTACTCA TCAAACCAGA TGGAACAAATC ACCTGGGGAG				
msa237456.2{328_CJB110}	CATTCTGTGCT GACTTACTCA TCAAACCAGA TGGAACAAATC ACCTGGGGAG				
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	1301	CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT			1350
msa237456.2{328_2603}	CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT				
msa237456.2{328_18RS21}	CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT				
msa237456.2{328_H36B}	CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT				
msa237456.2{328_COH1}	CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT				
msa237456.2{328_M732}	CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT				
msa237456.2{328_M781}	CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT				
msa237456.2{328_JM9130013}	CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT				
msa237456.2{328_A909}	CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT				
msa237456.2{328_090}	CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT				
msa237456.2{328_CJB110}	CTGCACAAGC AGTTCAACCT TTTGGTAATA TCTTACAAGT CGTCGAAATT				
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	1351	ACTGGTAGAG ATCTTTATAA AGCACTCAAC GAACAATACG ACCAAAAACA			1400

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_2603}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA	
msa237456.2{328_18RS21}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA	
msa237456.2{328_H36B}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA	
msa237456.2{328_COH1}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA	
msa237456.2{328_M732}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA	
msa237456.2{328_M781}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA	
msa237456.2{328_JM9130013}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA	
msa237456.2{328_A909}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA	
msa237456.2{328_090}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA	
msa237456.2{328_CJB110}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA	
Consensus	*****	*****	*****	*****	*****	
msa237456.2{328_1169NT}	1401	AAATTTCITC	CTTCAAATAG	CTGGTCTCGG	ATACACTTAC	ACAGATAATA
msa237456.2{328_2603}		AAATTTCITC	CTTCAAATAG	CTGGTCTCGG	ATACACTTAC	ACAGATAATA
msa237456.2{328_18RS21}		AAATTTCITC	CTTCAAATAG	CTGGTCTCGG	ATACACTTAC	ACAGATAATA
msa237456.2{328_H36B}		AAATTTCITC	CTTCAAATAG	CTGGTCTCGG	ATACACTTAC	ACAGATAATA
msa237456.2{328_COH1}		AAATTTCITC	CTTCAAATAG	CTGGTCTCGG	ATACACTTAC	ACAGATAATA
msa237456.2{328_M732}		AAATTTCITC	CTTCAAATAG	CTGGTCTCGG	ATACACTTAC	ACAGATAATA
msa237456.2{328_M781}		AAATTTCITC	CTTCAAATAG	CTGGTCTCGG	ATACACTTAC	ACAGATAATA
msa237456.2{328_JM9130013}		AAATTTCITC	CTTCAAATAG	CTGGTCTCGG	ATACACTTAC	ACAGATAATA
msa237456.2{328_A909}		AAATTTCITC	CTTCAAATAG	CTGGTCTCGG	ATACACTTAC	ACAGATAATA
msa237456.2{328_090}		AAATTTCITC	CTTCAAATAG	CTGGTCTCGG	ATACACTTAC	ACAGATAATA
msa237456.2{328_CJB110}		AAATTTCITC	CTTCAAATAG	CTGGTCTCGG	ATACACTTAC	ACAGATAATA
Consensus	*****	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	1451	AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_2603}		AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_18RS21}		AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_H36B}		AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_COH1}		AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_M732}		AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_M781}		AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_JM9130013}		AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_A909}		AAGAGGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_090}		AAGAGGGCGG	aGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
msa237456.2{328_CJB110}		AAGAGGGCGG	aGAAGAAACA	CCATTTAAAG	TTGTAAAAGC	TTATAAATCA
Consensus	*****	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	1501	AATGGTGAgG	AAATCAATCC	TGATGAAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_2603}		AATGGTGAgG	AAATCAATCC	TGATGAAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_18RS21}		AATGGTGAgG	AAATCAATCC	TGATGAAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_H36B}		AATGGTGAgG	AAATCAATCC	TGATGAAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_COH1}		AATGGTGAgG	AAATCAATCC	TGATGAAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_M732}		AATGGTGAgG	AAATCAATCC	TGATGAAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_M781}		AATGGTGAgG	AAATCAATCC	TGATGAAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_JM9130013}		AATGGTGAgG	AAATCAATCC	TGATGAAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_A909}		AATGGTGAgG	AAATCAATCC	TGATGAAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_090}		AATGGTGAgG	AAATCAATCC	TGATGAAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_CJB110}		AATGGTGAgG	AAATCAATCC	TGATGAAAAA	TACAAATTAG	TTATCAATGA
Consensus	*****	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	1551	CTTTTTATTTC	GGTGGTGGGT	ATGGCTTTC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_2603}		CTTTTTATTTC	GGTGGTGGGT	ATGGCTTTC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_18RS21}		CTTTTTATTTC	GGTGGTGGGT	ATGGCTTTC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_H36B}		CTTTTTATTTC	GGTGGTGGGT	ATGGCTTTC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_COH1}		CTTTTTATTTC	GGTGGTGGGT	ATGGCTTTC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_M732}		CTTTTTATTTC	GGTGGTGGGT	ATGGCTTTC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_M781}		CTTTTTATTTC	GGTGGTGGGT	ATGGCTTTC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_JM9130013}		CTTTTTATTTC	GGTGGTGGGT	ATGGCTTTC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_A909}		CTTTTTATTTC	GGTGGTGGGT	ATGGCTTTC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_090}		CTTTTTATTTC	GGTGGTGGGT	ATGGCTTTC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_CJB110}		CTTTTTATTTC	GGTGGTGGGT	ATGGCTTTC	AAGCTTCAGA	AATGCCAAAC
Consensus	*****	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	1601	TTCTAGGAGC	CATTAACCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_2603}		TTCTAGGAGC	CATTAACCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_18RS21}		TTCTAGGAGC	CATTAATCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_H36B}		TTCTAGGAGC	CATTAATCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_COH1}		TTCTAGGAGC	CATTAATCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_M732}		TTCTAGGAGC	CATTAATCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_M781}		TTCTAGGAGC	CATTAATCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_JM9130013}		TTCTAGGAGC	CATTAATCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_A909}		TTCTAGGAGC	CATTAATCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_090}		TTCTAGGAGC	CATTAATCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_CJB110}		TTCTAGGAGC	CATTAATCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
Consensus	*****	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	1651	1601	1651	1601	1650	1700

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_1169NT}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_2603}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_18RS21}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_H36B}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_COH1}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_M732}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_M781}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_JM9130013}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_A909}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_090}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_CJB110}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
Consensus	*****	*****	*****	-*****	*****
	1701			1750	
msa237456.2{328_1169NT}	AACTCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAATGATG
msa237456.2{328_2603}	AACTCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAATGATG
msa237456.2{328_18RS21}	AACTCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAATGATG
msa237456.2{328_H36B}	AACTCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAATGATG
msa237456.2{328_COH1}	AACTCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAATGATG
msa237456.2{328_M732}	AACTCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAATGATG
msa237456.2{328_M781}	AACTCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAATGATG
msa237456.2{328_JM9130013}	AACTCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAATGATG
msa237456.2{328_A909}	AACTCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAATGATG
msa237456.2{328_090}	AACTCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAATGATG
msa237456.2{328_CJB110}	AACTCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAATGATG
Consensus	*****	*****	*****	*****	*****
	1751			1800	
msa237456.2{328_1169NT}	GTACACATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_2603}	GTACACATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_18RS21}	GTACACATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_H36B}	GTACACATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_COH1}	GTACACATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_M732}	GTACACATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_M781}	GTACACATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_JM9130013}	GTACACATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_A909}	GTACACATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_090}	GTACACATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_CJB110}	GTACACATAG	CATTATTaAG	AAACTTTATT	TAGATCGACA	AGGAAATATT
Consensus	*****	*****	*****	*****	*****
	1801			1850	
msa237456.2{328_1169NT}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_2603}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_18RS21}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_H36B}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_COH1}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_M732}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_M781}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_JM9130013}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_A909}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_090}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
msa237456.2{328_CJB110}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAAATC
Consensus	*****	*****	*****	*****	*****
	1851			1900	
msa237456.2{328_1169NT}	TACAAAAATC	AACCCGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_2603}	TACAAAAATC	AACCCGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_18RS21}	TACAAAAATC	AACCCGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_H36B}	TACAAAAATC	AACCCGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_COH1}	TACAAAAATC	AACCCGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_M732}	TACAAAAATC	AACCCGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_M781}	TACAAAAATC	AACCCGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_JM9130013}	TACAAAAATC	AACCCGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_A909}	TACAAAAATC	AACCCGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_090}	TACAAAAATC	AACCCGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_CJB110}	TACAAAAATC	AACCCGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
Consensus	*****	*****	*****	*****	*****
	1901			1950	
msa237456.2{328_1169NT}	TTACAGCTAT	TAACCTATG	AGAAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_2603}	TTACAGCTAT	TAACCTATG	AGAAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_18RS21}	TTACAGCTAT	TAACCTATG	AGAAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_H36B}	TTACAGCTAT	TAACCTATG	AGAAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_COH1}	TTACAGCTAT	TAACCTATG	AGAAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_M732}	TTACAGCTAT	TAACCTATG	AGAAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_M781}	TTACAGCTAT	TAACCTATG	AGAAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_JM9130013}	TTACAGCTAT	TAACCTATG	AGAAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_A909}	TTACAGCTAT	TAACCTATG	AGAAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_090}	TTACAGCTAT	TAACCTATG	AGAAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_CJB110}	TTACAGCTAT	TAACCTATG	AGAAAATTATG	GCAAACCATC	AAACTCCACT
Consensus	*****	*****	*****	*****	*****

Table 71: Comparative Sequences relating to SAG1333

	1951	2000
msa237456.2{328_1169NT}	ACTGTAAAAT	Caaa-----
msa237456.2{328_2603}	ACTGTAAAAT	CAaaACAAat
msa237456.2{328_18RS21}	ACTGTAAAAT	accaaaaaca
msa237456.2{328_H36B}	ACTGTAAAAT	aactctgaat
msa237456.2{328_COH1}	ACTGTAAAAT	atggacaatc
msa237456.2{328_M732}	ACTGTAAAAT	CAaaA-----
msa237456.2{328_M781}	ACTGTAAAAT	CAaaACAA-
msa237456.2{328_JM9130013}	ACTGTAAAAT	CAaaA-----
msa237456.2{328_A909}	ACTGTAAAAT	CAaaACAA-
msa237456.2{328_090}	ACTGTAAAAT	CAaaACAA-
msa237456.2{328_CJB110}	ACTGTAAAAT	CA-----
Consensus	*****	*****
	2001	2050
msa237456.2{328_1169NT}	-----	-----
msa237456.2{328_2603}	attccttatg	tctgtctttg
msa237456.2{328_18RS21}	-----	gtgttggact
msa237456.2{328_H36B}	-----	tataggaatt
msa237456.2{328_COH1}	-----	gccttaata
msa237456.2{328_M732}	-----	-----
msa237456.2{328_M781}	-----	-----
msa237456.2{328_JM9130013}	-----	-----
msa237456.2{328_A909}	-----	-----
msa237456.2{328_090}	-----	-----
msa237456.2{328_CJB110}	-----	-----
Consensus	*****	*****
	2051	2070
msa237456.2{328_1169NT}	-----	-----
msa237456.2{328_2603}	caaagaaaa	acatatgaaa
msa237456.2{328_18RS21}	-----	-----
msa237456.2{328_H36B}	-----	-----
msa237456.2{328_COH1}	-----	-----
msa237456.2{328_M732}	-----	-----
msa237456.2{328_M781}	-----	-----
msa237456.2{328_JM9130013}	-----	-----
msa237456.2{328_A909}	-----	-----
msa237456.2{328_090}	-----	-----
msa237456.2{328_CJB110}	-----	-----
Consensus	*****	*****

SEQ ID NO. 7112

STRAIN 2603 frame: 1

MKKKI ILKSSVLLVAGTSIMFSSVFADQVGVQVIGVNDFHGALDNTGTANMPDGKVANA
 GAAQDAQLDAYMDMAQKDFQTKTNPNGESIRVQAGDMVGASPANSGLLQDEPTVKNFNAMNVE
 YGTLGNHBFDEGLAEVNRIVTGKAPAPDSNINNITKSYPHEAAKQEIVVANVIDKVNKQI
 PYNWKPYAIKNIPVNNSKSVNVGFIGIVTKDIPNLVLRKNYEQYEFLEDEAETIVVKYAKELQ
 AKNVKAIVVLAHPATSKNDIAEGEAAEMMKVNVQLPENSVDIVFAGHNHQYTNGLVGK
 TRIVQALSQGKAYADVRGLVLDTQDFIETPSAKVIAVPGKKTGSADIQAIVDQANTITV
 KQVTEAKIGTAEVSVMITRSVDQDNVPVGSLITEAQIARSKSWPDIDFAMTNNGGIRA
 DLLIKPDGTITWGAAQAVQPFGNILQVVEITGRDLYKALNEQYDQKQNFQLIAGLRYTY
 TDNKEGGEEETPKVVKAYKSNGEEINPDAKYKLVINDFLFGGGDFASFRAKLLGAINP
 DTEVFMAYITDLEKAGKKVSPVNPKIYVTMKMVNETITQNDGTHSIIKKLYLDRQGNI
 VAQEIVSDTLNQTKSKTKINPVITIHKKQLHQFTAINPMRNYGKPSNSTTVKSQKLPKT
 NSEYQGSFLMSVFGVGLIGIALNTKKHHMK

SEQ ID NO. 7113

STRAIN 090 frame: 3

VGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRV
 QAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGNHEFDEGLAEVNRIVTGKAPAPDS
 NINNITKSYPHEAAKQEIVVANVIDKVNKQI PYNWKPYAIKNIPVNNSKSVNVGFIGIVTK
 DIPNLVLRKNYEQYEFLEDEAETIVVKYAKELQAKNVKAIVVLAHPATSKDDIAEGEAAEM
 MKKVNQLPENSVDIDFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGLVLDTQDFIETPSAKV
 GSLITEAQIARSKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVVE
 ITGRDLYKALNEQYDQKQNFQLIAGLRYTYTDNKEGGEEETPKVVKAYKSNGEEINPDA
 KYKLVINDFLFGGGDFASFRAKLLGAINPDTEVFMAYITDLEKAGKKVSPVNPKIYVTMKMV
 NETITQNDGTHSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKTKINPVTTIHKK
 QLHQFTAINPMRNYGKPSNSTTVKSQ

SEQ ID NO. 7114

STRAIN A909 frame: 3

VNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVG
 ASPANSGLLQDEPTVKTFNAMNVEYGTGNHEFDEGLAEVNRIVTGKAPAPDSNINNITK
 SYPHEAAKQEIVVANVIDKVNKQI PYNWKPYAIKNIPVNNSKSVNVGFIGIVTKDIPNL
 RKNYEQYEFLEDEAETIVVKYAKELQAKNVKAIVVLAHPATSKDDIAEGEAAEMMKVNVQ
 LPENSVDIDFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGLVLDTQDFIETPSAKV
 IAVPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVPVGSLITEA
 QLIAARKSWPDIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPFGNILQVVEITGRDLY
 KALNEQYDQKQNFQLIAGLRYTYTDNKEGGEEETPKVVKAYKSNGEEINPDAKYKLV
 INDFFGGGDFASFRAKLLGAINPDTEVFMAYITDLEKAGKKVSPVNPKIYVTMKMV
 ETITQNDGTHSIIKKLYLDRQGNIVAQEIVSDTLNQTKSKTKINPVTTIHKKQLHQFTA

Table 71: Comparative Sequences relating to SAG1333

INPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7115

STRAIN H36B frame: 2

QVGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGLNHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHEAAKQEIVVANVIDKVNQIIPYNWKPYTIKNIPVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIIVLAHVPATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDLTDQDFI
 ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLLITEAQLAIIARKSWPDIIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPGNILQVV
 EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVVKAYKSNGEEINPD
 AKYKLVINDFLFGGGDGFAFRNAKLLGAINPDTEVFMAITYTDLEKAGKKVSIPNNPKI
 YVTMKMVNETITQNDGTYSI IKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHK
 KQLHQFTAIPMRNYGKPSNSTTVKS

SEQ ID NO. 7116

STRAIN I8RS21 frame: 1

DQVGVQVIGVNDFHGALDNTGTANMPDGKVXNAGTAAQLDAYMDDAQKDFKQTNPNGESI
 RVQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGLNHEFDEGLAEYNRIVTGKAPAP
 DSNINNITKSYPHEAAKQEIVVANVIDKVNQIIPYNWKPYTIKNIPVNNKSVNVGFIGIV
 TKDI PNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIIVLAHVPATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDLTDQDFI
 ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLLITEAQLAIIARKSWPDIIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPGNILQVV
 EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVVKAYKSNGEEINPD
 AKYKLVINDFLFGGGDGFAFRNAKLLGAINPDTEVFMAITYTDLEKAGKKVSIPNNPKI
 YVTMKMVNETITQNDGTYSI IKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIH
 KQLHQFTAIPMRNYGKPSNSTTVKS

SEQ ID NO. 7117

STRAIN M732 frame: 3

QVGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGLNHEFDEGLAEYNRIVTGKAPAPD
 SNINNITKSYPHEAAKQEIVVANVIDKVNQIIPYNWKPYTIKNIPVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIIVLAHVPATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDLTDQDFI
 ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLLITEAQLAIIARKSWPDIIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPGNILQVV
 EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVVKAYKSNGEEINPD
 AKYKLVINDFLFGGGDGFAFRNAKLLGAINPDTEVFMAITYTDLEKAGKKVSIPNNPKI
 YVTMKMVNETITQNDGTYSI IKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIH
 KQLHQFTAIPMRNYGKPSNSTTVKS

SEQ ID NO. 7118

STRAIN COH1 frame: 3

QVGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGLNHEFDEGLAEYNRIVTGKAPAP
 DSNINNITKSYPHEAAKQEIVVANVIDKVNQIIPYNWKPYTIKNIPVNNKSVNVGFIGIV
 KDI PNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIIVLAHVPATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDLTDQDFI
 ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLLITEAQLAIIARKSWPDIIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPGNILQVV
 EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVVKAYKSNGEEINPD
 AKYKLVINDFLFGGGDGFAFRNAKLLGAINPDTEVFMAITYTDLEKAGKKVSIPNNPKI
 YVTMKMVNETITQNDGTYSI IKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIH
 KQLHQFTAIPMRNYGKPSNSTTVKS

SEQ ID NO. 7119

STRAIN M781 frame: 1

QVGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
 VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGLNHEFDEGLAEYNRIVTGKAPAPD
 DSNINNITKSYPHEAAKQEIVVANVIDKVNQIIPYNWKPYTIKNIPVNNKSVNVGFIGIVT
 KDI PNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIIVLAHVPATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDLTDQDFI
 ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLLITEAQLAIIARKSWPDIIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPGNILQVV
 EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVVKAYKSNGEEINPD
 AKYKLVINDFLFGGGDGFAFRNAKLLGAINPDTEVFMAITYTDLEKAGKKVSIPNNPKI
 YVTMKMVNETITQNDGTYSI IKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIH
 KQLHQFTAIPMRNYGKPSNSTTVKS

SEQ ID NO. 7120

STRAIN CJB110 frame: 1

DQVGVQVIGVNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESI
 RVQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTGLNHEFDEGLAEYNRIVTGKAPAP
 DSNINNITKSYPHEAAKQEIVVANVIDKVNQIIPYNWKPYTIKNIPVNNKSVNVGFIGIV
 KDI PNLVLRKNYEQYEFLDEAETIVKYAKELQAKNVKAIIVLAHVPATSKDDIAEGEAAE
 MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRIVQALSQGKAYADVRGVLDLTDQDFI
 ETPSAKVIAVAPGKKTGSADIQAIVDQANTIVKQVTEAKIGTAEVSGMITRSVDQDNVSP
 VGSLLITEAQLAIIARKSWPDIIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQPGNILQVV
 EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVVKAYKSNGEEINP

Table 71: Comparative Sequences relating to SAG1333

DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVF MAYITDLEKAGKKVSVPPNNPK
IYVTMVMVNETTITQNDGTHS1IKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIH
KKQLHQFTAIPMRNYGKPSNSTTVKS

SEQ ID NO. 7121

STRAIN 1169NT frame: 1

QGVQVIGVNDFHGALDNTGTANMPDGKVNAGTAQQLDAYMDAQQDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKNFNAMNVEYGTGLNHEFDEGLAEYNRIVTGKAPAD
SNINNITKSYPHEAAKQEIVVANVIDKVNKQI PYNWKPYAIKNIPVNNKSVNVGFIGIVT
KDIPLNLVRKNEYEQYFLDEAETIVKYAKELQAKNVKAIUVALAHVPATSKDDIAEGEEAEM
MMKKVNLFPENSVDIVFAGHNHQYTNGLGVGKTRIVQALSGQKAYADVRGLDQDFIET
ETPSAKVIAVAPGKKTGSADIQAVIDQANTIVKQVTEAKIGTAEVSMITRSVDQDNVSP
VGSLITEAQLAIAKSWPDIQAMTNNNGGIRADLLIKPDGITTWGAAQAVQPFQGNILQVV
EITGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVF MAYITDLEKAGKKVSVPPNNPKI
YVTMVMVNETITQNDGTHS1IKKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIH
KKQLHQFTAIPMRNYGKPSNSTTVKS

SEQ ID NO. 7122

STRAIN JM9130013 frame: 2

GVQVIGVNDFHGALDNTGTANMPDGKVNAGTAQQLDAYMDAQQDFKQTNPNGESIRVQ
AGDMVGASPANSGLLQDEPTVKFTFNAMNVEYGTGLNHEFDEGLAEYNRIVTGKAPADSN
INNITKSYPHEAAKQEIVVANVIDKVNKQI PYNWKPYTIKNIPVNNKSVNVGFIGIVTKD
IPLNLVRKNEYEQYFLDEAETIVKYAKELQAKNVKAIUVALAHVPATSKDDIAEGEEAEMM
KKVNQLFPENSVDIVFAGHNHQYTNGLGVGKTRIVQALSGQKAYADVRGLDQDFIET
PSAKVIAVAPGKKTGSADIQAVIDQANTIVKQVTEAKIGTAEVSMITRSVDQDNVSPVG
SLITEAQLAIAKSWPDIQAMTNNNGGIRADLLIKPDGITTWGAAQAVQPFQGNILQVVEI
TGRDLYKALNEQYDQKQNFFLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGEEINPD
YKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVF MAYITDLEKAGKKVSVPPNNPKIY
TMKVMVNETITQNDGTHS1IEKLYLDRQGNIVAQEIVSDTLNQTKSKSTKINPVTTIHKKQ
LHQFTAIPMRNYGKPSNSTTVKS

Pretty of: /biotmp/msa237615.2{*} May 14, 2003 03:22 ..

	1	50
msa237615.2{328_1169NT}	-----	-----qv gvqvigvndf HGALDNTGTA
msa237615.2{328_2603}	mkkkiilkss vlgvagtsi mfssvfaDqv	gvqvigvndf HGALDNTGTA
msa237615.2{328_A909}	-----	-----vndf HGALDNTGTA
msa237615.2{328_M732}	-----	-----qv gvqvigvndf HGALDNTGTA
msa237615.2{328_COH1}	-----	-----qv gvqvigvndf HGALDNTGTA
msa237615.2{328_M781}	-----	-----qv gvqvigvndf HGALDNTGTA
msa237615.2{328_H36B}	-----	-----qv gvqvigvndf HGALDNTGTA
msa237615.2{328_JM9130013}	-----	-----qv gvqvigvndf HGALDNTGTA
msa237615.2{328_18RS21}	-----	-----Dqv gvqvigvndf HGALDNTGTA
msa237615.2{328_090}	-----	-----v gvqvigvndf HGALDNTGTA
msa237615.2{328_CJB110}	-----	-----Dqv gvqvigvndf HGALDNTGTA
Consensus	*****	*****
	51	100
msa237615.2{328_1169NT}	GTAQQQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA	
msa237615.2{328_2603}	GTAQQQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA	
msa237615.2{328_A909}	GMPDGKVtNA GTAQQQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA	
msa237615.2{328_M732}	GMPDGKVtNA GTAQQQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA	
msa237615.2{328_COH1}	GMPDGKVtNA GTAQQQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA	
msa237615.2{328_M781}	GMPDGKVtNA GTAQQQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA	
msa237615.2{328_H36B}	GMPDGKVtNA GTAQQQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA	
msa237615.2{328_JM9130013}	GMPDGKVtNA GTAQQQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA	
msa237615.2{328_18RS21}	GMPDGKVtNA GTAQQQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA	
msa237615.2{328_090}	GMPDGKVtNA GTAQQQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA	
msa237615.2{328_CJB110}	GMPDGKVtNA GTAQQQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA	
Consensus	*****	*****
	101	150
msa237615.2{328_1169NT}	NSGLLQDEPT VKnFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN	
msa237615.2{328_2603}	NSGLLQDEPT VKnFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN	
msa237615.2{328_A909}	NSGLLQDEPT VktFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN	
msa237615.2{328_M732}	NSGLLQDEPT VktFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN	
msa237615.2{328_COH1}	NSGLLQDEPT VktFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN	
msa237615.2{328_M781}	NSGLLQDEPT VktFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN	
msa237615.2{328_H36B}	NSGLLQDEPT VktFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN	
msa237615.2{328_JM9130013}	NSGLLQDEPT VktFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN	
msa237615.2{328_18RS21}	NSGLLQDEPT VktFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN	
msa237615.2{328_090}	NSGLLQDEPT VktFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN	
msa237615.2{328_CJB110}	NSGLLQDEPT VktFNAMNVE YGTLGNHEFD EGLAEYNRIV TGKAPAPDSN	
Consensus	*****	*****
	151	200
msa237615.2{328_1169NT}	INNITKSYPH EAAKQEIVVA NVIDKVNKQI PYNWKPYAIK NIPVNNKSVN	
msa237615.2{328_2603}	INNITKSYPH EAAKQEIVVA NVIDKVNKQI PYNWKPYAIK NIPVNNKSVN	
msa237615.2{328_A909}	INNITKSYPH EAAKQEIVVA NVIDKVNKQI PYNWKPYAIK NIPVNNKSVN	
msa237615.2{328_M732}	INNITKSYPH EAAKQEIVVA NVIDKVNKQI PYNWKPYAIK NIPVNNKSVN	
msa237615.2{328_COH1}	INNITKSYPH EAAKQEIVVA NVIDKVNKQI PYNWKPYAIK NIPVNNKSVN	
msa237615.2{328_M781}	INNITKSYPH EAAKQEIVVA NVIDKVNKQI PYNWKPYAIK NIPVNNKSVN	

Table 71: Comparative Sequences relating to SAG1333

msa237615.2{328_H36B}	INNITKSYPH	EEAKQEIVVA	NVIDKVNQKI	PYNWKPYTIK	NIPVNNKSVN
msa237615.2{328_JM9130013}	INNITKSYPH	EEAKQEIVVA	NVIDKVNQKI	PYNWKPYTIK	NIPVNNKSVN
msa237615.2{328_18RS21}	INNITKSYPH	EEAKQEIVVA	NVIDKVNQKI	PYNWKPYTIK	NIPVNNKSVN
msa237615.2{328_090}	INNITKSYPH	EEAKQEIVVA	NVIDKVNQKI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_CJB110}	INNITKSYPH	EEAKQEIVVA	NVIDKVNQKI	PYNWKPYaIK	NIPVNNKSVN
Consensus	*****	*****	*****	*****	*****
	201			250	
msa237615.2{328_1169NT}	VGFFIGIVTKD	I PNVLVRKNY	E Q Y E F L D E A E	T I V K Y A K E L Q	A K N V K A I V V L
msa237615.2{328_2603}	VGFFIGIVTKD	I PNVLVRKNY	E Q Y E F L D E A E	T I V K Y A K E L Q	A K N V K A I V V L
msa237615.2{328_A909}	VGFFIGIVTKD	I PNVLVRKNY	E Q Y E F L D E A E	T I V K Y A K E L Q	A K N V K A I V V L
msa237615.2{328_M732}	VGFFIGIVTKD	I PNVLVRKNY	E Q Y E F L D E A E	T I V K Y A K E L Q	A K N V K A I V V L
msa237615.2{328_COH1}	VGFFIGIVTKD	I PNVLVRKNY	E Q Y E F L D E A E	T I V K Y A K E L Q	A K N V K A I V V L
msa237615.2{328_M781}	VGFFIGIVTKD	I PNVLVRKNY	E Q Y E F L D E A E	T I V K Y A K E L Q	A K N V K A I V V L
msa237615.2{328_H36B}	VGFFIGIVTKD	I PNVLVRKNY	E Q Y E F L D E A E	T I V K Y A K E L Q	A K N V K A I V V L
msa237615.2{328_JM9130013}	VGFFIGIVTKD	I PNVLVRKNY	E Q Y E F L D E A E	T I V K Y A K E L Q	A K N V K A I V V L
msa237615.2{328_18RS21}	VGFFIGIVTKD	I PNVLVRKNY	E Q Y E F L D E A E	T I V K Y A K E L Q	A K N V K A I V V L
msa237615.2{328_090}	VGFFIGIVTKD	I PNVLVRKNY	E Q Y E F L D E A E	T I V K Y A K E L Q	A K N V K A I V V L
msa237615.2{328_CJB110}	VGFFIGIVTKD	I PNVLVRKNY	E Q Y E F L D E A E	T I V K Y A K E L Q	A K N V K A I V V L
Consensus	*****	*****	*****	*****	*****
	251			300	
msa237615.2{328_1169NT}	AHPATSKnD	I A E G E A A E M M	K K V N Q L F P E N	S D I V F A G H N	H Q Y T N G L V G K
msa237615.2{328_2603}	AHPATSKnD	I A E G E A A E M M	K K V N Q L F P E N	S D I V F A G H N	H Q Y T N G L V G K
msa237615.2{328_A909}	AHPATSKdD	I A E G E A A E M M	K K V N Q L F P E N	S D I V F A G H N	H Q Y T N G L V G K
msa237615.2{328_M732}	AHPATSKdD	I A E G E A A E M M	K K V N Q L F P E N	S D I V F A G H N	H Q Y T N G L V G K
msa237615.2{328_COH1}	AHPATSKdD	I A E G E A A E M M	K K V N Q L F P E N	S D I V F A G H N	H Q Y T N G L V G K
msa237615.2{328_M781}	AHPATSKdD	I A E G E A A E M M	K K V N Q L F P E N	S D I V F A G H N	H Q Y T N G L V G K
msa237615.2{328_H36B}	AHPATSKdD	I A E G E A A E M M	K K V N Q L F P E N	S D I V F A G H N	H Q Y T N G L V G K
msa237615.2{328_JM9130013}	AHPATSKdD	I A E G E A A E M M	K K V N Q L F P E N	S D I V F A G H N	H Q Y T N G L V G K
msa237615.2{328_18RS21}	AHPATSKdD	I A E G E A A E M M	K K V N Q L F P E N	S D I V F A G H N	H Q Y T N G L V G K
msa237615.2{328_090}	AHPATSKdD	I A E G E A A E M M	K K V N Q L F P E N	S D I V F A G H N	H Q Y T N G L V G K
msa237615.2{328_CJB110}	AHPATSKdD	I A E G E A A E M M	K K V N Q L F P E N	S D I V F A G H N	H Q Y T N G L V G K
Consensus	*****	*****	*****	*****	*****
	301			350	
msa237615.2{328_1169NT}	TRIVQALSQG	K A Y A D V R G V L	D T D T Q D F I E T	P S A K V I A V A P	G K K T G S A D I Q
msa237615.2{328_2603}	TRIVQALSQG	K A Y A D V R G V L	D T D T Q D F I E T	P S A K V I A V A P	G K K T G S A D I Q
msa237615.2{328_A909}	TRIVQALSQG	K A Y A D V R G V L	D T D T Q D F I E T	P S A K V I A V A P	G K K T G S A D I Q
msa237615.2{328_M732}	TRIVQALSQG	K A Y A D V R G V L	D T D T Q D F I E T	P S A K V I A V A P	G K K T G S A D I Q
msa237615.2{328_COH1}	TRIVQALSQG	K A Y A D V R G V L	D T D T Q D F I E T	P S A K V I A V A P	G K K T G S A D I Q
msa237615.2{328_M781}	TRIVQALSQG	K A Y A D V R G V L	D T D T Q D F I E T	P S A K V I A V A P	G K K T G S A D I Q
msa237615.2{328_H36B}	TRIVQALSQG	K A Y A D V R G V L	D T D T Q D F I E T	P S A K V I A V A P	G K K T G S A D I Q
msa237615.2{328_JM9130013}	TRIVQALSQG	K A Y A D V R G V L	D T D T Q D F I E T	P S A K V I A V A P	G K K T G S A D I Q
msa237615.2{328_18RS21}	TRIVQALSQG	K A Y A D V R G V L	D T D T Q D F I E T	P S A K V i A V A P	G K K T G S A D I Q
msa237615.2{328_090}	TRIVQALSQG	K A Y A D V R G V L	D T D T Q D F I E T	P S A K V v A V A P	G K K T G S A D I Q
msa237615.2{328_CJB110}	TRIVQALSQG	K A Y A D V R G V L	D T D T Q D F I E T	P S A K V v A V A P	G K K T G S A D I Q
Consensus	*****	*****	*****	*****	*****
	351			400	
msa237615.2{328_1169NT}	AIVDQANTIV	K Q V T E A K I G T	A E V S v M I T R S	V D Q D N V S P V G	S L I T E A Q L A I
msa237615.2{328_2603}	AIVDQANTIV	K Q V T E A K I G T	A E V S v M I T R S	V D Q D N V S P V G	S L I T E A Q L A I
msa237615.2{328_A909}	AIVDQANTIV	K Q V T E A K I G T	A E V S g M I T R S	V D Q D N V S P V G	S L I T E A Q L A I
msa237615.2{328_M732}	AIVDQANTIV	K Q V T E A K I G T	A E V S g M I T R S	V D Q D N V S P V G	S L I T E A Q L A I
msa237615.2{328_COH1}	AIVDQANTIV	K Q V T E A K I G T	A E V S g M I T R S	V D Q D N V S P V G	S L I T E A Q L A I
msa237615.2{328_M781}	AIVDQANTIV	K Q V T E A K I G T	A E V S g M I T R S	V D Q D N V S P V G	S L I T E A Q L A I
msa237615.2{328_H36B}	AIVDQANTIV	K Q V T E A K I G T	A E V S g M I T R S	V D Q D N V S P V G	S L I T E A Q L A I
msa237615.2{328_JM9130013}	AIVDQANTIV	K Q V T E A K I G T	A E V S g M I T R S	V D Q D N V S P V G	S L I T E A Q L A I
msa237615.2{328_18RS21}	AIVDQANTIV	K Q V T E A K I G T	A E V S g M I T R S	V D Q D N V S P V G	S L I T E A Q L A I
msa237615.2{328_090}	AIVDQANTIV	K Q V T E A K I G T	A E V S g M I T R S	V D Q D N V S P V G	S L I T E A Q L A I
msa237615.2{328_CJB110}	AIVDQANTIV	K Q V T E A K I G T	A E V S g M I T R S	V D Q D N V S P V G	S L I T E A Q L A I
Consensus	*****	*****	*****	*****	*****
	401			450	
msa237615.2{328_1169NT}	ARKSWPDIDF	A M T N N G G I R A	D L L I K P D G T I	T W G A A Q A V Q P	F G N I L Q V V E I
msa237615.2{328_2603}	ARKSWPDIDF	A M T N N G G I R A	D L L I K P D G T I	T W G A A Q A V Q P	F G N I L Q V V E I
msa237615.2{328_A909}	ARKSWPDIDF	A M T N N G G I R A	D L L I K P D G T I	T W G A A Q A V Q P	F G N I L Q V V E I
msa237615.2{328_M732}	ARKSWPDIDF	A M T N N G G I R A	D L L I K P D G T I	T W G A A Q A V Q P	F G N I L Q V V E I
msa237615.2{328_COH1}	ARKSWPDIDF	A M T N N G G I R A	D L L I K P D G T I	T W G A A Q A V Q P	F G N I L Q V V E I
msa237615.2{328_M781}	ARKSWPDIDF	A M T N N G G I R A	D L L I K P D G T I	T W G A A Q A V Q P	F G N I L Q V V E I
msa237615.2{328_H36B}	ARKSWPDIDF	A M T N N G G I R A	D L L I K P D G T I	T W G A A Q A V Q P	F G N I L Q V V E I
msa237615.2{328_JM9130013}	ARKSWPDIDF	A M T N N G G I R A	D L L I K P D G T I	T W G A A Q A V Q P	F G N I L Q V V E I
msa237615.2{328_18RS21}	ARKSWPDIDF	A M T N N G G I R A	D L L I K P D G T I	T W G A A Q A V Q P	F G N I L Q V V E I
msa237615.2{328_090}	ARKSWPDIDF	A M T N N G G I R A	D L L I K P D G T I	T W G A A Q A V Q P	F G N I L Q V V E I
msa237615.2{328_CJB110}	ARKSWPDIDF	A M T N N G G I R A	D L L I K P D G T I	T W G A A Q A V Q P	F G N I L Q V V E I
Consensus	*****	*****	*****	*****	*****
	451			500	
msa237615.2{328_1169NT}	T G R D L Y K A L N	E Q Y D Q K Q N F F	L Q I A G L R Y T Y	T D N K E G G E E T	P F K V V K A Y K S
msa237615.2{328_2603}	T G R D L Y K A L N	E Q Y D Q K Q N F F	L Q I A G L R Y T Y	T D N K E G G E E T	P F K V V K A Y K S
msa237615.2{328_A909}	T G R D L Y K A L N	E Q Y D Q K Q N F F	L Q I A G L R Y T Y	T D N K E G G E E T	P F K V V K A Y K S
msa237615.2{328_M732}	T G R D L Y K A L N	E Q Y D Q K Q N F F	L Q I A G L R Y T Y	T D N K E G G E E T	P F K V V K A Y K S
msa237615.2{328_COH1}	T G R D L Y K A L N	E Q Y D Q K Q N F F	L Q I A G L R Y T Y	T D N K E G G E E T	P F K V V K A Y K S

Table 71: Comparative Sequences relating to SAG1333

msa237615.2{328_M781}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_H36B}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_JM9130013}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_18RS21}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_090}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_CJB110}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
Consensus	*****	*****	*****	*****	*****
	501			550	
msa237615.2{328_1169NT}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAVIT
msa237615.2{328_2603}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAVIT
msa237615.2{328_A909}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAVIT
msa237615.2{328_M732}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAVIT
msa237615.2{328_COH1}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAVIT
msa237615.2{328_M781}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAVIT
msa237615.2{328_H36B}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAVIT
msa237615.2{328_JM9130013}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAVIT
msa237615.2{328_18RS21}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAVIT
msa237615.2{328_090}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAVIT
msa237615.2{328_CJB110}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAVIT
Consensus	*****	*****	*****	*****	*****
	551			600	
msa237615.2{328_1169NT}	DLEKAGKKVS	vPNNNPKPIYY	TMKMVNETIT	QNDGThSIIk	KLYLDRQGNi
msa237615.2{328_2603}	DLEKAGKKVS	vPNNKPKIYY	TMKMVNETIT	QNDGThSIIk	KLYLDRQGNi
msa237615.2{328_A909}	DLEKAGKKVS	vPNNKPKIYY	TMKMVNETIT	QNDGTsIIk	KLYLDRQGNi
msa237615.2{328_M732}	DLEKAGKKVS	iPNNNPKPIYY	TMKMVNETIT	QNDGTsIIk	KLYLDRQGNi
msa237615.2{328_COH1}	DLEKAGKKVS	iPNNNPKPIYY	TMKMVNETIT	QNDGTsIIk	KLYLDRQGNi
msa237615.2{328_M781}	DLEKAGKKVS	iPNNNPKPIYY	TMKMVNETIT	QNDGTsIIk	KLYLDRQGNi
msa237615.2{328_H36B}	DLEKAGKKVS	vPNNKPKIYY	TMKMVNETIT	QNDGTsIIk	KLYLDRQGNi
msa237615.2{328_JM9130013}	DLEKAGKKVS	vPNNKPKIYY	TMKMVNETIT	QNDGTsIIk	KLYLDRQGNi
msa237615.2{328_18RS21}	DLEKAGKKVS	vPNNKPKIYY	TMKMVNETIT	QNDGTsIIk	KLYLDRQGNi
msa237615.2{328_090}	DLEKAGKKVS	vPNNKPKIYY	TMKMVNETIT	QNDGTsIIk	KLYLDRQGNi
msa237615.2{328_CJB110}	DLEKAGKKVS	vPNNKPKIYY	TMKMVNETIT	QNDGTsIIk	KLYLDRQGNi
Consensus	*****	*****	*****	*****	*****
	601			650	
msa237615.2{328_1169NT}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_2603}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_A909}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_M732}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_COH1}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_M781}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_H36B}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_JM9130013}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_18RS21}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_090}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_CJB110}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
Consensus	*****	*****	*****	*****	*****
	651			690	
msa237615.2{328_1169NT}	TVKS-----	-----	-----	-----	-----
msa237615.2{328_2603}	TVKSKQlpkt	nseygqsfilm	svfgvgligi	alntkkhmk	-----
msa237615.2{328_A909}	TVKSKQ-----	-----	-----	-----	-----
msa237615.2{328_M732}	TVKSKQ-----	-----	-----	-----	-----
msa237615.2{328_COH1}	TVKS-----	-----	-----	-----	-----
msa237615.2{328_M781}	TVKS-----	-----	-----	-----	-----
msa237615.2{328_H36B}	TVKS-----	-----	-----	-----	-----
msa237615.2{328_JM9130013}	TVKS-----	-----	-----	-----	-----
msa237615.2{328_18RS21}	TVKS-----	-----	-----	-----	-----
msa237615.2{328_090}	TVKSQ-----	-----	-----	-----	-----
msa237615.2{328_CJB110}	TVKS-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****

Table 72: Comparative Sequences relating to SAG0941**SEQ ID NO. 7201****STRAIN 2603**

ATGAATAAAACCGCTAAAAATCGTTGCAACACTTGGCTCTCGGGTTGAATTCCGTGGTG
 GTAAAGAAGTTGGTGAGTCGGATACTGGGTGAAAGCCTTGACGTAGAACGTTCAACAG
 AAAAAATTGCTCAATTGATTAAAGAAGGTGCTAACGTTTCCGTTCAACTTCTCACATG
 GAGATCATGCTGAGCAAGGGCTGAAAGCAGGTTGCTACTGTTGCTAAAGCAGAACGATTG
 GACAAAAAGTTGGCTTCCCTGATGACTTAAGGACCTGAAATTGCTACAGAACCTTTTG
 AAGATGGTGAGATTCCATTGATATAACACAGGTACAAAATTACGTGTTGCTACTAACG
 AAGGTATCAAATCAAACCTGGAAAGTGAATTGCAATTGATGTTGCTGGGACTTGACATCT
 TTGATGACGTTGAAAGTGGTAAGCAATTCTTGTGATGATGTTAAACTTAGGTCTTACTG
 TGTGTCAGTAAAGGATAAAGACACTCGTGAATTGAGTGGTAAACTTAGGTCTTACTG
 TTGGTAACACAAAAGGTGTAACATCCCATACTAAATTCTTCCAGCAGCTTGAG
 AACGCATAATGCTGATATGCCATTGGACTTGGACATTGAGCAAGGACTTAACCTTATTGCTAICT
 CATTGTCAGCTACTGCTAAAGATGTTAATGAGTTGCTGCTATTGTAAGAAACTGGsm
 ATGGACACGTTAAGTTGCTAAATTGAAAATCAACAAGGTATCGATAATTGATG
 AGAATTATCGAAGCAGCAGCTGTTATTGATGTTGCTGGTATATGGGTATCGAAGTTC
 CATTGAAATGGTCCAGTTACAAAAAAATGATCATTAACGTTAAAGTAAATGAGCTGGTA
 AACGAGTTTACAGCAACAAATATGCTGAAACAAATGACTGATAACACAGTGCAGACTC
 GTTCAAGAAGTACTGATGTCATGCTGTTGATGTTGACTGATGCTACAAATGCTT
 CAGTGAGTCAGCTAAAGGTTAACCCAGTTGAGTCAGTTGCTACAATGGCTACTATTTG
 ATAACAAATGCTCAACATTACTCAATGAGTATTGTCGTTAGACTCATGCAATTCCCAC
 GTAATAACAAAAGTATGTTGCTATTGCACTGCGGTTAAAGATGCAACACACTCAATGGATA
 TCAACATTGTTGAAACAAATGCTGAAACAGGTAAATACAGCTGCTGCAATTCTAAATTCC
 GTTCAAGATGCAAGCATTGGCTTACATTGATGAGAAAAGTACAACGTTCAATTGATG
 TTAACCTGGGTGTTATCCCTGCTTGCAGACAAACCAGCATCTACAGATGATAATTGTTG
 AGGTTGCAAGAACCTGTTAGCAACTGAGCAGGATTGAGTCAAGGCGATAATATCGTTA
 TCGTTGCAAGGTGTTCTGAGGTGAACTAACACATGCGTGTGACTGTTA
 AA

SEQ ID NO. 7202**STRAIN 090****AATAAACCGCTAAAAATCGTTGCAACACT**

TGGTCTCGCGTAGAAGTGGTAAGAAGTTGGTGAAGTCTGGAT
 ACTGGGTGAAAGCCTTGACCTGAGCTAACGTTTCAGCAGAAAAAAATTGCTCAA
 TTGATTAAGAAGGTGCTAACGTTTCCGTTCAACTTCTCACATGGAGA
 TCATGCTGAGCAAGGAGCTCTATGGCTACTGTTGCTAAAGCAGAACGAGA
 TTGAGGACAAAAGTTGGCTTCCCTGATGACTAAAGGACCTGAAATT
 CGTACAGAACTTTGAAAGATGGTTGAGTTCAATTGATGAGCTGGTAAAG
 TACAGAAATTACGTGTTGCTACTAACGCAAGGTATCAAATCAACTCCAGAAC
 TGATGAGCTGATGTTGCTGAGCTGACATTTGATGACGTTGAA
 GTTGGTAAGCAATCCTTGTGATGATGTTAAACTAGGTCTTACTGTTG
 TGCAAAAGATAAAAGACACTGAGTAAAGTGGAGTGTGAGAATGATG
 GCCTTATTGGTAAACAAAAAGTGTAAACATCCCTTATACTAAATTCT
 TTCCCAgCACTGAGAACCGGATAATGCTGATATCCGTTTGGACTTGA
 GCAAGGACTTAACTTTATTGCTATCTCATTTGACTGCTAACAGATG
 TTAATGAGTTGCTGCTATTGTAAGGAAACTGGCAATGGACATGTTAAG
 TTGTTGCTAAATTGAAACATCAACAGGTATCGATAATTGATGAGAT
 TATCGAGCAGCACATGGTATTATGATGCTCGTGTGATAATGGGTATCG
 AAGTTCCATTGAAATGGTTCCAGTTTACCAAAAAATGATCATTACTAA
 GTTAATGAGCTGTTGAGTAAAGCAGTTATTACAGCAACAAATGCTTGAAC
 AATGACTGATAACCCACGTGGACTCGITCAGAAAGTATCTGATGTCCTCA
 ATGCTGTTATTGATGGTACTGATGCTACATGCTTCAAGGTGAGTCAGCT
 AATGGTAAATACCCAGTTGACTCGTACATGCTACAAATGGCTACTATTGATAAA
 AATGCTCAACATTACTCAATGAGTATTGCTCGCTTAGACTCATCTGCA
 TCCCACTGTAATAACAAAATGATGTTATTGATCTGCGGTTAACAGTGA
 ACACACTCAATGGATATCAAACATTGTTGACAATTACTGAAACAGGAA
 TACAGCTGTCGCAATTCTCAATTCCGTCAGATGCGAGACATTGGCTG
 TTACATTGATGAAAAAGTACAACAGTCTATTGATGATTAACGGGTGTT
 ATCCCTGTCCTGAGACAAACCAGCATCTACAGATGATAATTGTTGAGGT
 TGAGCAAGCTGTTAGCAAGGACTGTTGAGTCAAGGCGATAATA
 TCGTTATGTTGAGGTGTTCTGAGGTACAGGTGAACTAACACAAATG
 CGTTCGTACTGTTAAA

SEQ ID NO. 7203**STRAIN A909**

AATAAACCGCTAAAAATCGTTGCAACACTTGGTC
 CTGCGCTGAAATCCGGTAGAAGAAGTGTGGAGCTCTGGATACTGG
 GGTAAAGGCTTGTACGTAGAAAGCTTCAGCAGAAAAAAATTGCTCAATTGAT
 TAAAGAAGGTGCTAACGTTTCCGTTCAACTTCTCACATGGAGATCATG
 CTGAGCAAGGAGCTGCTATGGCTACTGTTGCTAAAGCAGAACGAGATTGCA
 GGACAAAAAGTTGGCTTCCCTGATGACTAAAGGACCTGAAATTGCTAC
 AGAACCTTTGAAAGATGGTGCAGATTCTTCAATTGATACACAGGTACAA
 AATTACGTGTTGCTACTAACGAGGTATCAAATCAACTCCAGAACGTTGATT
 GCATTTGAAATGTTGCTGGTGGACTTGACATTTGATGACGTTGAGAATTG
 TAAGCAATTCTTGTGATGATGTTGAAACTAGGTCTTACTGTTTGC
 AAAGATAAAAGACACTGCTGAAATTGAGTGTGTTGAGAATGATGGCCTT
 ATTGGTAAACAAAAAGGTGTAACACATCCCTTATACTAAATTCTTCCC
 AGCAGTTGCAAGAACCGGATAATGCTGATATCCGTTTGGACTTGAGCAAG
 GACTTAACTTAACTGCTATCTCATTTGACTGCTAACAGTGTAAAT
 GAAGTTGCTGCTATTGTAAGGAAACTGGCAATGGACACGTTAAGGTTG
 TGCTAAATTGAAACAAACAGGTATCGATAATTGATGAGATTATCG
 AACGACCAAGATGGTATTATGATGCTCGTGTGATAATTGGTATCGAAGT
 CCATTGAAATGGTCCAGTTACCAAAAAATGATCATTACTAAAGTTAA

Table 72: Comparative Sequences relating to SAG0941

TGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGAACAACTGA
 CTGATAAACCAACGTGCGACTGTTAGAAGTATCTGATGTCCTCAATGCT
 GTTATTGATGGTACTGATGCTACAATGCTTCAAGTGAGTCAGCTAATGG
 TAAATACCCAGTGTAGTCAGTACATGGCTACTATTTGATAAAATG
 CTCAAACATTACTCAATGAGTATGGTCGTTAGACTCATCTGCATTCCC
 CGTATAAACAAACTGATGTTATTGATCTGCCGTTAAAGATGCAACACA
 CTCATGGATATCAAACCTGTTGTAACAATTACTGAAACAGGTAAATACAG
 CTGCTGCCATTCTAAATCCGTCAGATGCAGACATTTGGCTTAC
 TTGATGAAAAGTACAACGTTCAATTGATGATTAACGGGGTGTATCCC
 TGTCITGCAGAACACCAGCATCACAGTATGTTGAGGTTGCAG
 AACCTGTAGCACTTGAAGCAGGATTGTTGAATCAGGCATAATATCGT
 ATCGTGCAGGTGTTCTGTAGGTACAGGTGGAACTAACACAATGCGTGT
 TCGTACTGTTAAA

SEQ ID NO. 7204

STRAIN H36B

AATAAACCGCTAAAAATCGTGCAC
 ACTTGGTCTGGGTTGAATTGGTGGTGAAGAAGTTGGTGAGTC
 GATACTGGGGTGAAGCCTGACGTTAGAACGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAGAAGGTGCTAACGTTTCAGTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGAGGACAAAAGTGGCTTCTCTTGTATGACTAAAGGACCTGAA
 ATTGCTACAGAACCTTGGATGGTCAAGTTCATTGATGACATTTGATGACGTT
 AGGTACACAAATTACGTGTTGCTACTAACGAAAGGTATCAAATCAACTCCAG
 AAGTGATTGATGTTGAGTGTCTGGTGGACTTGACATTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTGT
 GTTGGTAAAGGAAACTTGGTGAAGTGTGAGTACTGTTGAGAATG
 ATGGCCTTATTGCTAAACAAAAGGTGTAACATCCTTATACTAAAATT
 CCTTCCAGCACTTGCAGAACCGGATAATGCTGATATCGTTGGACT
 TGAGCAAGGAAACTTGGTACATGTTGATGTTGAGTGTGAAACTGGGGT
 ATGTTAATGAGTTGCTGTTATTGTAAGGAAACTGGCAATGCTAAAG
 AAGTTGTTGCTAAATTGAAATCAACAAAGGTATCGATAATATTGATGA
 GATTATCGAACGAGATGGTATTATGCTGTTGGTGTATGGGTA
 TCGAAGTTCATTGAAATGGTCCAGTTACCAAAATGATCATTACT
 AAAGTTAATGCAAGCTGGTAAAGCAGTTATACAGCAACAAATATGCTG
 AACATGACTGATAAACCAACCGTGGACTCCTCAGAAGTATCTGATGCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTCAAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTTACATGGCTACTATTGA
 TAAAATGCTCAAACATTACTCAATGAGTATGGTCGTTAGACTCATCTG
 CATTCCCACGTAATAACAAAACGTGATGTTATTGCACTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACITGTTGTAACAAATTACTGAAACAGG
 TAATACAGCTCGGCCATTCTAAATCCGTCAGATGCAGACATTTGG
 CTGTTACATTGATGAAAAGTACAACGTTCAATTGATGATGTTAACCTGGGGT
 GTTACCTGCTTGCAGAACACCAGCATCTACAGATGATATGTTGA
 GGTGCAAGACGTGAGCACTTGAAGCAGGATTGTTGAATCAGGCATA
 ATATCGTATCGTGCAGGTGTTCTGTAGGTACAGGTGGAACAAACACA
 ATGCGTGTTCGTTACTGTTAAA

SEQ ID NO. 7205

STRAIN 18RS21

AATAAACCGCTAAAAATCGTGCAC
 ACTTGGTCTGGGTTGAATTGGTGGTGAAGAAGTTGGTGAGTC
 GATACTGGGGTGAAGCCTGACGTTAGAACGCTTCAGCAGAAAAAATTGCT
 CAATTGATTAAGAAGGTGCTAACGTTTCAGTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTGTAAGCAGAAG
 AGATTGAGGACAAAAGTGGCTTCTCTTGTATGACTAAAGGACCTGAA
 ATTGCTACAGAACCTTGGATGGTCAAGTTCATTGATGACATTTGATGACGTT
 AGGTACACAAATTACGTGTTGCTACTAACGAAAGGTATCAAATCAACTCCAG
 AAGTGATTGATGTTGAGTGTCTGGTGGACTTGACATTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTTGATGATGGTAAACTAGGTCTTACTGT
 GTTGGTAAAGGAAACTTGGTGAAGTGTGAGTACTGTTGAGAATG
 ATGGCCTTATTGCTAAACAAAAGGTGTAACATCCTTATACTAAAATT
 CCTTCCAGCACTTGCAGAACCGGATAATGCTGATATCGTTGGACT
 TGAGCAAGGAAACTTGGTACATGTTGATGTTGAGTGTGAAACTGGGGT
 ATGTTAATGAGTTGCTGTTATTGTAAGGAAACTGGCAATGACACGTT
 AAGTTGTTGCTAAATTGAAATCAACAAAGGTATCGATAATATTGATGA
 GATTATCGAACGAGATGGTATTATGCTGTTGGTGTATGGGTA
 TCGAAGTTCATTGAAATGGTCCAGTTACCAAAATGATCATTACT
 AAAGTTAATGCAAGCTGGTAAAGCAGTTATACAGCAACAAATATGCTG
 AACATGACTGATAAACCAACCGTGGACTCCTCAGAAGTATCTGATGCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTCAAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTTACATGGCTACTATTGA
 TAAAATGCTCAAACATTACTCAATGAGTATGGTCGTTAGACTCATCTG
 CATTCCCACGTAATAACAAAACGTGATGTTATTGCACTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACITGTTGTAACAAATTACTGAAACAGG
 TAATACAGCTCGGCCATTCTAAATCCGTCAGATGCAGACATTTGG
 CTGTTACATTGATGAAAAGTACAACGTTCAATTGATGATGTTAACCTGGGGT
 GTTACCTGCTTGCAGAACACCAGCATCTACAGATGATATGTTGA
 GGTGCAAGACGTGAGCACTTGAAGCAGGATTGTTGAATCAGGCATA
 ATATCGTATCGTGCAGGTGTTCTGTAGGTACAGGTGGAACAAACACA
 ATGCGTGTTCGTTACTGTTAAA

SEQ ID NO. 7206

Table 72: Comparative Sequences relating to SAG0941**STRAIN M732**

AATAAACCGCTAAAAATCGTTGCAAC
 ACTTGGTCCCTGCCGTAGAATTCCGTGGTGAAGAAGTTGGTAGCTG
 GATACTGGGGTGAAGCCTTGACGTAGAACGTTCACGAGAAAAATTGCT
 CAATTGATTAAGAAGGTGCTAACGTTTCGTTCAACTTCACATGG
 AGATCATGCTGAGCAAGGGACTCGTACTGTTCGTAAAGCAGAAAG
 AGATTGCAGGACAAAAGTTGGCTTCCCTCTTGATACTAAAGGACCTGAA
 ATTGTCACAGAACCTTTGAAGATGGTGCAGATTTCCATTATACAAAC
 AGGTACAAAATTACGTGTTGCTACTAACGCAAGGTATCAAATCAACTCCAG
 AAGTGTGGTACGTTGATGAGCTGGGACTTGTACATCTTGTGACGTT
 GAAGTTGGTAAAGCAAATCTTGTGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAGACACTCGTGAAGTTGAAGTAGTTGAGAAATG
 ATGGCCTTATTGTTAAACAAAAGGTAAACATCCCTTATACAAATTAAATT
 CCTTCCCAGCACTTGCAAGACCGCATAATGCTGATATCCGTTGGACT
 TGAGCAAGGACTTAACCTTATGCTATCTCATTGTACGTACTGCTAAAG
 ATGTTAATGAAAGTTGCTGCTATTGTAAGGAAACTGGCAATGGACACGTT
 AAGTTGTTGATGAAATTGAAACACTCGTGAATTTGAGTATGGTAAACTAGGTCTTACTGT
 GATTATCGAAGCAGCAGATGGTATTATGATGCTGTTGATGGTAA
 TCAGGAACTTCCATTGAAATGGTCCAGTTACCAAAAATGATCATTACT
 AAAGTTAATGCAAGCTGGTAAGCAGTTACAGCAACAAATATGCTTGA
 AACAACTGACTGATAACACCAGCTGCGACTCGTCAAGTATCTGATGCT
 TCAATGCTGTTATTGATGGTACTGATGCTAACATGCTTCAGGTGAGTC
 GCTAATGGTAAATACCCAGTTGAGTCAGTTGCTAACATGGTACTATTG
 TAAAGGCTTAACTACATTACTCAATGAGTATGGCTTACAGTCTCATCTG
 CATTCCCACGTAAATAACAAAACGTATGTTATTGATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACACTTGTGAACAATTACTGAAACAGG
 TAATACAGCTGGCCATTCTAAATTCCGTCCAGATGCAAGACATTGG
 CTGTTACATTGATGAAAGGAAACTACAGCTTACATTGATGATTAACGGGGT
 GTTATCCCTGTCCTTGCAGACAAACCCAGCATCTACAGATGATATGTTGA
 GGTTGCAGAACGTGTAAGCAGGACTTGTGAATCAGGGCATA
 ATATGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACAAACACA
 ATGCGTGTTCGACTGTTAAA

SEQ ID NO. 7207**STRAIN COH1**

AATAAACCGCTAAAAATCGTTGCAAC
 ACTTGGTCCCTGCCGTAGAATTCCGTGGTGAAGAAGTTGGTAGCTG
 GATACTGGGGTGAAGCCTTGACGTAGAACGTTCACGAGAAAAATTGCT
 CAATTGATTAAGAAGGTGCTAACGTTTCGTTCAACTTCACATGG
 AGATCATGCTGAGCAAGGGACTCGTACTGTTCGTAAAGCAGAAAG
 AGATTGCAGGACAAAAGTTGGCTTCCCTCTTGATACTAAAGGACCTGAA
 ATTGTCACAGAACCTTTGAAGATGGTGCAGATTTCCATTATACAAAC
 AGGTACAAAATTACGTGTTGCTACTAACGCAAGGTATCAAATCAACTCCAG
 AAGTGTGGTACGTTGATGAGCTGGGACTTGTACATCTTGTGACGTT
 GAAGTTGGTAAAGCAAATCTTGTGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAGACACTCGTGAATTGAGTAGTTGAGAAATG
 ATGGCCTTATTGTTAAACAAAAGGTAAACATCCCTTATACAAATTAAATT
 CCTTCCCAGCACTTGCAAGACCGCATAATGCTGATATCCGTTGGACT
 TGAGCAAGGACTTAACCTTATGCTATCTCATTGTTACGTACTGCTAAAG
 ATGTTAATGAAAGTTGCTGCTATTGTAAGGAAACTGGCAATGGACACGTT
 AAGTTGTTGCTAAATTGAAACACTCAACAGGTATGATAATATTGATG
 GATTATCGAAGCAGCAGATGGTATTATGATGCTGTTGATGGTAA
 TCAGGAACTTCCATTGAAATGGTCCAGTTACCAAAAATGATCATTACT
 AAAGTTAATGCAAGCTGGTAAGCAGTTACAGCAACAAATATGCTTGA
 AACAACTGACTGATAACACCAGCTGCGACTCGTCAAGTATCTGATGCT
 TCAATGCTGTTATTGATGGTACTGATGCTAACATGCTTCAGGTGAGTC
 GCTAATGGTAAATACCCAGTTGAGTCAGTTGCTAACATGGTACTATTG
 TAAAGGCTTAACTACATTACTCAATGAGTATGGCTTACAGTCTCATCTG
 CATTCCCACGTAAATAACAAAACGTATGTTATTGCTGTTGAGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACACTTGTGAACAATTACTGAAACAGG
 TAATACAGCTGGCCATTCTAAATTCCGTCCAGATGCAAGACATTGG
 CTGTTACATTGATGAAAGGAAACTACAGCTTACATTGATGATTAACGGGGT
 GTTATCCCTGTCCTTGCAGACAAACCCAGCATCTACAGATGATAATTGTTGA
 GGTTGCAGAACGTGTAAGCAGGACTTGTGAATCAGGGCATA
 ATATGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACAAACACA
 ATGCGTGTTCGACTGTTAAA

SEQ ID NO. 7208**STRAIN M781**

AATAAACCGCTAAAAATCGTTGCAAC
 ACTTGGTCCCTGCCGTAGAATTCCGTGGTGAAGAAGTTGGTAGCTG
 GATACTGGGGTGAAGCCTTGACGTAGAACGTTCACGAGAAAAATTGCT
 CAATTGATTAAGAAGGTGCTAACGTTTCGTTCAACTTCACATGG
 AGATCATGCTGAGCAAGGGACTCGTACTGTTCGTAAAGCAGAAAG
 AGATTGCAGGACAAAAGTTGGCTTCCCTCTTGATACTAAAGGACCTGAA
 ATTGTCACAGAACCTTTGAAGATGGTGCAGATTTCCATTATACAAAC
 AGGTACAAAATTACGTGTTGCTACTAACGCAAGGTATCAAATCAACTCCAG
 AAGTGTGGTACGTTGATGAGCTGGGACTTGTACATCTTGTGACGTT
 GAAGTTGGTAAAGCAAATCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAGACACTCGTGAATTGAGTAGTTGAGAAATG
 ATGGCCTTATTGTTAAACAAAAGGTAAACATCCCTTATACAAATTAAATT
 CCTTCCCAGCACTTGCAAGACACTCGTATCTGATATCCGTTGGACT
 TGAGCAAGGACTTAACCTTATGCTATCTCATTGTTACGTACTGCTAAAG

Table 72: Comparative Sequences relating to SAG0941

ATGTTAATGAAGTTCGTGCTTGTGAAGAAACTGGCAATGGCACACGTT
 AAGTTTGTCAAATTGAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTGATGCTCGTGGTATATGGGTA
 TCGAAGTTCCATTGAAATGGTCCAGTTACCAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAGCAGTTAACAGCAACAAATATGCTTGA
 AACATGACTGAAACCTGGCAGTCAGAAGTATCTGATGTC
 TCAATGCTGTTAATTGATGGTACTGATGCTAACATGCTTCAGGTGAGTC
 GCTAATGGTAATACCCAGTTGAGTCAGTCTGACAATGGCTACTATTGA
 TAAAAATGCTCAACATTACTCAATGAGTATGGTCCAGTAACTGGCT
 CATTCCCACGTTAACATGATGTTATTCATCTGCCGTTAAAGAT
 GCAACACACTCAATGGATATCAAACCTGTTGAACAATTACTGAAACAGG
 TAATACAGCTCGTCCATTCTAAGTTCGGTCCAGATGCAGACATTGGT
 CTGTTACATTGATGAAACCTGAGTCAGTCTGACAATGGCTACTATTGA
 GTTATCCCTGCTTGCAGACAAACAGCATCTACAGATGATAATGTTGA
 GGTGAGAAGCTGTAGCACTTGAAAGCAGGACTTGTGAATCAGGCGATA
 ATATCGTATCGTGCAGGTCTGTAGGTACAGGTGGAACAAACACA
 ATGCGTGTCTGACTGTTAAA

SEQ ID NO. 7209**STRAIN CJB110**

AATAAACCGTAAATCGTGCAC
 ACTTGGTCTGGGTTGAATTCGTGGTGAAGAAGTTGGTAGTC
 GATACTGGGGTGAAGCCTGACGTAAGGCTTCAGCAGAAAAAAATTGCT
 CAATTGATTAAGAAGGTGCTAACGTTCCGTTCAACTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGTACTGTTGCTAAAGCAGAAG
 AGATTGAGGACAAAAAGTGGCTTCTCTTGTACTAAAGGACCTGAA
 ATTGCTACAGAACCTTGTGAGTGGTAAACTGATGTTATTCATTACAAAC
 AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCTGAACTCCAG
 AAGTGAATGCTGATGAAATGTTGCTGGACTTGCACATCTTGATGACGTT
 GAAGTGTGTAAGCAAATCTTGTGATGGTAAACTAGGTCTTACTGT
 GTTGCAGAAAGATAAGACACTCGTGAATTGAAAGTAGTGTGAGAAATG
 ATGGCTTATGGTAAACAAAAGGTGTAACATCCCTTATACTAAAATT
 CCTTCCACGACTTGCAGAACGGGATATGCTGATATCCGTTGGACT
 TGAAACAAGGACTTAACCTTATGCTATCTCATTTGATGCTACTGCTAAAG
 ATGTTAATGAAGTTCGTGCTTGTGAAGAAACTGGCAATGGCACACGTT
 AAGTTGTGCTAAATTGAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTGCTCGTGGTATATGGGTA
 TCGAAGTTCCATTGAAATGGTCCAGTTACCAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAGCAGTTAACAGCAACAAATATGCTTGA
 AACATGACTGAAACCCACTGGCAGTCAGAAGTATCTGATGTC
 TCAATGCTGTTAATTGATGGTACTGATGCTAACATGCTTCAGGTGAGTC
 GCTAATGGTAATACCCAGTTGAGTCAGTCTGACAATGGCTACTATTGA
 TAAAAATGCTCAAACATTACTCAATGAGTATGGTCTTAACTGGCT
 CATTCCCACGTTAACAAACACTGATGTTATTCATCTGCCGTTAAAGAT
 GCAACACACTCAATGGATATCAAACCTGTTGAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCTTCAAAATCCGTCAGATGCAGACATTGGT
 CTGTTACATTGATGAAAGAAGTACAACGTTCAATTGATGATGTTAACTGGG
 GTTATCCCTGCTTGCAGACAAACAGCATCTACAGATGATAATGTTGA
 GGTGAGAAGCTGTAGCACTTGAAAGCAGGATTGTGAATCAGGCGATA
 ATATCGTATCGTGCAGGTCTGTAGGTACAGGTGGAACAAACACA
 ATGCGTGTCTGACTGTTAAA

SEQ ID NO. 7210**STRAIN 1169NT**

AATAAACCGTAAATCGTGCAC
 ACTTGGTCTGGGTTGAATTCGTGGTGAAGAAGTTGGTAGTC
 GATACTGGGGTGAAGCCTGACGTAAGGCTTCAGCAGAAAAAAATTGCT
 CAATTGATTAAGAAGGTGCTAACGTTCCGTTCAACTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGTACTGTTGCTAAAGCAGAAG
 AGATTGAGGACAAAAAGTGGCTTCTCTTGTACTAAAGGACCTGAA
 ATTGCTACAGAACCTTGTGAGTGGTCAAGTGGACTTCCATTACAAAC
 AGGTACAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCACTCCAG
 AAGTGAATGCTGATGAAATGTTGCTGGTGGACTTGCACATCTTGATGACGTT
 GAAGTGTGTAAGCAAATCTTGTGATGGTAAACTAGGTCTTACTGT
 GTTGCAGAAAGATAAGACACTCGTGAATTGAAAGTAGTGTGAGAAATG
 ATGGCTTATGGTAAACAAAAGGTGTAACATCCCTTATACTAAAATT
 CCTTCCACGACTTGCAGAACCCGATAATGCTGATATCCGTTGGACT
 TGAGCAAGGACTTAACCTTATGCTATCTCATTTGATGCTACTGCTAAAG
 ATGTTAATGAAGTTCGTGCTTGTGAAGAAACTGGCAATGGCACACGTT
 AAGTTGTGCTAAATTGAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTGCTCGTGGTATATGGGTA
 TCGAAGTTCCATTGAAATGGTCCAGTTACCAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAGCAGTTAACAGCAACAAATATGCTTGA
 AACATGACTGATAAAACCACGTCAGTCAGAAGTATCTGATGTC
 TCAATGCTGTTAATTGATGGTACTGATGCTAACATGCTTCAGGTGAGTC
 GCTAATGGTAATACCCAGTTGAGTCAGTCTGACAATGGCTACTATTGA
 TAAAAATGCTCAAACATTACTCAATGAGTATGGTCTTAACTGGCT
 CATTCCCACGTTAACAAACACTGATGTTATTCATCTGCCGTTAAAGAT
 GCAACACACTCAATGGATATCAAACCTGTTGAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCTTCAAAATCCGTCAGATGCAGACATTGGT
 CTGTTACATTGATGAAAGAAGTACAACGTTCAATTGATGATGTTAACTGGG
 GTTATCCCTGCTTGCAGACAAACAGCATCTACAGATGATAATGTTGA
 GGTGAGAAGCTGTAGCACTTGAAAGCAGGATTGTGAATCAGGCGATA

Table 72: Comparative Sequences relating to SAG0941

ATATCGTTATCGTGCAGGTGTCCTGAGGTACAGGTGAACTAACACA
ATCGTGTCTACTGTTAAA

SEQ ID NO. 7211

STRAIN JM9130013

AATAAACCGTAAAGAACACTCGTCAAC
ACTGGTCTGCGTAGAATTCCGTGGTGGTAAGAAGTTGGTGAGTCG
GATACTGGGTGAAAGCCTGAGCTAGAAGCTTCAGCAGAAAAATTGCT
CAAATGATTAAAGAAGGTGCTACGTTTCCGTTTCAACTCTCATGG
AGATCATGCTGAGGACGCTCGTATGGCTACTGTTCTAAACGCCAG
AGATTGAGGACAAAAGTGGCTCCCTCTGATACTAAAGGACCTGAA
ATTGTCAGAACCTTTGAGGAGCTCGTATGGCTACTGTTCTAAACGCCAG
AGTACACAAATTACGTGCTACTAAGCAAGGTATCAAATCAACTCCAG
AAGTGATTGATTGATTGTCAGGACTGACATCTGATGACGTT
GAAGTTGGTAAGCAAATCCTGTTGATGATGGTAAACTAGGTCTTACTGT
GTTGAGGAAAGGACACTCGTCAAGTGGTGAAGGAAACTGGCAATGGACATGTT
ATGGCCTTATTGTTAAACAAAAGGTGTAACATCCCTTAACTAAATT
CCTTCCGACACTGAGCAGCAGATACTGCTGATATCCGTTTGGACT
TGAGCAAGGACTTAACCTTATGCTATCTCATTTGACCTACTGCTAAAG
ATGTTAATGAGGTTCTGCTATTGAGGAAACTGGCAATGGACATGTT
AAGTTGTTGCTAAAATTGAAATCAACAGTATGATAATTGATGAA
GATTATGCAAGCAGCAGATGGTATTATGATTGCTCGTGGTATATGGTA
TCAAGGTTCCATTGAAATGGTCCAGTTACCAAAAATGATCATTACT
AAAGTTAATGAGCTGTTAAAGCAGTTAACAGCAACAAATATGCTGAA
AACATGACTGATAAACACACGTGCGACTCGTCAAGTATCTGATGTC
TCAATGCTGTTATTGATGGTACTGATGCTAACATGCTTCAAGGTGACTCA
GCTAATGGTAAATACCCAGTTGACTCAGTTGCTACAATGCTACTATTGAA
TAAAAATGCTAACACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
CATTCCCACGTAATAACAAAATGATGTTATTGACATCTGCGTTAAAGAT
GCAACACACTCAATGGATCAAACCTGTTGACAAATTACTGAAACAGG
TAATACAGCTGTCGCTATTCTAAATTCCGTCAGATGCGACACATTG
CTGTTACATTGATGAAAAGTACAACGTTATTGATGATGTTAAACTGGGT
GTTATCCTGTCAGACAAACCGAGCATCTACAGATGATATGTTGAA
GGTGCAGAACGTGTAAGCTGAAGCAGGACTGTTGAATCAGGGATA
ATATCGTTATCGTGCAGGTGTCCTGAGGTACAGGTGAACTAACACA
ATCGTGTCTACTGTTAAA

PRETTY OF: /biotmp/msa277466.2[*] February 24, 2003 01:44 ..

<p>msa277466.2{330_090}</p> <p>msa277466.2{330_JM9130013}</p> <p>msa277466.2{330_18RS21}</p> <p>msa277466.2{330_2603}</p> <p>msa277466.2{330_A909}</p> <p>msa277466.2{330_H36B}</p> <p>msa277466.2{330_CJB110}</p> <p>msa277466.2{330_COH1}</p> <p>msa277466.2{330_M732}</p> <p>msa277466.2{330_1169NT}</p> <p>msa277466.2{330_M781}</p>	<p>1</p> <pre>---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCCTG CGGTaGAATT</pre> <p>---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCCTG CGGTaGAATT</p> <p>---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCCTG CGGTaGAATT</p> <p>atgAATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCCTG CGGTaGAATT</p> <p>---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCCTG CGGTaGAATT</p> <p>*****</p>	<p>50</p>
<p>Consensus</p>	<p>51</p> <pre>*****</pre>	<p></p>
<p>msa277466.2{330_090}</p> <p>msa277466.2{330_JM9130013}</p> <p>msa277466.2{330_18RS21}</p> <p>msa277466.2{330_2603}</p> <p>msa277466.2{330_A909}</p> <p>msa277466.2{330_H36B}</p> <p>msa277466.2{330_CJB110}</p> <p>msa277466.2{330_COH1}</p> <p>msa277466.2{330_M732}</p> <p>msa277466.2{330_1169NT}</p> <p>msa277466.2{330_M781}</p>	<pre>CCGTGGTGGT AAGAAGTTG GTGAGTCTGG ATACTGGGGT GAAAGCCTTG</pre> <p>*****</p>	<p>100</p>
<p>Consensus</p>	<p>101</p> <pre>*****</pre>	<p></p>
<p>msa277466.2{330_090}</p> <p>msa277466.2{330_JM9130013}</p> <p>msa277466.2{330_18RS21}</p> <p>msa277466.2{330_2603}</p> <p>msa277466.2{330_A909}</p> <p>msa277466.2{330_H36B}</p> <p>msa277466.2{330_CJB110}</p> <p>msa277466.2{330_COH1}</p> <p>msa277466.2{330_M732}</p> <p>msa277466.2{330_1169NT}</p> <p>msa277466.2{330_M781}</p>	<pre>ACGTAGAAC TTTCAGCAGAA AAAATTGCTC ATTGATTA AGAAGGTGCT</pre> <p>*****</p>	<p>150</p>
<p>Consensus</p>	<p>151</p> <pre>*****</pre>	<p></p>
<p>msa277466.2{330_090}</p>	<pre>AACGTTTCC GTTTCAACTT CTCACATGGA GATCATGCTG AGCAAGGAGC</pre>	<p>200</p>

Table 72: Comparative Sequences relating to SAG0941

msa277466.2{330_JM9130013}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_18RS21}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_2603}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_A909}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_H36B}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_CJB110}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_COH1}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_M732}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_1169NT}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_M781}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
Consensus	*****	*****	*****	*****	*****
					250
msa277466.2{330_090}	TCGTATGGCT	ACTGTCGTA	AAGCAGAAGA	GATTGCAGGA	AAAAAAGTTG
msa277466.2{330_JM9130013}	TCGTATGGCT	ACTGTCGTA	AAGCAGAAGA	GATTGCAGGA	AAAAAAGTTG
msa277466.2{330_18RS21}	TCGTATGGCT	ACTGTCGTA	AAGCAGAAGA	GATTGCAGGA	AAAAAAGTTG
msa277466.2{330_2603}	TCGTATGGCT	ACTGTCGTA	AAGCAGAAGA	GATTGCAGGA	AAAAAAGTTG
msa277466.2{330_A909}	TCGTATGGCT	ACTGTCGTA	AAGCAGAAGA	GATTGCAGGA	AAAAAAGTTG
msa277466.2{330_H36B}	TCGTATGGCT	ACTGTCGTA	AAGCAGAAGA	GATTGCAGGA	AAAAAAGTTG
msa277466.2{330_CJB110}	TCGTATGGCT	ACTGTCGTA	AAGCAGAAGA	GATTGCAGGA	AAAAAAGTTG
msa277466.2{330_COH1}	TCGTATGGCT	ACTGTCGTA	AAGCAGAAGA	GATTGCAGGA	AAAAAAGTTG
msa277466.2{330_M732}	TCGTATGGCT	ACTGTCGTA	AAGCAGAAGA	GATTGCAGGA	AAAAAAGTTG
msa277466.2{330_1169NT}	TCGTATGGCT	ACTGTCGTA	AAGCAGAAGA	GATTGCAGGA	AAAAAAGTTG
msa277466.2{330_M781}	TCGTATGGCT	ACTGTCGTA	AAGCAGAAGA	GATTGCAGGA	AAAAAAGTTG
Consensus	*****	*****	*****	*****	*****
					300
msa277466.2{330_090}	GCTTCCTCCT	TGATACTAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_JM9130013}	GCTTCCTCCT	TGATACTAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_18RS21}	GCTTCCTCCT	TGATACTAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_2603}	GCTTCCTCCT	TGATACTAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_A909}	GCTTCCTCCT	TGATACTAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_H36B}	GCTTCCTCCT	TGATACTAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_CJB110}	GCTTCCTCCT	TGATACTAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_COH1}	GCTTCCTCCT	TGATACTAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_M732}	GCTTCCTCCT	TGATACTAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_1169NT}	GCTTCCTCCT	TGATACTAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_M781}	GCTTCCTCCT	TGATACTAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
Consensus	*****	*****	*****	*****	*****
					350
msa277466.2{330_090}	GATGGTtCAG	ATTTCCATT	ATATACAACA	GGTACAgAAT	TACGTGTTGC
msa277466.2{330_JM9130013}	GATGGTtCAG	ATTTCCATT	ATATACAACA	GGTACAAAT	TACGTGTTGC
msa277466.2{330_18RS21}	GATGGTgCAG	ATTTCCATT	ATATACAACA	GGTACAAAT	TACGTGTTGC
msa277466.2{330_2603}	GATGGTgCAG	ATTTCCATT	ATATACAACA	GGTACAAAT	TACGTGTTGC
msa277466.2{330_A909}	GATGGTgCAG	ATTTCCATT	ATATACAACA	GGTACAAAT	TACGTGTTGC
msa277466.2{330_H36B}	GATGGTgCAG	ATTTCCATT	ATATACAACA	GGTACAAAT	TACGTGTTGC
msa277466.2{330_CJB110}	GATGGTgCAG	ATTTCCATT	ATATACAACA	GGTACAAAT	TACGTGTTGC
msa277466.2{330_COH1}	GATGGTgCAG	ATTTCCATT	ATATACAACA	GGTACAAAT	TACGTGTTGC
msa277466.2{330_M732}	GATGGTgCAG	ATTTCCATT	ATATACAACA	GGTACAAAT	TACGTGTTGC
msa277466.2{330_1169NT}	GATGGTgCAG	ATTTCCATT	ATATACAACA	GGTACAAAT	TACGTGTTGC
msa277466.2{330_M781}	GATGGTgCAG	ATTTCCATT	ATATACAACA	GGTACAAAT	TACGTGTTGC
Consensus	*****	*****	*****	*****	*****
					400
msa277466.2{330_090}	TACTAACCAA	GGTATCAAAT	CAACTCCAGA	AGTGATGCA	TTGAATGTTG
msa277466.2{330_JM9130013}	TACTAACCAA	GGTATCAAAT	CAACTCCAGA	AGTGATGCA	TTGAATGTTG
msa277466.2{330_18RS21}	TACTAACCAA	GGTATCAAAT	CAACTCCAGA	AGTGATGCA	TTGAATGTTG
msa277466.2{330_2603}	TACTAACCAA	GGTATCAAAT	CAACTCCAGA	AGTGATGCA	TTGAATGTTG
msa277466.2{330_A909}	TACTAACCAA	GGTATCAAAT	CAACTCCAGA	AGTGATGCA	TTGAATGTTG
msa277466.2{330_H36B}	TACTAACCAA	GGTATCAAAT	CAACTCCAGA	AGTGATGCA	TTGAATGTTG
msa277466.2{330_CJB110}	TACTAACCAA	GGTATCAAAT	CAACTCCAGA	AGTGATGCA	TTGAATGTTG
msa277466.2{330_COH1}	TACTAACCAA	GGTATCAAAT	CAACTCCAGA	AGTGATGCA	TTGAATGTTG
msa277466.2{330_M732}	TACTAACCAA	GGTATCAAAT	CAACTCCAGA	AGTGATGCA	TTGAATGTTG
msa277466.2{330_1169NT}	TACTAACCAA	GGTATCAAAT	CAACTCCAGA	AGTGATGCA	TTGAATGTTG
msa277466.2{330_M781}	TACTAACCAA	GGTATCAAAT	CAACTCCAGA	AGTGATGCA	TTGAATGTTG
Consensus	*****	*****	*****	*****	*****
					450
msa277466.2{330_090}	CTGGTGGACT	TGACATCTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCIT
msa277466.2{330_JM9130013}	CTGGTGGACT	TGACATCTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCIT
msa277466.2{330_18RS21}	CTGGTGGACT	TGACATCTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCIT
msa277466.2{330_2603}	CTGGTGGACT	TGACATCTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCIT
msa277466.2{330_A909}	CTGGTGGACT	TGACATCTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCIT
msa277466.2{330_H36B}	CTGGTGGACT	TGACATCTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCIT
msa277466.2{330_CJB110}	CTGGTGGACT	TGACATCTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCIT
msa277466.2{330_COH1}	CTGGTGGACT	TGACATCTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCIT
msa277466.2{330_M732}	CTGGTGGACT	TGACATCTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCIT
msa277466.2{330_1169NT}	CTGGTGGACT	TGACATCTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCIT
msa277466.2{330_M781}	CTGGTGGACT	TGACATCTT	GATGACGTTG	AAGTTGGTAA	GCAAATCCIT
Consensus	*****	*****	*****	*****	*****

Table 72: Comparative Sequences relating to SAG0941

msa277466.2{330_090}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_JM9130013}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_18RS21}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_2603}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_A909}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_H36B}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_CJB110}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_COH1}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_M732}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_1169NT}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
msa277466.2{330_M781}	GTTGATGATG	GTAAACTAGG	TCTTACTGTG	TTTGCAAAAG	ATAAAGACAC
Consensus	*****	*****	*****	*****	*****
501					550
msa277466.2{330_090}	TCGTGAATT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_JM9130013}	TCGTGAATT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_18RS21}	TCGTGAATT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_2603}	TCGTGAATT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_A909}	TCGTGAATT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_H36B}	TCGTGAATT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_CJB110}	TCGTGAATT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_COH1}	TCGTGAATT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_M732}	TCGTGAATT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_1169NT}	TCGTGAATT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_M781}	TCGTGAATT	GAAGTAGTTG	TTGAGAATGA	TGGCCTTATT	GGTAAACAAA
Consensus	*****	*****	*****	*****	*****
551					600
msa277466.2{330_090}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTTCCCGAGC	ACTTGCAGAA
msa277466.2{330_JM9130013}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTTCCCGAGC	ACTTGCAGAA
msa277466.2{330_18RS21}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTTCCCGAGC	ACTTGCAGAA
msa277466.2{330_2603}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTTCCCGAGC	ACTTGCAGAA
msa277466.2{330_A909}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTTCCCGAGC	ACTTGCAGAA
msa277466.2{330_H36B}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTTCCCGAGC	ACTTGCAGAA
msa277466.2{330_CJB110}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTTCCCGAGC	ACTTGCAGAA
msa277466.2{330_COH1}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTTCCCGAGC	ACTTGCAGAA
msa277466.2{330_M732}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTTCCCGAGC	ACTTGCAGAA
msa277466.2{330_1169NT}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTTCCCGAGC	ACTTGCAGAA
msa277466.2{330_M781}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CTTTCCCGAGC	ACTTGCAGAA
Consensus	*****	*****	*****	*****	*****
601					650
msa277466.2{330_090}	CCCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACCTTTAT
msa277466.2{330_JM9130013}	CCCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACCTTTAT
msa277466.2{330_18RS21}	CCCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACCTTTAT
msa277466.2{330_2603}	CCCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACCTTTAT
msa277466.2{330_A909}	CCCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACCTTTAT
msa277466.2{330_H36B}	CCCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACCTTTAT
msa277466.2{330_CJB110}	CCCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACCTTTAT
msa277466.2{330_COH1}	CCCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACCTTTAT
msa277466.2{330_M732}	CCCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACCTTTAT
msa277466.2{330_1169NT}	CCCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACCTTTAT
msa277466.2{330_M781}	CCCGATAATG	CTGATATCCG	TTTGGACTT	GAGCAAGGAC	TTAACCTTTAT
Consensus	*****	*****	*****	*****	*****
651					700
msa277466.2{330_090}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	TTTCGTGCTA
msa277466.2{330_JM9130013}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	TTTCGTGCTA
msa277466.2{330_18RS21}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	TTTCGTGCTA
msa277466.2{330_2603}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	TTTCGTGCTA
msa277466.2{330_A909}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	TTTCGTGCTA
msa277466.2{330_H36B}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	TTTCGTGCTA
msa277466.2{330_CJB110}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	TTTCGTGCTA
msa277466.2{330_COH1}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	TTTCGTGCTA
msa277466.2{330_M732}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	TTTCGTGCTA
msa277466.2{330_1169NT}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	TTTCGTGCTA
msa277466.2{330_M781}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	TTTCGTGCTA
Consensus	*****	*****	*****	*****	*****
701					750
msa277466.2{330_090}	TTTGTGAAGA	AACTGGcaAT	GGACATGTGA	AGTTGTTTGC	AAAAATTGAA
msa277466.2{330_JM9130013}	TTTGTGAAGA	AACTGGcaAT	GGACATGTGA	AGTTGTTTGC	AAAAATTGAA
msa277466.2{330_18RS21}	TTTGTGAAGA	AACTGGcaAT	GGACATGTGA	AGTTGTTTGC	AAAAATTGAA
msa277466.2{330_2603}	TTTGTGAAGA	AACTGGcaAT	GGACATGTGA	AGTTGTTTGC	AAAAATTGAA
msa277466.2{330_A909}	TTTGTGAAGA	AACTGGcaAT	GGACATGTGA	AGTTGTTTGC	AAAAATTGAA
msa277466.2{330_H36B}	TTTGTGAAGA	AACTGGcaAT	GGACATGTGA	AGTTGTTTGC	AAAAATTGAA
msa277466.2{330_CJB110}	TTTGTGAAGA	AACTGGcaAT	GGACATGTGA	AGTTGTTTGC	AAAAATTGAA
msa277466.2{330_COH1}	TTTGTGAAGA	AACTGGcaAT	GGACATGTGA	AGTTGTTTGC	AAAAATTGAA
msa277466.2{330_M732}	TTTGTGAAGA	AACTGGcaAT	GGACATGTGA	AGTTGTTTGC	AAAAATTGAA
msa277466.2{330_1169NT}	TTTGTGAAGA	AACTGGcaAT	GGACATGTGA	AGTTGTTTGC	AAAAATTGAA
msa277466.2{330_M781}	TTTGTGAAGA	AACTGGcaAT	GGACATGTGA	AGTTGTTTGC	AAAAATTGAA
Consensus	*****	*****	*****	*****	*****

Table 72: Comparative Sequences relating to SAG0941

msa277466.2{330_090}	751				800
msa277466.2{330_JM9130013}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_18RS21}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_2603}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_A909}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_H36B}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_CJB110}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_COH1}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_M732}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_1169NT}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
msa277466.2{330_M781}	AATCAACAAG	GTATCGATAA	TATTGATGAG	ATTATCGAAG	CAGCAGATGG
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	801				850
msa277466.2{330_JM9130013}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAAGTTCCA	TTTGAAATGG
msa277466.2{330_18RS21}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAAGTTCCA	TTTGAAATGG
msa277466.2{330_2603}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAAGTTCCA	TTTGAAATGG
msa277466.2{330_A909}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAAGTTCCA	TTTGAAATGG
msa277466.2{330_H36B}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAAGTTCCA	TTTGAAATGG
msa277466.2{330_CJB110}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAAGTTCCA	TTTGAAATGG
msa277466.2{330_COH1}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAAGTTCCA	TTTGAAATGG
msa277466.2{330_M732}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAAGTTCCA	TTTGAAATGG
msa277466.2{330_1169NT}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAAGTTCCA	TTTGAAATGG
msa277466.2{330_M781}	TATTATGATT	GCTCGTGGTG	ATATGGGTAT	CGAAAGTTCCA	TTTGAAATGG
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	851				900
msa277466.2{330_JM9130013}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_18RS21}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_2603}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_A909}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_H36B}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_CJB110}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_COH1}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_M732}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_1169NT}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
msa277466.2{330_M781}	TTCCAGTTTA	CCAAAAAATG	ATCATTACTA	AAGTTAATGC	AGCTGGTAAA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	901				950
msa277466.2{330_JM9130013}	GCAGTTATTAA	CAGCAACAAA	TATGCTTGA	ACAATGACTG	ATAAACCACG
msa277466.2{330_18RS21}	GCAGTTATTAA	CAGCAACAAA	TATGCTTGA	ACAATGACTG	ATAAACCACG
msa277466.2{330_2603}	GCAGTTATTAA	CAGCAACAAA	TATGCTTGA	ACAATGACTG	ATAAACCACG
msa277466.2{330_A909}	GCAGTTATTAA	CAGCAACAAA	TATGCTTGA	ACAATGACTG	ATAAACCACG
msa277466.2{330_H36B}	GCAGTTATTAA	CAGCAACAAA	TATGCTTGA	ACAATGACTG	ATAAACCACG
msa277466.2{330_CJB110}	GCAGTTATTAA	CAGCAACAAA	TATGCTTGA	ACAATGACTG	ATAAACCACG
msa277466.2{330_COH1}	GCAGTTATTAA	CAGCAACAAA	TATGCTTGA	ACAATGACTG	ATAAACCACG
msa277466.2{330_M732}	GCAGTTATTAA	CAGCAACAAA	TATGCTTGA	ACAATGACTG	ATAAACCACG
msa277466.2{330_1169NT}	GCAGTTATTAA	CAGCAACAAA	TATGCTTGA	ACAATGACTG	ATAAACCACG
msa277466.2{330_M781}	GCAGTTATTAA	CAGCAACAAA	TATGCTTGA	ACAATGACTG	ATAAACCACG
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	951				1000
msa277466.2{330_JM9130013}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_18RS21}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_2603}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_A909}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_H36B}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_CJB110}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_COH1}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_M732}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_1169NT}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCCTT	CAATGCTGTT	ATTGATGGTA
msa277466.2{330_M781}	TGCGACTCGT	TCAGAAAGTAT	CTGATGTCCTT	CAATGCTGTT	ATTGATGGTA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	1001				1050
msa277466.2{330_JM9130013}	CTGATGCTAC	AATGCTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_18RS21}	CTGATGCTAC	AATGCTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_2603}	CTGATGCTAC	AATGCTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_A909}	CTGATGCTAC	AATGCTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_H36B}	CTGATGCTAC	AATGCTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_CJB110}	CTGATGCTAC	AATGCTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_COH1}	CTGATGCTAC	AATGCTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_M732}	CTGATGCTAC	AATGCTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_1169NT}	CTGATGCTAC	AATGCTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
msa277466.2{330_M781}	CTGATGCTAC	AATGCTTCA	GGTGAGTCAG	CTAATGGTAA	ATACCCAGTT
Consensus	*****	*****	*****	*****	*****

Table 72: Comparative Sequences relating to SAG0941

			1051		1100
msa277466.2{330_090}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_JM9130013}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_18RS21}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_2603}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_A909}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_H36B}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_CJB110}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_COH1}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_M732}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_1169NT}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_M781}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
Consensus	*****	*****	*****	*****	*****
			1101		1150
msa277466.2{330_090}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCACACGT	AATAACAAAA
msa277466.2{330_JM9130013}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCACACGT	AATAACAAAA
msa277466.2{330_18RS21}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCACACGT	AATAACAAAA
msa277466.2{330_2603}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCACACGT	AATAACAAAA
msa277466.2{330_A909}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCACACGT	AATAACAAAA
msa277466.2{330_H36B}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCACACGT	AATAACAAAA
msa277466.2{330_CJB110}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCACACGT	AATAACAAAA
msa277466.2{330_COH1}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCACACGT	AATAACAAAA
msa277466.2{330_M732}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCACACGT	AATAACAAAA
msa277466.2{330_1169NT}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCACACGT	AATAACAAAA
msa277466.2{330_M781}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCACACGT	AATAACAAAA
Consensus	*****	*****	*****	*****	*****
			1151		1200
msa277466.2{330_090}	CTGATGTTAT	TGCATCTGGC	GTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_JM9130013}	CTGATGTTAT	TGCATCTGGC	GTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_18RS21}	CTGATGTTAT	TGCATCTGGC	GTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_2603}	CTGATGTTAT	TGCATCTGGC	GTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_A909}	CTGATGTTAT	TGCATCTGGC	GTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_H36B}	CTGATGTTAT	TGCATCTGGC	GTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_CJB110}	CTGATGTTAT	TGCATCTGGC	GTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_COH1}	CTGATGTTAT	TGCATCTGGC	GTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_M732}	CTGATGTTAT	TGCATCTGGC	GTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_1169NT}	CTGATGTTAT	TGCATCTGGC	GTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_M781}	CTGATGTTAT	TGCATCTGGC	GTAAAGATG	CAACACACTC	AATGGATATC
Consensus	*****	*****	*****	*****	*****
			1201		1250
msa277466.2{330_090}	AAACTTGTG	TgACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_JM9130013}	AAACTTGTG	TgACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_18RS21}	AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_2603}	AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_A909}	AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_H36B}	AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_CJB110}	AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_COH1}	AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_M732}	AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_1169NT}	AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_M781}	AAACTTGTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
Consensus	*****	*****	*****	*****	*****
			1251		1300
msa277466.2{330_090}	TAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_JM9130013}	TAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_18RS21}	TAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_2603}	TAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_A909}	TAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_H36B}	TAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_CJB110}	TAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_COH1}	TAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_M732}	TAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_1169NT}	TAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_M781}	TAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
Consensus	*****	*****	*****	*****	*****
			1301		1350
msa277466.2{330_090}	TACAACGTTC	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_JM9130013}	TACAACGTTC	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_18RS21}	TACAACGTTC	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_2603}	TACAACGTTC	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_A909}	TACAACGTTC	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_H36B}	TACAACGTTC	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_CJB110}	TACAACGTTC	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_COH1}	TACAACGTTC	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_M732}	TACAACGTTC	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_1169NT}	TACAACGTTC	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_M781}	TACAACGTTC	ATTGATGATT	AACTGGGGTG	TTATCCCTGT	CCTTGCAGAC

Table 72: Comparative Sequences relating to SAG0941

Consensus	*****	*****	*****	*****	*****	*****	*****
msa277466.2{330_090}	1351	AAACAGCAT	CTACAGATGA	TATGTTGAG	GTTGCAGAAC	GTGTAGCACT	.1400
msa277466.2{330_JM9130013}		AAACAGCAT	CTACAGATGA	TATGTTGAG	GTTGCAGAAC	GTGTAGCACT	
msa277466.2{330_18RS21}		AAACAGCAT	CTACAGATGA	TATGTTGAG	GTTGCAGAAC	GTGTAGCACT	
msa277466.2{330_2603}		AAACAGCAT	CTACAGATGA	TATGTTGAG	GTTGCAGAAC	GTGTAGCACT	
msa277466.2{330_A909}		AAACAGCAT	CTACAGATGA	TATGTTGAG	GTTGCAGAAC	GTGTAGCACT	
msa277466.2{330_H36B}		AAACAGCAT	CTACAGATGA	TATGTTGAG	GTTGCAGAAC	GTGTAGCACT	
msa277466.2{330_CJB110}		AAACAGCAT	CTACAGATGA	TATGTTGAG	GTTGCAGAAC	GTGTAGCACT	
msa277466.2{330_COH1}		AAACAGCAT	CTACAGATGA	TATGTTGAG	GTTGCAGAAC	GTGTAGCACT	
msa277466.2{330_M732}		AAACAGCAT	CTACAGATGA	TATGTTGAG	GTTGCAGAAC	GTGTAGCACT	
msa277466.2{330_1169NT}		AAACAGCAT	CTACAGATGA	TATGTTGAG	GTTGCAGAAC	GTGTAGCACT	
msa277466.2{330_M781}		AAACAGCAT	CTACAGATGA	TATGTTGAG	GTTGCAGAAC	GTGTAGCACT	
Consensus	*****	*****	*****	*****	*****	*****	*****
msa277466.2{330_090}	1401	TGAAAGCAGGA	cTTGTTGAAT	CAGGGCATAA	TATCGTTATC	GTTGCAGGTG	1450
msa277466.2{330_JM9130013}		TGAAAGCAGGA	cTTGTTGAAT	CAGGGCATAA	TATCGTTATC	GTTGCAGGTG	
msa277466.2{330_18RS21}		TGAAAGCAGGA	tTTGTTGAAT	CAGGGCATAA	TATCGTTATC	GTTGCAGGTG	
msa277466.2{330_2603}		TGAAAGCAGGA	tTTGTTGAAT	CAGGGCATAA	TATCGTTATC	GTTGCAGGTG	
msa277466.2{330_A909}		TGAAAGCAGGA	tTTGTTGAAT	CAGGGCATAA	TATCGTTATC	GTTGCAGGTG	
msa277466.2{330_H36B}		TGAAAGCAGGA	tTTGTTGAAT	CAGGGCATAA	TATCGTTATC	GTTGCAGGTG	
msa277466.2{330_CJB110}		TGAAAGCAGGA	tTTGTTGAAT	CAGGGCATAA	TATCGTTATC	GTTGCAGGTG	
msa277466.2{330_COH1}		TGAAAGCAGGA	cTTGTTGAAT	CAGGGCATAA	TATCGTTATC	GTTGCAGGTG	
msa277466.2{330_M732}		TGAAAGCAGGA	cTTGTTGAAT	CAGGGCATAA	TATCGTTATC	GTTGCAGGTG	
msa277466.2{330_1169NT}		TGAAAGCAGGA	cTTGTTGAAT	CAGGGCATAA	TATCGTTATC	GTTGCAGGTG	
msa277466.2{330_M781}		TGAAAGCAGGA	cTTGTTGAAT	CAGGGCATAA	TATCGTTATC	GTTGCAGGTG	
Consensus	*****	*****	*****	*****	*****	*****	*****
msa277466.2{330_090}	1451	TCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA	1500
msa277466.2{330_JM9130013}		TCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA	
msa277466.2{330_18RS21}		TCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA	
msa277466.2{330_2603}		TCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA	
msa277466.2{330_A909}		TCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA	
msa277466.2{330_H36B}		TCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA	
msa277466.2{330_CJB110}		TCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA	
msa277466.2{330_COH1}		TCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA	
msa277466.2{330_M732}		TCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA	
msa277466.2{330_1169NT}		TCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA	
msa277466.2{330_M781}		TCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA	
Consensus	*****	*****	*****	*****	*****	*****	*****

SEQ ID NO. 7212

STRAIN 2603 frame: 1

MNKRVKIVATLGPRAVEFRGGKKFGESEGYWGESLDVEASAECIAQLIKEGANVFRFNFSHG
 DHAEGQARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEADGDFHSYTGTKLRVATKQ
 GIKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTVFAKDKDTRFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAEVDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 GHVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVFEMVPVYQKMIITKVNAAGKA
 AVITATNMLETMTDKPRATRSEVDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLNNEYGRLDSSAFPRNNKTDVIASAVKDATHSMIDLKVVTITETGNTARAIISKFRP
 DADILAVTFDEKVQRSLMINWGVI PVLADKPASTDDMFVAERVALEAGFVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7213

STRAIN 090 frame: 1

NKRVKIVATLGPRAVEFRGGKKFGESEGYWGESLDVEASAECIAQLIKEGANVFRFNFSHG
 HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEADGDFHSYTGTKLRVATKQ
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTVFAKDKDTRFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAEVDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKILENQQGIDNIDEIIEAADGIMIARGDMGIEVFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLNNEYGRLDSSAFPRNNKTDVIASAVKDATHSMIDLKVVTITETGNTARAIISKFRP
 DADILAVTFDEKVQRSLMINWGVI PVLADKPASTDDMFVAERVALEAGFVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7214

STRAIN A909 frame: 1

NKRVKIVATLGPRAVEFRGGKKFGESEGYWGESLDVEASAECIAQLIKEGANVFRFNFSHG
 HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEADGDFHSYTGTKLRVATKQ
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTVFAKDKDTRFEVVVENDGLIG
 KQKGVNIPYTKIPFPALAEVDNADIRFGLEQGLNFIAISFVRTAKDVNEVRAICEETGNG
 HVKLFAKILENQQGIDNIDEIIEAADGIMIARGDMGIEVFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMTDKPRATRSEVDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLNNEYGRLDSSAFPRNNKTDVIASAVKDATHSMIDLKVVTITETGNTARAIISKFRP
 DADILAVTFDEKVQRSLMINWGVI PVLADKPASTDDMFVAERVALEAGFVESGDNIVIV
 AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7215

STRAIN H36B frame: 1

Table 72: Comparative Sequences relating to SAG0941

NKRVKIVATLGPRAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDEGADFHSHYTTGTKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKGLLTFAKDKDTRFEVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLQEGLNFIASFVRTAKDVNEVRAICEETCNG
 HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMDKPRATRSESDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTVDVIASAVKDATHSMDIKLWVITETGNTARAIISKRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVIV
 AGPVGTGGTNTMRVRTVK

SEQ ID NO. 7216

STRAIN 18RS21 frame: 1

NKRVKIVATLGPRAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDEGADFHSHYTTGTKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKGLLTFAKDKDTRFEVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLQEGLNFIASFVRTAKDVNEVRAICEETCNG
 HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMDKPRATRSESDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTVDVIASAVKDATHSMDIKLWVITETGNTARAIISKRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVIV
 AGPVGTGGTNTMRVRTVK

SEQ ID NO. 7217

STRAIN M732 frame: 1

NKRVKIVATLGPRAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDEGADFHSHYTTGTKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKGLLTFAKDKDTRFEVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLQEGLNFIASFVRTAKDVNEVRAICEETCNG
 HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMDKPRATRSESDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTVDVIASAVKDATHSMDIKLWVITETGNTARAIISKRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGPVGTGGTNTMRVRTVK

SEQ ID NO. 7218

STRAIN COH1 frame: 1

NKRVKIVATLGPRAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDEGADFHSHYTTGTKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKGLLTFAKDKDTRFEVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLQEGLNFIASFVRTAKDVNEVRAICEETCNG
 HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMDKPRATRSESDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTVDVIASAVKDATHSMDIKLWVITETGNTARAIISKRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGPVGTGGTNTMRVRTVK

SEQ ID NO. 7219

STRAIN M781 frame: 1

NKRVKIVATLGPRAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDEGADFHSHYTTGTKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKGLLTFAKDKDTRFEVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLQEGLNFIASFVRTAKDVNEVRAICEETCNG
 HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMDKPRATRSESDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTVDVIASAVKDATHSMDIKLWVITETGNTARAIISKRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGPVGTGGTNTMRVRTVK

SEQ ID NO. 7220

STRAIN CJB110 frame: 1

NKRVKIVATLGPRAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDEGADFHSHYTTGTKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKGLLTFAKDKDTRFEVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLQEGLNFIASFVRTAKDVNEVRAICEETCNG
 HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMDKPRATRSESDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTVDVIASAVKDATHSMDIKLWVITETGNTARAIISKRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGPVGTGGTNTMRVRTVK

SEQ ID NO. 7221

STRAIN 1169NT frame: 1

NKRVKIVATLGPRAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDEGADFHSHYTTGTKLRVATKQG
 IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKGLLTFAKDKDTRFEVVENDGLIG
 KQKGVNIPYTKIPFPALAERDNADIRFGLQEGLNFIASFVRTAKDVNEVRAICEETCNG
 HVKLFAKIENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMVPVYQKMIITKVNAAGKA
 VITATNMLETMDKPRATRSESDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
 NAQTLLNEYGRLDSSAFPRNNKTVDVIASAVKDATHSMDIKLWVITETGNTARAIISKRP
 DADILAVTFDEKVQRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGFVESGDNIVIV
 AGPVGTGGTNTMRVRTVK

Table 72: Comparative Sequences relating to SAG0941

SEQ ID NO. 7222

STRAIN JM9130013 frame: 1

NKRVKIVATLGPAVEFRGGKKFGESGYWGESLDVEASAECIAQLIKEGANVFRFNFSHGD
 HAEQGARMATVRKAEEIAGQKVGFLDTKGPEIRTELFFEDGSDFHSYTTGTLRVAATKQG
 IKSPEVIALNVAGGLIDFDDVEVGKQILVDDGKLGLTVFAKDKDTREFEVVVENDGLIG
 KQGVNI PYTKI PFPALABERDNADIRFGLQGLNFIAISFRTAKDVNEVRAICEETGNG
 HVKLFAKIEENQQGIDNIDEIIEAADGIMIARGDMGIEVPFEMPVYQKMIITKVNAAGKA
 VITATNMLETMDKPRATRSVDVFNAVILDGTDATMLSGESANGKYPESVRTMATIDK
 NAQTLNNEYGRDSSAFPRNKTVDVIASAVKDATHSMDIKLVVTITETGNTARAI SKRPP
 DAI LAVTFDEKVRSLSMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIVIV
 AGVPVGTTGGTNTMRVRTVK

PRETTY of: /biotmp/msa277662.2{*} February 24, 2003 01:49 ..

msa277662.2{330_18RS21}	-NKRVKIVAT	LGPAVEFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	50
msa277662.2{330_A909}	-NKRVKIVAT	LGPAVEFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_CJB110}	-NKRVKIVAT	LGPAVEFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_H36B}	-NKRVKIVAT	LGPAVEFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_1169NT}	-NKRVKIVAT	LGPAVEFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_COH1}	-NKRVKIVAT	LGPAVEFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_M732}	-NKRVKIVAT	LGPAVEFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_M781}	-NKRVKIVAT	LGPAVEFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_JM9130013}	-NKRVKIVAT	LGPAVEFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_090}	-NKRVKIVAT	LGPAVEFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
msa277662.2{330_2603}	mNKRVKIVAT	LGPAVEFRGG	KKFGESGYWG	ESLDVEASAE	KIAQLIKEGA	
Consensus	*****	*****	*****	*****	*****	
msa277662.2{330_18RS21}	NVFRFNFSHG	DHAEQGARMA	TVRKAEIIAG	QKVGFLLDTK	GPEIRTELFE	100
msa277662.2{330_A909}	NVFRFNFSHG	DHAEQGARMA	TVRKAEIIAG	QKVGFLLDTK	GPEIRTELFE	
msa277662.2{330_CJB110}	NVFRFNFSHG	DHAEQGARMA	TVRKAEIIAG	QKVGFLLDTK	GPEIRTELFE	
msa277662.2{330_H36B}	NVFRFNFSHG	DHAEQGARMA	TVRKAEIIAG	QKVGFLLDTK	GPEIRTELFE	
msa277662.2{330_1169NT}	NVFRFNFSHG	DHAEQGARMA	TVRKAEIIAG	QKVGFLLDTK	GPEIRTELFE	
msa277662.2{330_COH1}	NVFRFNFSHG	DHAEQGARMA	TVRKAEIIAG	QKVGFLLDTK	GPEIRTELFE	
msa277662.2{330_M732}	NVFRFNFSHG	DHAEQGARMA	TVRKAEIIAG	QKVGFLLDTK	GPEIRTELFE	
msa277662.2{330_M781}	NVFRFNFSHG	DHAEQGARMA	TVRKAEIIAG	QKVGFLLDTK	GPEIRTELFE	
msa277662.2{330_JM9130013}	NVFRFNFSHG	DHAEQGARMA	TVRKAEIIAG	QKVGFLLDTK	GPEIRTELFE	
msa277662.2{330_090}	NVFRFNFSHG	DHAEQGARMA	TVRKAEIIAG	QKVGFLLDTK	GPEIRTELFE	
msa277662.2{330_2603}	NVFRFNFSHG	DHAEQGARMA	TVRKAEIIAG	QKVGFLLDTK	GPEIRTELFE	
Consensus	*****	*****	*****	*****	*****	
msa277662.2{330_18RS21}	DGADFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	101
msa277662.2{330_A909}	DGADFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_CJB110}	DGADFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_H36B}	DGADFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_1169NT}	DGADFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_COH1}	DGADFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_M732}	DGADFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_M781}	DGADFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_JM9130013}	DGADFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_090}	DGADFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_2603}	DGADFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
Consensus	*****	*****	*****	*****	*****	
msa277662.2{330_18RS21}	DGSDFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	102
msa277662.2{330_A909}	DGSDFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_CJB110}	DGSDFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_H36B}	DGSDFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_1169NT}	DGSDFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_COH1}	DGSDFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_M732}	DGSDFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_M781}	DGSDFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_JM9130013}	DGSDFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_090}	DGSDFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
msa277662.2{330_2603}	DGSDFHSYT	GTKLRVATKQ	GIKSTPEVIA	LNVAGGLDIF	DDVEVGKQIL	
Consensus	*****	*****	*****	*****	*****	
msa277662.2{330_18RS21}	VDDGKLGTV	FAKDKDTRF	EVVVENDGLI	GKQKGVNIPY	TKIPFPALAE	103
msa277662.2{330_A909}	VDDGKLGTV	FAKDKDTRF	EVVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_CJB110}	VDDGKLGTV	FAKDKDTRF	EVVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_H36B}	VDDGKLGTV	FAKDKDTRF	EVVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_1169NT}	VDDGKLGTV	FAKDKDTRF	EVVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_COH1}	VDDGKLGTV	FAKDKDTRF	EVVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_M732}	VDDGKLGTV	FAKDKDTRF	EVVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_M781}	VDDGKLGTV	FAKDKDTRF	EVVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_JM9130013}	VDDGKLGTV	FAKDKDTRF	EVVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_090}	VDDGKLGTV	FAKDKDTRF	EVVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
msa277662.2{330_2603}	VDDGKLGTV	FAKDKDTRF	EVVVENDGLI	GKQKGVNIPY	TKIPFPALAE	
Consensus	*****	*****	*****	*****	*****	
msa277662.2{330_18RS21}	RDNADIRFGL	EQGLNFI	FVRTAKDVNE	VRAICEETGn	GHVKLFAKIE	104
msa277662.2{330_A909}	RDNADIRFGL	EQGLNFI	FVRTAKDVNE	VRAICEETGn	GHVKLFAKIE	
msa277662.2{330_CJB110}	RDNADIRFGL	EQGLNFI	FVRTAKDVNE	VRAICEETGn	GHVKLFAKIE	
msa277662.2{330_H36B}	RDNADIRFGL	EQGLNFI	FVRTAKDVNE	VRAICEETGn	GHVKLFAKIE	
msa277662.2{330_1169NT}	RDNADIRFGL	EQGLNFI	FVRTAKDVNE	VRAICEETGn	GHVKLFAKIE	
msa277662.2{330_COH1}	RDNADIRFGL	EQGLNFI	FVRTAKDVNE	VRAICEETGn	GHVKLFAKIE	
msa277662.2{330_M732}	RDNADIRFGL	EQGLNFI	FVRTAKDVNE	VRAICEETGn	GHVKLFAKIE	
msa277662.2{330_M781}	RDNADIRFGL	EQGLNFI	FVRTAKDVNE	VRAICEETGn	GHVKLFAKIE	
msa277662.2{330_JM9130013}	RDNADIRFGL	EQGLNFI	FVRTAKDVNE	VRAICEETGn	GHVKLFAKIE	
msa277662.2{330_090}	RDNADIRFGL	EQGLNFI	FVRTAKDVNE	VRAICEETGn	GHVKLFAKIE	
msa277662.2{330_2603}	RDNADIRFGL	EQGLNFI	FVRTAKDVNE	VRAICEETGx	GHVKLFAKIE	
Consensus	*****	*****	*****	*****	*****	

Table 72: Comparative Sequences relating to SAG0941

		251		300
msa277662.2{330_18RS21}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM
msa277662.2{330_A909}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM
msa277662.2{330_CJB110}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM
msa277662.2{330_H36B}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM
msa277662.2{330_1169NT}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM
msa277662.2{330_COH1}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM
msa277662.2{330_M732}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM
msa277662.2{330_M781}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM
msa277662.2{330_JM9130013}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM
msa277662.2{330_090}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM
msa277662.2{330_2603}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVPVYQKM
Consensus	*****	*****	*****	*****
		301		350
msa277662.2{330_18RS21}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS
msa277662.2{330_A909}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS
msa277662.2{330_CJB110}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS
msa277662.2{330_H36B}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS
msa277662.2{330_1169NT}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS
msa277662.2{330_COH1}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS
msa277662.2{330_M732}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS
msa277662.2{330_M781}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS
msa277662.2{330_JM9130013}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS
msa277662.2{330_090}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS
msa277662.2{330_2603}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS
Consensus	*****	*****	*****	*****
		351		400
msa277662.2{330_18RS21}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA
msa277662.2{330_A909}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA
msa277662.2{330_CJB110}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA
msa277662.2{330_H36B}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA
msa277662.2{330_1169NT}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA
msa277662.2{330_COH1}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA
msa277662.2{330_M732}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA
msa277662.2{330_M781}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA
msa277662.2{330_JM9130013}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA
msa277662.2{330_090}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA
msa277662.2{330_2603}	ESVRTMATID	KNAQTLLNEY	GRLDSSAFPR	NNKTDVIASA
Consensus	*****	*****	*****	*****
		401		450
msa277662.2{330_18RS21}	KLVVTITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI
msa277662.2{330_A909}	KLVVTITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI
msa277662.2{330_CJB110}	KLVVTITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI
msa277662.2{330_H36B}	KLVVTITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI
msa277662.2{330_1169NT}	KLVVTITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI
msa277662.2{330_COH1}	KLVVTITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI
msa277662.2{330_M732}	KLVVTITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI
msa277662.2{330_M781}	KLVVTITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI
msa277662.2{330_JM9130013}	KLVVTITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI
msa277662.2{330_090}	KLVVTITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI
msa277662.2{330_2603}	KLVVTITETG	NTARAISKFR	PDADILAVTF	DEKVQRSLMI
Consensus	*****	*****	*****	*****
		451		500
msa277662.2{330_18RS21}	KPASTDDMFE	VAERVALEAG	fVESGDNIVI	VAGVPVGTGG
msa277662.2{330_A909}	KPASTDDMFE	VAERVALEAG	fVESGDNIVI	VAGVPVGTGG
msa277662.2{330_CJB110}	KPASTDDMFE	VAERVALEAG	fVESGDNIVI	VAGVPVGTGG
msa277662.2{330_H36B}	KPASTDDMFE	VAERVALEAG	fVESGDNIVI	VAGVPVGTGG
msa277662.2{330_1169NT}	KPASTDDMFE	VAERVALEAG	fVESGDNIVI	VAGVPVGTGG
msa277662.2{330_COH1}	KPASTDDMFE	VAERVALEAG	fVESGDNIVI	VAGVPVGTGG
msa277662.2{330_M732}	KPASTDDMFE	VAERVALEAG	fVESGDNIVI	VAGVPVGTGG
msa277662.2{330_M781}	KPASTDDMFE	VAERVALEAG	fVESGDNIVI	VAGVPVGTGG
msa277662.2{330_JM9130013}	KPASTDDMFE	VAERVALEAG	fVESGDNIVI	VAGVPVGTGG
msa277662.2{330_090}	KPASTDDMFE	VAERVALEAG	fVESGDNIVI	VAGVPVGTGG
msa277662.2{330_2603}	KPASTDDMFE	VAERVALEAG	fVESGDNIVI	VAGVPVGTGG
Consensus	*****	*****	*****	*****

Table 73: Comparative Sequences relating to SAG0981**SEQ ID NO. 7301****STRAIN 2603**

TTCGCTATAATAGACAAAAGGTGGTGTATTTATGTATTAGCATTAATCGGTGAT
ATCATTAATTCAAAACAGATACTTGAAACGTGAAACTTCCAACAGCTTTCCAGCAACTA
ATGACCGAACTATCTGATCTATGGTGAAGAGCTGATTCTCCATTCACTATTACAGCT
GGTGTGAAATTCAAGCTTATTGAAACCATCAAAAAGGTATTCAAAATTATTGACCAT
ATTCAACTAGCCTCTAAACCTGTTAATGTAAGGTCGGCCTCGGTACAGGAAACATTATA
ACATCCCATCAATCAAAATGAAAGTATCGGTGCTGATGGTCTGCCACTGGCATGCTCGC
TCAGCTTAAATCATACATGATAAAAATGATTATGGAACAGTTCAAGTAGCTATTGC
CTTGATGATGAAGACCAAAACCTGAAATTAAACACTAAATAGCTCATTTCAAGCTGGTGTAT
TTTATCAAGTCAAAATGGACTACAAACCATTTCAATGCTGAGCCTTAATACITCAA
GATAATTATCAAGAACATTCACATCAAAGTTAGGCCAACTGGAAAATATTGAAACCT
AGTCGCTGACTAAACGCTTAAAGCAAGCGGTCTGAAGATTACITAAGAACGAGAAC
CAGGCAGCCGATCTATTAGTTAAAGGGGAAGCTATGATT

SEQ ID NO. 7302**STRAIN 090**

TCTGCTATAATAGACAAAAGGTGGTGTATTTATGTATT
AGCTTAAACAGCTTTCCAGCAACTAATGACCGAACTATCTGATGTATAT
GGTGAAGAGCTGATTCTCCATTCACTATTACAGCTGGTGTGATGAATTCA
AGCTTATTGAAACCATCAAAAAGGTATTCAAAATTATTGACCATATTCT
AACTAGCTTAAACCTGTTAATGTAAGGTCGGCCTCGGTACAGGAAAC
ATTATAACATCCATCAATTAAATGAAAGTATCGGTGCTGATGGTCTGC
CTACTGGCATGCTCGCTCAGCTATTAAATCATACATGATAAAAATGATT
ATGGAAACAGTCTCAAGTAGCTATTGGCCTTGATGATGAAGACCAAAACCTT
GAATTAAACACTAAATAGTCTCATTTCACTGGTGTATTATCAAGTC
ATGGACTACAACCATTTCAATGCTGAGCCTTAATACITCAAAGATA
ATTATCAAGAACATTTCAACATCAAAGTTAGGCCAACTGGAAAATATT
GAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCTGAAGATT
CTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAGTTGCACTC
AAACTAAAGGGGAAGCTATGATT

SEQ ID NO. 7303**STRAIN A909**

TCTGCTATAATAGACAAAAGGTGGTGTATTTATGTATT
TTAGCATTAATCGGTGTATCATTAATTCAAAACAGATACTTGAAACGTGAA
AACTTCCAAACAGCTTTCCAGCAACTAATGACCGAACTATCTGATGTAT
ATGGTGAAGAGCTGATTCTCCATTCACTATTACAGCTGGTGTGATGAATT
CAAGCTTATTGAAACCATCAAAAAGGTATTCAAAATTATTGACCATAT
TCAACTAGCTTAAACCTGTTAATGTAAGGTCGGCCTCGGTACAGGAA
ACATTATAACATCCATCAATTCAAAATGAAAGTATCGGTGCTGATGGTCT
GCCACTGGCATGCTCGCTCAGCTATTAAATCATACATGATAAAAATGAA
TTATGGAAACAGTCTCAAGTAGCTATTGGCCTTGATGATGAAGACCAAAACC
TTGAATTAAACACTAAATAGTCTCATTTCACTGGTGTATTATCAAGTC
AAATGGACTACAACCATTTCAAAATGCTGAGCCTTAATACITCAAAGA
TAATTATCAAGAACATTTCAACATCAAAGTTAGGCCAACTGGAAAATA
TTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCTGAAGATT
TACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAGTTGCAC
TCAAACTAAAGGGGAAGCTATGATT

SEQ ID NO. 7304**STRAIN H36B**

TCTGCTATAATAGACAAAAGGTGGTGTATTT
ATGTATTTAGCATTAATCGGTGTATCATTAATTCAAAACAGATACTTGAA
ACGTGAAACACTTCCAAACAGCTTTCCAGCAACTAATGACCGAACTATCTG
ATGTATATGGTGAAGAGCTGATTCTCCATTCACTATTACAGCTGGTGT
GAATTTCAGCTTATTGAAACCATCAAAAAGGTATTCAAAATTATTGAA
CCATATTCAACTAGCTTAAACCTGTTAATGTAAGGTCGGCCTCGGT
CAGGAAACATTATAACATCCATCAATTCAAAATGAAAGTATCGGTGCTGAT
GGTCTGGCTACTGGCATGCTCGCTCAGCTATTAAATCATACATGATAAA
AAATGATTATGGAAACAGTCTCAAGTAGCTATTGGCCTTGATGATGAAGACC
AAAACCTTGAATTAACACTAAATAGTCTCATTTCACTGGTGTATTATC
AAAGTCAAATGGACTACAACCATTTCAATGCTTGAGCCTTAATACIT
TCAAGATAATTATCAAGAACATTTCAACATCAAAGTTAGGCCAACTGG
AAAATATTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCTG
AAGATTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
TTGCACTCAAACATAAGGGGAAGCTATGATT

SEQ ID NO. 7305**STRAIN 18RS21**

TCTGCTATAATAGACAAAAGGTGGTGTATTT
ATGTATTTAGCATTAATCGGTGTATCATTAATTCAAAACAGATACTTGAA
ACGTGAAACACTTCCAAACAGCTTTCCAGCAACTAATGACCGAACTATCTG
ATGTATATGGTGAAGAGCTGATTCTCCATTCACTATTACAGCTGGTGT
GAATTTCAGCTTATTGAAACCATCAAAAAGGTATTCAAAATTATTGAA
CCATATTCAACTAGCTTAAACCTGTTAATGTAAGGTCGGCCTCGGT
CAGGAAACATTATAACATCCATCAATTCAAAATGAAAGTATCGGTGCTGAT
GGTCTGGCTACTGGCATGCTCGCTCAGCTATTAAATCATACATGATAAA
AAATGATTATGGAAACAGTCTCAAGTAGCTATTGGCCTTGATGATGAAGACC
AAAACCTTGAATTAACACTAAATAGTCTCATTTCACTGGTGTATTATC
AAAGTCAAATGGACTACAACCATTTCAATGCTTGAGCCTTAATACIT

Table 73: Comparative Sequences relating to SAG0981

TCAGATAATTATCAAGAACATTCAACATCAAAAGTTAGCCAACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7306

STRAIN M732

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 TATGTATTAGCATTAATCGGTGATATCATTAAATTCAAAACAGATACTTG
 AACGTGAAACTTCCAACAGTCTTTCAAGCAACTAATGACCGAACTATCT
 GATGTATATGGTGAAGAGCTGATTCTCCATTCACTATTACAGCTGGTGA
 TGAATTCAGCTTATTGAAACAcATCRAAAAAGGTATTCAAAATTATTG
 ACCATATTCAACTAGCTCTAAACACCTGTTAATGTAAGGTTGCCCTCGGT
 ACAGGAAACATTATAACATCCATCAATTCAATGAAAGTATCGGTGCTGA
 TGGCTCTGCCCTACTGGCATGCTCAGCTTAAATCATATACTGATA
 AAAATGATTATGAAACAGTCAAGTAGCTATTGCTTGTGATGAAGAC
 CAAAACCTTGAATTAAACACTAAATAGTCATTTCAATGCTTGAGCACCTTAATAC
 CAAGTCAAAATGGACTACAAACCAATTTCACATCAAAAGTTAGCCCAACTG
 GAAAATATTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCT
 GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAA
 GTGCACTCAAACAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7307

STRAIN COH1

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 TATGTATTAGCATTAATCGGTGATATCATTAAATTCAAAACAGATACTTG
 AACGTGAAACTTCCAACAGTCTTTCAAGCAACTAATGACCGAACTATCT
 GATGTATATGGTGAAGAGCTGATTCTCCATTCACTATTACAGCTGGTGA
 TGAATTCAGCTTATTGAAACAcATCRAAAAAGGTATTCAAAATTATTG
 ACCATATTCAACTAGCTCTAAACACCTGTTAATGTAAGGTTGCCCTCGGT
 ACAGGAAACATTATAACATCCATCAATTCAATGAAAGTATCGGTGCTGA
 TGGCTCTGCCCTACTGGCATGCTCAGCTTAAATCATATACTGATA
 AAAATGATTATGAAACAGTCAAGTAGCTATTGCTTGTGATGAAGAC
 CAAAACCTTGAATTAAACACTAAATAGTCATTTCAATGCTTGAGCACCTTAATAC
 CAAGTCAAAATGGACTACAAACCAATTTCACATCAAAAGTTAGCCCAACTG
 GAAAATATTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCT
 GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAA
 GTGCACTCAAACAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7308

STRAIN M781

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 ATGTATTAGCATTAATCGGTGATATCATTAAATTCAAAACAGATACTTG
 AACGTGAAACTTCCAACAGTCTTTCAAGCAACTAATGACCGAACTATCT
 ATGTATATGGTGAAGAGCTGATTCTCCATTCACTATTACAGCTGGTGA
 GAATTCAGCTTATTGAAACAcATCRAAAAAGGTATTCAAAATTATTG
 CCATATTCAACTAGCTCTAAACCTGTTAATGTAAGGTTGCCCTCGGT
 CAGGAAACATTATAACATCCATCAATTCAATGAAAGTATCGGTGCTGA
 GGTCCTGCCCTACTGGCATGCTCAGCTTAAATCATATACTGATA
 AAATGATTATGAAACAGTCAAGTAGCTATTGCTTGTGATGAAGACC
 AAAACCTTGAATTAAACACTAAATAGTCATTTCAATGCTTGAGCACCTTAATAC
 AAGTCAAAATGGACTACAAACCAATTTCACATCAAAAGTTAGCCCAACTG
 CAAGATAATTATCAAGAACAAATTCAACATCAAAAGTTAGCCCAACTG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCT
 AGAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAA
 TTGCACTCAAACAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7309

STRAIN CJB110

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 TTATGATTAGCATTAATCGGTGATATCATTAAATTCAAAACAGATACT
 TGAACCGTGAACACTTCCAACAGTCTTTCAAGCAACTAATGACCGAACTAT
 CTGATGTATATGGTGAAGAGCTGATTCTCTATTCACTATTACAGCTGGT
 GATGAATTCAACTGTTATTGAAACCATCAAAAAGGTATTCAAAATTAT
 TGACCATATTCAACTAGCTCTAAACCTGTTAATGTAAGGTTGCCCTCG
 GTACAGGAAACATTATAACATCCATCAATTCAATGAAAGTATCGGTGCT
 GATGGTCCTGCCCTACTGGCATGCTCAGCTTAAATCATATACTGATA
 TAAAATGATTATGAAACAGTCAAGTAGCTATTGCTTGTGATGAAG
 ACCAACACCTTGAATTAAACACTAAATAGTCATTTCACTGCTTGAGCACCTTAAT
 ATCAAGTCAAAATGGACTACTAAACCAATTTCACATCAAAAGTTAGCCCAAC
 ACTTCAGATAATTATCAAGAACAAATTTCACATCAAAAAGTTAGCCCAAC
 TGAAAATATTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGT
 CTGAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAA
 AGTTGCACTCAAACAAAGGGGAAGCTATGATTTC

SEQ ID NO. 7310

STRAIN JM9130013

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 ATGTATTAGCATTAATCGGTGATATCATTAAATTCAAAACAGATACTTG
 AACGTGAAACTTCCAACAGTCTTTCAAGCAACTAATGACCGAACTATCT

Table 73: Comparative Sequences relating to SAG0981

ATGTATATGGTGAAGAGCTGATTCTCCATTCACTATTACAGCTGGTGAT
 GAATTCAAGCTTATTGAAACCATCAAAAAGGTATTCATAATTATTGA
 CCATATTCAACTAGCTCTAAACCTGTTAATGTAAGGTCGGCTCGGT
 CAGGAACATTATAACATCCATTAACTGAAAGTATCGGTGCTGAT
 GGTCCTGCCTACTGGCATGCTCGTCAGCTTAAATCATACATGATAA
 AAATGATTATGGAACAGCTCAAGTAGCTATTGCTTGTGATGAAGACC
 AAAACCTGAAATTAAACACTAAATAGTCTCATTCAGCTGGTGAATTATC
 AAGTCAAAATGAACTACAAACATTTCATGCTTGGCACTTAAATACT
 TCAAGATAATTATCAAGAACATTTCACATCAAAGTTAGCCCCACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAACGGCTCG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCACTCAAACCTAAAGGGGGAAAGCTATGATITTC

PRETTY of: /biotmp/msa31912.2{*} February 18, 2003 08:19 ..

		1		50
msa31912.2{338_18RS21}	---	TCTGCTA TAATAGACAA	AAAGGTGGTG	aTATTTATGT ATTTAGCATT
msa31912.2{338_2603}	ttgt	TCTGCTA TAATAGACAA	AAAGGTGGTG	aTATTTATGT ATTTAGCATT
msa31912.2{338_A909}	---	TCTGCTA TAATAGACAA	AAAGGTGGTG	aTATTTATGT ATTTAGCATT
msa31912.2{338_H36B}	---	TCTGCTA TAATAGACAA	AAAGGTGGTG	aTATTTATGT ATTTAGCATT
msa31912.2{338_JM9130013}	---	TCTGCTA TAATAGACAA	AAAGGTGGTG	aTATTTATGT ATTTAGCATT
msa31912.2{338_COH1}	---	TCTGCTA TAATAGACAA	AAAGGTGGTG	aTATTTATGT ATTTAGCATT
msa31912.2{338_M732}	---	TCTGCTA TAATAGACAA	AAAGGTGGTG	aTATTTATGT ATTTAGCATT
msa31912.2{338_M781}	---	TCTGCTA TAATAGACAA	AAAGGTGGTG	aTATTTATGT ATTTAGCATT
msa31912.2{338_090}	---	TCTGCTA TAATAGACAA	AAAGGTGGTG	aTATTTATGT ATTTAGCATT
msa31912.2{338_CJB110}	---	TCTGCTA TAATAGACAA	AAAGGTGGTG	gTATTTATGT ATTTAGCATT
Consensus	*****	*****	*****	*****
		51		100
msa31912.2{338_18RS21}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAAACGT GAAACTTTCC
msa31912.2{338_2603}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAAACGT GAAACTTTCC
msa31912.2{338_A909}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAAACGT GAAACTTTCC
msa31912.2{338_H36B}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAAACGT GAAACTTTCC
msa31912.2{338_JM9130013}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAAACGT GAAACTTTCC
msa31912.2{338_COH1}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAAACGT GAAACTTTCC
msa31912.2{338_M732}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAAACGT GAAACTTTCC
msa31912.2{338_M781}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAAACGT GAAACTTTCC
msa31912.2{338_090}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAAACGT GAAACTTTCC
msa31912.2{338_CJB110}	AATCGGTGAT	ATCATTAATT	CAAAACAGAT	ACTTGAAACGT GAAACTTTCC
Consensus	*****	*****	*****	*****
		101		150
msa31912.2{338_18RS21}	AACAGTCTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT ATATGGTGA
msa31912.2{338_2603}	AACAGTCTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT ATATGGTGA
msa31912.2{338_A909}	AACAGTCTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT ATATGGTGA
msa31912.2{338_H36B}	AACAGTCTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT ATATGGTGA
msa31912.2{338_JM9130013}	AACAGTCTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT ATATGGTGA
msa31912.2{338_COH1}	AACAGTCTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT ATATGGTGA
msa31912.2{338_M732}	AACAGTCTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT ATATGGTGA
msa31912.2{338_M781}	AACAGTCTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT ATATGGTGA
msa31912.2{338_090}	AACAGTCTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT ATATGGTGA
msa31912.2{338_CJB110}	AACAGTCTT	TCAGCAACTA	ATGACCGAAC	TATCTGATGT ATATGGTGA
Consensus	*****	*****	*****	*****
		151		200
msa31912.2{338_18RS21}	GAGCTGATTT	CTCcATTCA	TATTACAGCT	GGTGTGATGAAT TTCAAGCTTT
msa31912.2{338_2603}	GAGCTGATTT	CTCcATTCA	TATTACAGCT	GGTGTGATGAAT TTCAAGCTTT
msa31912.2{338_A909}	GAGCTGATTT	CTCcATTCA	TATTACAGCT	GGTGTGATGAAT TTCAAGCTTT
msa31912.2{338_H36B}	GAGCTGATTT	CTCcATTCA	TATTACAGCT	GGTGTGATGAAT TTCAAGCTTT
msa31912.2{338_JM9130013}	GAGCTGATTT	CTCcATTCA	TATTACAGCT	GGTGTGATGAAT TTCAAGCTTT
msa31912.2{338_COH1}	GAGCTGATTT	CTCcATTCA	TATTACAGCT	GGTGTGATGAAT TTCAAGCTTT
msa31912.2{338_M732}	GAGCTGATTT	CTCcATTCA	TATTACAGCT	GGTGTGATGAAT TTCAAGCTTT
msa31912.2{338_M781}	GAGCTGATTT	CTCcATTCA	TATTACAGCT	GGTGTGATGAAT TTCAAGCTTT
msa31912.2{338_090}	GAGCTGATTT	CTCcATTCA	TATTACAGCT	GGTGTGATGAAT TTCAAGCTTT
msa31912.2{338_CJB110}	GAGCTGATTT	CTCcATTCA	TATTACAGCT	GGTGTGATGAAT TTCAAGCTTT
Consensus	*****	*****	*****	*****
		201		250
msa31912.2{338_18RS21}	ATTGAAACCA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT ATTCAACTAG
msa31912.2{338_2603}	ATTGAAACCA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT ATTCAACTAG
msa31912.2{338_A909}	ATTGAAACCA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT ATTCAACTAG
msa31912.2{338_H36B}	ATTGAAACCA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT ATTCAACTAG
msa31912.2{338_JM9130013}	ATTGAAACCA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT ATTCAACTAG
msa31912.2{338_COH1}	ATTGAAACCA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT ATTCAACTAG
msa31912.2{338_M732}	ATTGAAACCA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT ATTCAACTAG
msa31912.2{338_M781}	ATTGAAACCA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT ATTCAACTAG
msa31912.2{338_090}	ATTGAAACCA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT ATTCAACTAG
msa31912.2{338_CJB110}	ATTGAAACCA	TCAAAAAAGG	TATTTCAAAT	TATTGACCAT ATTCAACTAG
Consensus	*****	*****	*****	*****
		251		300
msa31912.2{338_18RS21}	CTCTAAAACC	TGTTAATGTA	AGGTTGGCC	TCGGTACAGG AAACATTATA
msa31912.2{338_2603}	CTCTAAAACC	TGTTAATGTA	AGGTTGGCC	TCGGTACAGG AAACATTATA

Table 73: Comparative Sequences relating to SAG0981

msa31912.2{338_A909}	CTCTAAAACC	TGTTAATGTA	AGGTTGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_H36B}	CTCTAAAACC	TGTTAATGTA	AGGTTGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_JM9130013}	CTCTAAAACC	TGTTAATGTA	AGGTTGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_COH1}	CTCTAAAACC	TGTTAATGTA	AGGTTGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_M732}	CTCTAAAACC	TGTTAATGTA	AGGTTGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_M781}	CTCTAAAACC	TGTTAATGTA	AGGTTGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_090}	CTCTAAAACC	TGTTAATGTA	AGGTTGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_CJB110}	CTCTAAAACC	TGTTAATGTA	AGGTTGGCC	TCGGTACAGG	AAACATTATA
Consensus	*****	*****	*****	*****	*****
	301				350
msa31912.2{338_18RS21}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_2603}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_A909}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_H36B}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_JM9130013}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_COH1}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_M732}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_M781}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_090}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_CJB110}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
Consensus	*****	*****	*****	*****	*****
	351				400
msa31912.2{338_18RS21}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_2603}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_A909}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_H36B}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_JM9130013}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_COH1}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_M732}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_M781}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_090}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_CJB110}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
Consensus	*****	*****	*****	*****	*****
	401				450
msa31912.2{338_18RS21}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_2603}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_A909}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_H36B}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_JM9130013}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_COH1}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_M732}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_M781}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_090}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_CJB110}	CAGTTCAAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
Consensus	*****	*****	*****	*****	*****
	451				500
msa31912.2{338_18RS21}	ACACTAAATA	GTCTCATTTC	AGCTGGTGT	TTTATCAAGT	AAAAATGGAC
msa31912.2{338_2603}	ACACTAAATA	GTCTCATTTC	AGCTGGTGT	TTTATCAAGT	AAAAATGGAC
msa31912.2{338_A909}	ACACTAAATA	GTCTCATTTC	AGCTGGTGT	TTTATCAAGT	AAAAATGGAC
msa31912.2{338_H36B}	ACACTAAATA	GTCTCATTTC	AGCTGGTGT	TTTATCAAGT	AAAAATGGAC
msa31912.2{338_JM9130013}	ACACTAAATA	GTCTCATTTC	AGCTGGTGT	TTTATCAAGT	AAAAATGGAC
msa31912.2{338_COH1}	ACACTAAATA	GTCTCATTTC	AGCTGGTGT	TTTATCAAGT	AAAAATGGAC
msa31912.2{338_M732}	ACACTAAATA	GTCTCATTTC	AGCTGGTGT	TTTATCAAGT	AAAAATGGAC
msa31912.2{338_M781}	ACACTAAATA	GTCTCATTTC	AGCTGGTGT	TTTATCAAGT	AAAAATGGAC
msa31912.2{338_090}	ACACTAAATA	GTCTCATTTC	AGCTGGTGT	TTTATCAAGT	AAAAATGGAC
msa31912.2{338_CJB110}	ACACTAAATA	GTCTCATTTC	AGCTGGTGT	TTTATCAAGT	AAAAATGGAC
Consensus	*****	*****	*****	*****	*****
	501				550
msa31912.2{338_18RS21}	TACAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAATTATC
msa31912.2{338_2603}	TACAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAATTATC
msa31912.2{338_A909}	TACAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAATTATC
msa31912.2{338_H36B}	TACAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAATTATC
msa31912.2{338_JM9130013}	TACAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAATTATC
msa31912.2{338_COH1}	TACAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAATTATC
msa31912.2{338_M732}	TACAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAATTATC
msa31912.2{338_M781}	TACAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAATTATC
msa31912.2{338_090}	TACAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAATTATC
msa31912.2{338_CJB110}	TACAACCAT	TTTCAAATGC	TTGAGCACIT	AATACTTCAA	GATAATTATC
Consensus	*****	*****	*****	*****	*****
	551				600
msa31912.2{338_18RS21}	AAGAACCAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_2603}	AAGAACCAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_A909}	AAGAACCAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_H36B}	AAGAACCAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_JM9130013}	AAGAACCAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_COH1}	AAGAACCAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_M732}	AAGAACCAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT

Table 73: Comparative Sequences relating to SAG0981

msa31912.2{338_M781}	AAGAACATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT	
msa31912.2{338_O90}	AAGAACATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT	
msa31912.2{338_CJB110}	AAGAACATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT	
Consensus	*****	*****	*****	*****	*****	
						601
msa31912.2{338_18RS21}	AGTGCCTGA	CTAAACGCC	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG	650
msa31912.2{338_2603}	AGTGCCTGA	CTAAACGCC	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG	
msa31912.2{338_A909}	AGTGCCTGA	CTAAACGCC	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG	
msa31912.2{338_H36B}	AGTGCCTGA	CTAAACGCC	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG	
msa31912.2{338_JM9130013}	AGTGCCTGA	CTAAACGCC	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG	
msa31912.2{338_COH1}	AGTGCCTGA	CTAAACGCC	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG	
msa31912.2{338_M732}	AGTGCCTGA	CTAAACGCC	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG	
msa31912.2{338_M781}	AGTGCCTGA	CTAAACGCC	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG	
msa31912.2{338_O90}	AGTGCCTGA	CTAAACGCC	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG	
msa31912.2{338_CJB110}	AGTGCCTGA	CTAAACGCC	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG	
Consensus	*****	*****	*****	*****	*****	
						651
msa31912.2{338_18RS21}	AACGAGAACAA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACTA	700
msa31912.2{338_2603}	AACGAGAACAA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACTA	
msa31912.2{338_A909}	AACGAGAACAA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACTA	
msa31912.2{338_H36B}	AACGAGAACAA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACTA	
msa31912.2{338_JM9130013}	AACGAGAACAA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACTA	
msa31912.2{338_COH1}	AACGAGAACAA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACTA	
msa31912.2{338_M732}	AACGAGAACAA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACTA	
msa31912.2{338_M781}	AACGAGAACAA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACTA	
msa31912.2{338_O90}	AACGAGAACAA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACTA	
msa31912.2{338_CJB110}	AACGAGAACAA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACTA	
Consensus	*****	*****	*****	*****	*****	
						701
msa31912.2{338_18RS21}	AAGGGGGAAAG	CTATGATTC				720
msa31912.2{338_2603}	AAGGGGGAAAG	CTATGATTC				
msa31912.2{338_A909}	AAGGGGGAAAG	CTATGATTC				
msa31912.2{338_H36B}	AAGGGGGAAAG	CTATGATTC				
msa31912.2{338_JM9130013}	AAGGGGGAAAG	CTATGATTC				
msa31912.2{338_COH1}	AAGGGGGAAAG	CTATGATTC				
msa31912.2{338_M732}	AAGGGGGAAAG	CTATGATTC				
msa31912.2{338_M781}	AAGGGGGAAAG	CTATGATTC				
msa31912.2{338_O90}	AAGGGGGAAAG	CTATGATTC				
msa31912.2{338_CJB110}	AAGGGGGAAAG	CTATGATTC				
Consensus	*****	*****				

SEQ ID NO. 7311

STRAIN 2603 frame: 1

LSAIIDKKVVI FMYLALIGDI INSKQILERETFQQSFQQLMTELSDDVYGEELISPFTITAG
 DEFQALLKPSKKVFOIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHAR
 SAIHIDKNDYGTQVAICLDDDEDQNLELTLNLSIISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEFOHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7312

STRAIN 090 frame: 1

SAIIDKKVVI FMYLALIGDI INSKQILERETFQQSFQQLMTELSDDVYGEELISPFTITAG
 DEFQALLKPSKKVFOIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHAR
 AINHIDKNDYGTQVAICLDDDEDQNLELTLNLSIISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEFOHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7313

STRAIN A909 frame: 1

SAIIDKKVVI FMYLALIGDI INSKQILERETFQQSFQQLMTELSDDVYGEELISPFTITAG
 DEFQALLKPSKKVFOIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHAR
 AINHIDKNDYGTQVAICLDDDEDQNLELTLNLSIISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEFOHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7314

STRAIN H36B frame: 1

SAIIDKKVVI FMYLALIGDI INSKQILERETFQQSFQQLMTELSDDVYGEELISPFTITAG
 DEFQALLKPSKKVFOIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHAR
 AINHIDKNDYGTQVAICLDDDEDQNLELTLNLSIISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEFOHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7315

STRAIN 18RS21 frame: 1

SAIIDKKVVI FMYLALIGDI INSKQILERETFQQSFQQLMTELSDDVYGEELISPFTITAG
 DEFQALLKPSKKVFOIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHAR
 AINHIDKNDYGTQVAICLDDDEDQNLELTLNLSIISAGDFIKSKWTTNHFQMLEHLILQD
 NYQEFOHQKLAQLENIEPSALTKRLKASGLKIYLRTRTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7316

STRAIN M732 frame: 1

SAIIDKKVVI FMYLALIGDI INSKQILERETFQQSFQQLMTELSDDVYGEELISPFTITAG

Table 73: Comparative Sequences relating to SAG0981

DEFQALLKOSKKVVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVAICLDDDEDQNLELTNSLISAGDFIKSKWITNFQMLEHLILQD
 NYQEQQFHOKLAQLENIEPSALTKRLKASGLKIYLRTTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7317

STRAIN COH1 frame: 1

SAIIDKKVVI FMYLALIGDIINSKQILERETFQOQSFOQLMTELSDVYGEELISPFTITAG
 DEFQALLKOSKKVVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVAICLDDDEDQNLELTNSLISAGDFIKSKWITNFQMLEHLILQD
 NYQEQQFHOKLAQLENIEPSALTKRLKASGLKIYLRTTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7318

STRAIN M781 frame: 1

SAIIDKKVVI FMYLALIGDIINSKQILERETFQOQSFOQLMTELSDVYGEELISPFTITAG
 DEFQALLKOSKKVVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVAICLDDDEDQNLELTNSLISAGDFIKSKWITNFQMLEHLILQD
 NYQEQQFHOKLAQLENIEPSALTKRLKASGLKIYLRTTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7319

STRAIN CJB110 frame: 1

SAIIDKKVVFMYLALIGDIINSKQILERETFOQSFOQLMTELSDVYGEELISPFTITAG
 DEFQALLKPSKVKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVAICLDDDEDQNLELTNSLISAGDFIKSKWITNFQMLEHLILQD
 NYQEQQFHOKLAQLENIEPSALTKRLKASGLKIYLRTTQAADLLVKSCTQTKGGSYDF

SEQ ID NO. 7320

STRAIN JM9130013 frame: 1

SAIIDKKVVI FMYLALIGDIINSKQILERETFOQSFOQLMTELSDVYGEELISPFTITAG
 DEFQALLKPSKVKVFQIIDHIQLALKPVNVRFGGLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTQVAICLDDDEDQNLELTNSLISAGDFIKSKWITNFQMLEHLILQD
 NYQEQQFHOKLAQLENIEPSALTKRLKASGLKIYLRTTQAADLLVKSCTQTKGGSYDF

PRETTY of: /biotmp/msa32053.2{(*)} February 18, 2003 08:25 ..

	1	50
msa32053.2{338_18RS21}	-SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE	
msa32053.2{338_2603}	1SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE	
msa32053.2{338_A909}	-SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE	
msa32053.2{338_CJB110}	-SAIIDKKVV vFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE	
msa32053.2{338_COH1}	-SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE	
msa32053.2{338_H36B}	-SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE	
msa32053.2{338_JM9130013}	-SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE	
msa32053.2{338_M732}	-SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE	
msa32053.2{338_M781}	-SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE	
msa32053.2{338_090}	-SAIIDKKVV iFMYLALIGD IINSKQILER ETFQQSFQQL MTELSDVYGE	
Consensus	***** - *****	*****
	51	100
msa32053.2{338_18RS21}	ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNI I	
msa32053.2{338_2603}	ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNI I	
msa32053.2{338_A909}	ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNI I	
msa32053.2{338_CJB110}	ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNI I	
msa32053.2{338_COH1}	ELISpFTITA GDEFQALLKq SKKVFQIIDH IQLALKPVNV RFGLGTGNI I	
msa32053.2{338_H36B}	ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNI I	
msa32053.2{338_JM9130013}	ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNI I	
msa32053.2{338_M732}	ELISpFTITA GDEFQALLKq SKKVFQIIDH IQLALKPVNV RFGLGTGNI I	
msa32053.2{338_M781}	ELISpFTITA GDEFQALLKq SKKVFQIIDH IQLALKPVNV RFGLGTGNI I	
msa32053.2{338_090}	ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNI I	
Consensus	***** - *****	*****
	101	150
msa32053.2{338_18RS21}	TSINsNESIG ADGPAYWHAR SAINHHIDKN DYGTQVAIC LDDEDQNLEL	
msa32053.2{338_2603}	TSINsNESIG ADGPAYWHAR SAINHHIDKN DYGTQVAIC LDDEDQNLEL	
msa32053.2{338_A909}	TSINsNESIG ADGPAYWHAR SAINHHIDKN DYGTQVAIC LDDEDQNLEL	
msa32053.2{338_CUB110}	TSINsNESIG ADGPAYWHAR SAINHHIDKN DYGTQVAIC LDDEDQNLEL	
msa32053.2{338_COH1}	TSINsNESIG ADGPAYWHAR SAINHHIDKN DYGTQVAIC LDDEDQNLEL	
msa32053.2{338_H36B}	TSINsNESIG ADGPAYWHAR SAINHHIDKN DYGTQVAIC LDDEDQNLEL	
msa32053.2{338_JM9130013}	TSINsNESIG ADGPAYWHAR SAINHHIDKN DYGTQVAIC LDDEDQNLEL	
msa32053.2{338_M732}	TSINsNESIG ADGPAYWHAR SAINHHIDKN DYGTQVAIC LDDEDQNLEL	
msa32053.2{338_M781}	TSINsNESIG ADGPAYWHAR SAINHHIDKN DYGTQVAIC LDDEDQNLEL	
msa32053.2{338_090}	TSIN1NESIG ADGPAYWHAR SAINHHIDKN DYGTQVAIC LDDEDQNLEL	
Consensus	***** - *****	*****
	151	200
msa32053.2{338_18RS21}	TLNLSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQQHQ KLAQLENIEP	
msa32053.2{338_2603}	TLNLSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQQHQ KLAQLENIEP	
msa32053.2{338_A909}	TLNLSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQQHQ KLAQLENIEP	
msa32053.2{338_CJB110}	TLNLSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQQHQ KLAQLENIEP	
msa32053.2{338_COH1}	TLNLSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQQHQ KLAQLENIEP	
msa32053.2{338_H36B}	TLNLSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQQHQ KLAQLENIEP	
msa32053.2{338_JM9130013}	TLNLSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQQHQ KLAQLENIEP	
msa32053.2{338_M732}	TLNLSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQQHQ KLAQLENIEP	
msa32053.2{338_M781}	TLNLSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQQHQ KLAQLENIEP	

Table 73: Comparative Sequences relating to SAG0981

msa32053.2{338_090}	TLNSLISAGD FIKSKWTTNH FQMLEHLILQ DNYQEQQFOHQ KLAQLENIEP
Consensus	***** * ***** * ***** * ***** * *****
	201 240
msa32053.2{338_18RS21}	SALT _K R _L KAS GLK _I YLRTRT QAADLLVKSC TQTKGGSYDF
msa32053.2{338_2603}	SALT _K R _L KAS GLK _I YLRTRT QAADLLVKSC TQTKGGSYDF
msa32053.2{338_A909}	SALT _K R _L KAS GLK _I YLRTRT QAADLLVKSC TQTKGGSYDF
msa32053.2{338_CJB110}	SALT _K R _L KAS GLK _I YLRTRT QAADLLVKSC TQTKGGSYDF
msa32053.2{338_COH1}	SALT _K R _L KAS GLK _I YLRTRT QAADLLVKSC TQTKGGSYDF
msa32053.2{338_H36B}	SALT _K R _L KAS GLK _I YLRTRT QAADLLVKSC TQTKGGSYDF
msa32053.2{338_JM9130013}	SALT _K R _L KAS GLK _I YLRTRT QAADLLVKSC TQTKGGSYDF
msa32053.2{338_M732}	SALT _K R _L KAS GLK _I YLRTRT QAADLLVKSC TQTKGGSYDF
msa32053.2{338_M781}	SALT _K R _L KAS GLK _I YLRTRT QAADLLVKSC TQTKGGSYDF
msa32053.2{338_090}	SALT _K R _L KAS GLK _I YLRTRT QAADLLVKSC TQTKGGSYDF
Consensus	***** * ***** * ***** * *****

Table 74: Comparative Sequences relating to SAG1572**SEQ ID NO. 7401****STRAIN 2603**

ATGGAATCGAACGTTCAAAAAGTTAAATCAAATATAACATTACGGAACACTCTAT
 CTAGTCCCAACTCAATTGGTAATCTAGATGATGACTTTCTGTGCCATTAGGATTITA
 AGAGAAGTGTGATTTCTGTGCCATTAGGATTITA
 TTTGATATTACTAAACAAATTAGTTCAACGACATGCTTACGATAAAATCTCT
 GGGTAATTGATTGTTAAAAGAAGGGAAATCTTAGGCCAAGTATCTGATGCAGGAATG
 CCCCTATTTCTGACCCAGGACATGACCTTGCAAGGCTGCTATTGAGGGGATATCCA
 GTTGATATTACTACAGGAGCTGCTGTTACTGCTCATCGCTCAGGTTAGCT
 CCACAACCTCATATTTCATGGCTTCTAACCTCGTAAGAAAGGTCAACAAATACTTC
 TTGAAACAAAGCAATTACCCCTGAAACACAAATCTTATGAGTCACCGTTTGCAGTC
 TCTGATACGCTAAACACATGAAAGAGATTACGGAGATCGCCAAGTTGTTTAGTACGC
 GAATTGAGGAAACTCTATGAAAGACTATCAAAGGAGAACATTAGTCAACTTTAGAGCAT
 ATTGAAAAGGTCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGTTAGAGAGATACC
 GAGCAGTGAAGAACAGATAGCCAAACAGACTAGTAAAGAATATATCGCT
 ATGGTGATAAAACTAACTACAGGATAAAAAAAAGTAGCAGAACAGATTAACTCAATAGA
 CAAGAACTCTATGCTAGTTCCATGATTTA

SEQ ID NO. 7402**STRAIN 090**

GAAATGCAAGTCAAAAAGTTAAATCAAATACACATTACGGGACACT
 CTATCTAGTCCAACTCAATTGGTAATCTAGATGATGACTTTCTGTGCCATTAGG
 CCAATTAGGATTITAAGAGAAGTTGATTTTATTGTGCCAGGAGATACCGA
 AATACGGGACTTTACTCAAGCACTTGTATTAATTACTAAACAAATTAG
 TTTCACGAAACAAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGT
 TAAAAGAAGGGAGATCTTAGGCCAAGTATCTGATGCAGGAATGCCCTCT
 ATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAGGGGGAT
 CCCGGTCGATCTATCACCGAGCTAGCGCTGGTATTACTGCTCTCATCG
 CTTCAAGGTTAGCTCCACAACTCATATTTTATGGCTTCTTACCGCGT
 AAGAAAGGTCACAAATAACTTTTTGAAACAAAGAAAGATTACCTCTGA
 AACACAAATCTTTATGAGTCACCGTTTCGAGTCTTGATACGCTAAAC
 ACATGAAAGAGATTACGGAGATCGCCAAGTTGTTTAGTACCGGAATTG
 ACCGAAactCTATGAAAGACTATCAAAGGAGAACATTAGTCAACTTTAGG
 GCATATTGAAAAGTCCCTCTAAAGGTGAATGCTTAATTATTGTTGATG
 GTAAGAGAGATACCGAGCGAGTGAAGAGACAGTAGCCAACAGATCCACTA
 GTATTAGTAA

SEQ ID NO. 7403**STRAIN A909**

AGTCAAAAGTTAAATCAAATATAACATTACGGAACACTCTATCTAG
 TCCAACCTCAATTGGTAATCTAGATGATGACTTTCTGTGCCATTAGG
 ATTGAGAGAAGTTGATTTTATTGTGCCAGGAGATACCGAAATACGG
 ACTTTACTCAAGCACTTGTATTAATTACTAAACAAATTAGTTTCTAG
 AACACAATCTTACGATAAAATCTCTGGGTTATTGATTTGTAAAGAA
 GGGAAATCTTAGGCCAAGTATCTGATGCAGGAATGCCCTCTATTCTGA
 CCCAGGACATGACCTTGCAAGGCTGCTATTGAGGGGATATCCCAGTIG
 TAATCTATACAGGAGCTAGCGCTGCTATTACTGCTCATCGCTTACGGT
 TTAGCTCCAAACCTCATATTTTATGGCTTCTTACACCGTAAGAAAGG
 TCAACAAATAACTTCTGAAACAAAGCAAGATTACCTGAAACACAAA
 TCTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAACACATGAAA
 GAGATTACGGAGATCGCCAAGTTGTTTAGTACCGGAATTGACGAAACT
 CTATGAAAGACTATCAAAGGAGAACATTAGTCAACTTTAGCAGTATTG
 AAAAGGTCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGTTAGAGA
 GATACCGAGCGAGTGAAGAGACAGTAGCCAACAGATCCACTAGTATTG
 AA

SEQ ID NO. 7404**STRAIN H36B**

GAAATGCAAGTCAAAAAGTTAAATCAAATACACATT
 ACGGGACACTCTATCTAGTCCAACTCAATTGGTAATCTAGATGATG
 ACTTTCTGTGCCATTAGGATTITAAGAGAAGTTGATTTTATTGTGCCAGA
 GGATACACGAAATACGGGACTTTACTCAAGCACTTGTATTAATTACTA
 AACAAATTAGTTCTCGAAACACATGCTTATGATAAAATCTCTGGGTTA
 ATTGATTGTTAAAGAAGGGAGATCTTAGGCCAAGTATCTGATGCAGG
 AATGCCCTCTATTCTGACCCAGGACATGACCTTGCAAGGCTGCTATTG
 AAGGGGAGATCTCGGCTGCTATACCGAGGAGCTAGCGCTGGTATTACT
 GCTCTCATCGCTTACGGTTAGCTCCACACCTCATATTTTATGGCTT
 CTACCGCGTAAGCAAGTCACAAATAACTTTTTGAAACAAAGAAAG
 ATTACCCCTGAAACACAAATCTTTATGAGTCACCGTTTCGAGTCTCTGAT
 ACGCTAAACACATGAAAGAGATTATGGAGATCGCCAAGTTGTTTAGT
 ACCGAAATTGAGCAACACTCTATGAAAGACTATCAAAGGAGAACATTACTC
 AACITTTAGGGCATATTGAAAAGGTCCCTCTAAAGGTGAATGCTTAATT
 ATTGTTGATGTTAGAGAGACTGAGCGAGTGAAGAGACAGTAGCCAACA
 AGATCCACTAGTATTGTA

SEQ ID NO. 7405**STRAIN 18RS21**

GAAATGCAAGTCAAAAAGTTAAATCAAATATAACATT
 ACGGAACACTCTATCTAGTCCAACTCAATTGGTAATCTGATGATG
 ACTTTCTGTGCCATTAGGATTITAAGAGAAGTTGATTTTATTGTGCCAGA
 GGATACACGAAATACGGGACTTTACTCAAGCACTTGTATTAATTACTA
 AACAAATTAGTTCTCGAAACACATGCTTACGATAAAATCTCTGGGTTA
 ATTGATTGTTAAAGAAGGGAAATCTTAGGCCAAGTATCTGATGCAGG

Table 74: Comparative Sequences relating to SAG1572

AATGCCCTCATTTCTGACCCAGGACATGACCTTGTCAAGGCCTGCTATTG
 AAGGGGATATCCCAGTTGATCTATACCAGGAGCTAGCCTGGTATTACT
 GCTCTCATCGCTTCAGGTTAGCTCCACAACCTCATATTTTATGGCTT
 CTACACAGTAAGAAGGTCAACAAATACTTCTTGTAAACAAAGCAAG
 ATACACAGTAAGAAGGTCAACAAATACTTCTTGTAAACAAAGCAAG
 ATGCTAAACACATGAAAGAGATTACGGAGATCGCCAAGTTGTTAGT
 ACAGCAGATTGACGAAACTCTATGAAGAGTATCAAAGAGAACCTAGTC
 AACCTTTAGAGCATATTGAAAGAGTCCCTCTCAAAGGTGAATGCTTAATT
 ATTGTTGATGGTAAGAGAGATACCGAGCAGTGAAAGACAGTAGCCAACA
 AGATCCACTAGTATTAGTAA

SEQ ID NO. 7406

STRAIN M732

GAAATGCAAGTCAAAAAAGTTTAAATCAAAT
 ATACATTACGGAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGA
 TGATATGACTTTCTGCCCCATTAGGATTTAAGAGAAAGTGATTTATT
 GTGCAGGAGATAACGAAATAACGGGACTTTACTCAAGCACTTGTATATT
 ACTACTAAACAAATACTTGTAAACGAAACAAATGCTTACGATAAAAATCTC
 TGGGTTAATTGATTTGTTAAAGAAGGGAAATCTTAGCCTAGTATCTG
 ATGCAGGAATGCCCTCATTTCTGACCCAGGACATGACCTTGTCAAGGT
 GCTATTGAAAGGGATATCCAGTTGATCTATACCAGGAGCTAGCCTGG
 TATTACTGCTCATCGCTTCAAGGTTAGCTCCACAACCTCATATTTTT
 ATGGCTTCTTACACAGTAAGAAGGTCAACAAATAACTTCTTGTAAACA
 AAGCAAGATTACCCGAAACACAAATACTTGTAAAGAGATCGCCAAGTGT
 CTCTGATACGCTAAACACATGAAAGAGATTACGGAGATCGCCAAGTGT
 TTGTTAGTACGCAATTGACGAAACTCTATGAAGAGTATCAAAGAGAAC
 ATTAGTCACTTTGTAGAGCATATTGAAAGAGTCCCTCTCAAAGGTGAATG
 CTTAATTATTGTTGATGGTAAGAGAGATACCGAGCAGTGAAAGACAGTA
 GCCAACAAAGATCCACTAGTATTAGTAA

SEQ ID NO. 7407

STRAIN COH1

GAAATGCAAGTCAAAAAAGTTTAAATCAAATATAACATTAC
 GGAAACACTCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGAC
 TTTCGIGCCATTAGGATTTAAGAGAAAGTGATTTATTGTCAGGAGG
 ATACACGAAATAACGGGAcTTTACTCAAGGACTTTGATATTACTAA
 CAAATTAGTTTCAACGAAACAAATGCTTACGATAAAATCTCTGGTTAAAT
 TGATTGTTAAAGAAGGGAAATCTTAGCCTAGTATCTGATGCAAGGAA
 TGCCCTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAA
 GGGGATATCCCAAGTTGATCTATACCAAGGAGCTAGCCTGGTATTACTGC
 TCTCATCGCTTCAAGGTTAGCTCCACAACCTCATATTTTATGGCCTCT
 TACCAAGCTAAGAAGGTCAACAAATAACTTCTTGAACAAAGCAAGAT
 TACCGTAAAGGATCTTATGAGTCACCGtTTCGAGTCTGATAC
 GCTAAAACACATGAAAGAGATTACGGAGATCGCCAAGTGTATTAGTAC
 GCGAATTGACGAAACTCTATGAAGAGTATCAAAGAGAACCTAGTCAA
 CTTTAGAGCATATTGAAAGAGTCCCTCTCAAAGGTGAATGCTTAATT
 TGGTGTAGGTAAGAGAGATACCGAGCAGTGAAAGACAGTAGCCAACAAG
 ATCCACTAGTATTAGTAA

SEQ ID NO. 7408

STRAIN M781

AAATGCAAGTCAAAAAAGTTTAAATCAAATATAACATTACGGAAACACTC
 TATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTCTGTC
 CATTAGGATTTAAGAGAAAGTGATTTATTGTCAGGAGATAACGAA
 ATACGGgACTTTACTCAAGCACTTGTATTTACTAAACAAATTAGT
 TTACGAAACAAATGCTTACGGGATAAAATCTGGTTATTGATTGTT
 AAAAGAAGGGAAATCTTACGGCAAGTATCTGATGCAAGGATGCCCTcTA
 TTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAAGGGGATATC
 CCAGTTGATCTATACCAAGGAGCTAGCCTGGTATTACTGCTCTCATCGC
 TTCAAGGTTAGCTCCACAACCTCATATTTTATGGCTTCTTACACGTA
 AGAAAGGTCAACAAATAACTTTTGAACAAAGCAAGATTACCCGTAA
 ACACAAATCTTTATGAGTCACGGTTTCAGTcTcTGATACGCTAAACAA
 CATGAAAGAGATTACGGAGATCGCCAAGTTGTTTAGTACGCGAATTG
 CGAAACTCTATGAAGAGTATCAAAGAGAACCTAGTCAACTTTAGAG
 CATATTGAAAGAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGG
 TAAAGAGAGATACCGAGCAGTGAAAGACAGTAGCCAACAAGATCCACTAG
 TATTAGTAA
 A

SEQ ID NO. 7409

STRAIN CJB110

GAAATGCAAGTCAAAAAAGTTTAAATCAAATACACATTACGGGACAC
 TCCTATCTAGTCCCAACTCCAATTGGTAATCTAGATGATATGACTTTCTG
 GCCATTAGGATTTAAGAGAAAGTGATTTATTGTCAGGAGGATACAG
 AAATACGGGACTTTACTCAAGCACTTGTATTTACTAAACAAATT
 GTTTCTCAGGAAACAAATGCTTACGATAAAATCTCTGGTTAATTGATTG
 TTAAAGAAGGGAGATCTTACGGGAGATCGCCAAGTATCTGATGCAAGGAA
 TCCGGCTGATCTATACCAAGGAGCTAGCCTGGTATTACTGCTCTCATC
 GCCTCAGGTTAGCTCCACAACCTCATATTGTTATGCTTCTTACCGCG
 TAAGAAAGGTCAACAAATAACTTTTTGAAACAAAGAAAGATTACCCGT
 AAACACAAATCTTATGAGTCACCGtTTGAGTCTGATACGCTAAAC
 CATGAAAGAGATTACGGAGATCGCCAAGTGTGTTAGTACGCGAATT

Table 74: Comparative Sequences relating to SAG1572

GACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCACCTTTAG
 GGATATTGAAAAGTCCCTCAAGGTGAATGCTTAATTATTGTTGAT
 GTTAAGAGAGATACCGAGCAGTGAAGACAGTAGCCAACAAGATCCACT
 AGTATTAGTAA

SEQ ID NO. 7410
STRAIN 1169NT
 TGCAAGTTCAAAAAAGTTTAAATCAAATACACATTATGGGACACTCTAT
 CTAGTCCCACCTCAATTGGTAATCTAGATGATATGACTTTCTGCCCCAT
 TAGGATTAAAGAAGTTGatTTTATTGTGCAGAGGATACACGAAATA
 CGGGACTTTACTCAAGCACTTGTATTAACAAATTAGTT
 cACGAACACAATGCTTACGATAAAATCTGGGTTAATTGATTGTTAA
 AGAAGGGAAATCTTACGCCAAGTATCTGATGCAGGAATGCCCTCTATT
 CTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGATATCCA
 GTTGATATTACCGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTC
 AGGTTAGCTCCACAACTCATTTTTATGGCTTCAACACGTAAGA
 AAGTCACAAATAACTTTTTGAAACAAGAACAGATTATCTGAAACA
 CAAATTTTATGAGTCACCGTttCGAGTCTCTGATACGCTAAACACAT
 GAAAGGAGATTACGGAGATGCCAAGTGTGTTAGTACCGAATTGACgA
 AACTCTATGAAGAGTATCAAAGAGAACCCATTaGTCACCTTTAGAGCAT
 ATTGAAAAGGTCCTCTAAAGGTGAATGCTTAATTATTGTTGATGGTAA
 GAGAGAtaCCGAGCGAGTGAAGAGACAGTAGCCAACAAGATCCACTAGTAT
 TAGTAA

SEQ ID NO. 7411
STRAIN JM9130013
 GAAATGCAAGTTCAAAAAAGTTTAAATCAAATAACACATTACGGGA
 CACTCTATCTAGTCCCACCTCAATTGGTAATCTAGATGATATGACTTT
 CGTCCATTAGGATTAAAGAGAAGTTGATTTTATTGTGCAGAGGATAC
 AGGAATAACGGGACTTTACTCAAGCACTTGTATGATAAAATCTGGGTTAATTGAT
 TTGTTAAAGAAGGGAGATCTTAGGCCAAGTGTGATGCAAGGAAATGCC
 CTCTATTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGG
 ATATCCGGTCTATCTATACAGGAGCTAGCGCTGGTATTCTGCTCTC
 ATCGCTTCAGGTTAGCTCCACAACCTCATTTTTATGGCTTCTTAC
 GCGTAAGCAAGGTTAGTCAACAAATAACTTTTGAAACAAAGAACAGATTACC
 CTGAAACACATGAAAGAGATTATGGAGATGCCAAGTGTGTTAGTACCGA
 ATGACGAAACTCTATGAAGAGTATCAAAGGAAACCAATTGCAACTTT
 TAGGGCATATTGAAAGGTCTCTCAAAGGTGAATGCTTAATTATTGTT
 GATGGTAAGAGAGATACTGAGCGAGTGAAGACAGTAGCCAACAAGATCC
 AGTAGTATTAGTAA

PRETTY of: /biotmp/msa323014.2{*} March 28, 2003 02:40 ..

msa323014.2{343_18RS21}	1	---gaaatgc aAGTTCAAAA AAGTTTAAA TCAAATAC ATTAcGGaAC	50
msa323014.2{343_A909}		-----AGTTCAAAA AAGTTTAAA TCAAATAC ATTAcGGaAC	
msa323014.2{343_COH1}		---gaaatgc aAGTTCAAAA AAGTTTAAA TCAAATAC ATTAcGGaAC	
msa323014.2{343_M732}		---gaaatgc aAGTTCAAAA AAGTTTAAA TCAAATAC ATTAcGGaAC	
msa323014.2{343_M781}		----aaatgc aAGTTCAAAA AAGTTTAAA TCAAATAC ATTAcGGaAC	
msa323014.2{343_2603}		atggaaatgc aAGTTCAAAA AAGTTTAAA TCAAATAC ATTAcGGaAC	
msa323014.2{343_1169NT}		-----tgc aAGTTCAAAA AAGTTTAAA TCAAATAC ATTAcGGgAC	
msa323014.2{343_090}		---gaaatgc aAGTTCAAAA AAGTTTAAA TCAAATAC ATTAcGGgAC	
msa323014.2{343_CJ8110}		---gaaatgc aAGTTCAAAA AAGTTTAAA TCAAATAC ATTAcGGgAC	
msa323014.2{343_H36B}		---gaaatgc aAGTTCAAAA AAGTTTAAA TCAAATAC ATTAcGGgAC	
msa323014.2{343_JM9130013}		---gaaatgc aAGTTCAAAA AAGTTTAAA TCAAATAC ATTAcGGgAC	
Consensus		*****-*****-*****-*****-*****-*****-*****	
msa323014.2{343_18RS21}	51	ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC	100
msa323014.2{343_A909}		ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC	
msa323014.2{343_COH1}		ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC	
msa323014.2{343_M732}		ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC	
msa323014.2{343_M781}		ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC	
msa323014.2{343_2603}		ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC	
msa323014.2{343_1169NT}		ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC	
msa323014.2{343_090}		ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC	
msa323014.2{343_CJ8110}		ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC	
msa323014.2{343_H36B}		ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC	
msa323014.2{343_JM9130013}		ACTCTATCTA GTCCCAACTC CAATTGGTAA TCTAGATGAT ATGACTTTTC	
Consensus		*****-*****-*****-*****-*****-*****-*****	
msa323014.2{343_18RS21}	101	GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA	150
msa323014.2{343_A909}		GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA	
msa323014.2{343_COH1}		GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA	
msa323014.2{343_M732}		GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA	
msa323014.2{343_M781}		GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA	
msa323014.2{343_2603}		GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA	
msa323014.2{343_1169NT}		GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA	
msa323014.2{343_090}		GTGCCATTAG GATTTTAAGA GAAGTTGATT TTATTTGTGC AGAGGATACA	

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_CJB110}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT	TTATTTGTGC	AGAGGATACA
msa323014.2{343_H36B}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT	TTATTTGTGC	AGAGGATACA
msa323014.2{343_JM9130013}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT	TTATTTGTGC	AGAGGATACA
Consensus	*****	*****	*****	*****	*****
	151			200	
msa323014.2{343_18RS21}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_A909}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_COH1}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_M732}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_M781}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_2603}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_1169NT}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_090}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_CJB110}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_H36B}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_JM9130013}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
Consensus	*****	*****	*****	*****	*****
	201			250	
msa323014.2{343_18RS21}	TAGTTTCAC	GAACACAATG	CTTACGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_A909}	TAGTTTCAC	GAACACAATG	CTTACGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_COH1}	TAGTTTCAC	GAACACAATG	CTTACGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_M732}	TAGTTTCAC	GAACACAATG	CTTACGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_M781}	TAGTTTCAC	GAACACAATG	CTTACGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_2603}	TAGTTTCAC	GAACACAATG	CTTACGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_1169NT}	TAGTTTCAC	GAACACAATG	CTTACGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_090}	TAGTTTCAC	GAACACAATG	CTTACGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_CJB110}	TAGTTTCAC	GAACACAATG	CTTACGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_H36B}	TAGTTTCAC	GAACACAATG	CTTACGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_JM9130013}	TAGTTTCAC	GAACACAATG	CTTACGATAA	AATCTCTGGG	TTAATTGATT
Consensus	*****	*****	*****	*****	*****
	251			300	
msa323014.2{343_18RS21}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_A909}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_COH1}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_M732}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_M781}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_2603}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_1169NT}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_090}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_CJB110}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_H36B}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_JM9130013}	TGTTAAAAGA	AGGGAAATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
Consensus	*****	*****	*****	*****	*****
	301			350	
msa323014.2{343_18RS21}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_A909}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_COH1}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_M732}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_M781}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_2603}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_1169NT}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_090}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_CJB110}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_H36B}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
msa323014.2{343_JM9130013}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGa
Consensus	*****	*****	*****	*****	*****
	351			400	
msa323014.2{343_18RS21}	tATCCCCaGTt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_A909}	tATCCCCaGTt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_COH1}	tATCCCCaGTt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_M732}	tATCCCCaGTt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_M781}	tATCCCCaGTt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_2603}	tATCCCCaGTt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_1169NT}	tATCCCCaGTt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_090}	tATCCCCaGTt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_CJB110}	tATCCCCaGTt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_H36B}	tATCCCCaGTt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_JM9130013}	tATCCCCaGTt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
Consensus	*****	*****	*****	*****	*****
	401			450	
msa323014.2{343_18RS21}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_A909}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_COH1}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_M732}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_M781}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_2603}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa
msa323014.2{343_1169NT}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCa

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_090}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCG
msa323014.2{343_CJB110}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCG
msa323014.2{343_COH1}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCG
msa323014.2{343_H36B}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCG
msa323014.2{343_JM9130013}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCG
Consensus	*****	*****	*****	*****	*****
	451				500
msa323014.2{343_18RS21}	CGTAAGAAG	GTCACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTACCC
msa323014.2{343_A909}	CGTAAGAAG	GTCACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTACCC
msa323014.2{343_COH1}	CGTAAGAAG	GTCACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTACCC
msa323014.2{343_M732}	CGTAAGAAG	GTCACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTACCC
msa323014.2{343_M781}	CGTAAGAAG	GTCACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTACCC
msa323014.2{343_2603}	CGTAAGAAG	GTCACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTACCC
msa323014.2{343_1169NT}	CGTAAGAAG	GTCACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTACCC
msa323014.2{343_090}	CGTAAGAAG	GTCACAAAT	AACTTTcTTT	GAAACAAAGa	AAGATTACCC
msa323014.2{343_CJB110}	CGTAAGAAG	GTCACAAAT	AACTTTcTTT	GAAACAAAGa	AAGATTACCC
msa323014.2{343_H36B}	CGTAAGAAG	GTCACAAAT	AACTTTcTTT	GAAACAAAGa	AAGATTACCC
msa323014.2{343_JM9130013}	CGTAAGAAG	GTCACAAAT	AACTTTcTTT	GAAACAAAGa	AAGATTACCC
Consensus	*****	*****	*****	*****	*****
	501				550
msa323014.2{343_18RS21}	TGAAACACAA	ATCTTTATG	AGTCACCGTT	TCGACTCTCT	GATACGCTAA
msa323014.2{343_A909}	TGAAACACAA	ATCTTTATG	AGTCACCGTT	TCGACTCTCT	GATACGCTAA
msa323014.2{343_COH1}	TGAAACACAA	ATCTTTATG	AGTCACCGTT	TCGACTCTCT	GATACGCTAA
msa323014.2{343_M732}	TGAAACACAA	ATCTTTATG	AGTCACCGTT	TCGACTCTCT	GATACGCTAA
msa323014.2{343_M781}	TGAAACACAA	ATCTTTATG	AGTCACCGTT	TCGACTCTCT	GATACGCTAA
msa323014.2{343_2603}	TGAAACACAA	ATCTTTATG	AGTCACCGTT	TCGACTCTCT	GATACGCTAA
msa323014.2{343_1169NT}	TGAAACACAA	ATCTTTATG	AGTCACCGTT	TCGACTCTCT	GATACGCTAA
msa323014.2{343_090}	TGAAACACAA	ATCTTTATG	AGTCACCGTT	TCGACTCTCT	GATACGCTAA
msa323014.2{343_CJB110}	TGAAACACAA	ATCTTTATG	AGTCACCGTT	TCGACTCTCT	GATACGCTAA
msa323014.2{343_H36B}	TGAAACACAA	ATCTTTATG	AGTCACCGTT	TCGACTCTCT	GATACGCTAA
msa323014.2{343_JM9130013}	TGAAACACAA	ATCTTTATG	AGTCACCGTT	TCGACTCTCT	GATACGCTAA
Consensus	*****	*****	*****	*****	*****
	551				600
msa323014.2{343_18RS21}	AACACATGAA	AGAGATTTAC	GGAGATGCC	AAGTTGTTT	AGTACCGGAA
msa323014.2{343_A909}	AACACATGAA	AGAGATTTAC	GGAGATGCC	AAGTTGTTT	AGTACCGGAA
msa323014.2{343_COH1}	AACACATGAA	AGAGATTTAC	GGAGATGCC	AAGTTGTTT	AGTACCGGAA
msa323014.2{343_M732}	AACACATGAA	AGAGATTTAC	GGAGATGCC	AAGTTGTTT	AGTACCGGAA
msa323014.2{343_M781}	AACACATGAA	AGAGATTTAC	GGAGATGCC	AAGTTGTTT	AGTACCGGAA
msa323014.2{343_2603}	AACACATGAA	AGAGATTTAC	GGAGATGCC	AAGTTGTTT	AGTACCGGAA
msa323014.2{343_1169NT}	AACACATGAA	AGAGATTTAC	GGAGATGCC	AAGTTGTTT	AGTACCGGAA
msa323014.2{343_090}	AACACATGAA	AGAGATTTAC	GGAGATGCC	AAGTTGTTT	AGTACCGGAA
msa323014.2{343_CJB110}	AACACATGAA	AGAGATTTAC	GGAGATGCC	AAGTTGTTT	AGTACCGGAA
msa323014.2{343_H36B}	AACACATGAA	AGAGATTTAC	GGAGATGCC	AAGTTGTTT	AGTACCGGAA
msa323014.2{343_JM9130013}	AACACATGAA	AGAGATTTAC	GGAGATGCC	AAGTTGTTT	AGTACCGGAA
Consensus	*****	*****	*****	*****	*****
	601				650
msa323014.2{343_18RS21}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACACTTT
msa323014.2{343_A909}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACACTTT
msa323014.2{343_COH1}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACACTTT
msa323014.2{343_M732}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACACTTT
msa323014.2{343_M781}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACACTTT
msa323014.2{343_2603}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACACTTT
msa323014.2{343_1169NT}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACACTTT
msa323014.2{343_090}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACACTTT
msa323014.2{343_CJB110}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACACTTT
msa323014.2{343_H36B}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACACTTT
msa323014.2{343_JM9130013}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACACTTT
Consensus	*****	*****	*****	*****	*****
	651				700
msa323014.2{343_18RS21}	AGAGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_A909}	AGAGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_COH1}	AGAGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_M732}	AGAGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_M781}	AGAGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_2603}	AGAGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_1169NT}	AGAGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_090}	AGgGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_CJB110}	AGgGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_H36B}	AGgGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_JM9130013}	AGgGCATATT	GAAAAGGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
Consensus	*****	*****	*****	*****	*****
	701				750
msa323014.2{343_18RS21}	ATGGTAAGAG	AGATAccGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_A909}	ATGGTAAGAG	AGATAccGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_COH1}	ATGGTAAGAG	AGATAccGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_M732}	ATGGTAAGAG	AGATAccGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_M781}	ATGGTAAGAG	AGATAccGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_2603}	ATGGTAAGAG	AGATAccGAG	CGAGTGAAG	ACAGTAGCCA	ACAAGATCCA

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_1169NT}	ATGGTAAGAG AGATACCGAG CGAGTGAAAG ACAGTAGCCA ACAAGATCCA
msa323014.2{343_090}	ATGGTAAGAG AGATACCGAG CGAGTGAAAG ACAGTAGCCA ACAAGATCCA
msa323014.2{343_CJB110}	ATGGTAAGAG AGATACCGAG CGAGTGAAAG ACAGTAGCCA ACAAGATCCA
msa323014.2{343_H36B}	ATGGTAAGAG AGATACTGAG CGAGTGAAAG ACAGTAGCCA ACAAGATCCA
msa323014.2{343_JM9130013}	ATGGTAAGAG AGATACTGAG CGAGTGAAAG ACAGTAGCCA ACAAGATCCA
Consensus	***** * ***** * ***** * ***** * ***** * *****
	751
msa323014.2{343_18RS21}	CTAGTATTAG TAA-----
msa323014.2{343_A909}	CTAGTATTAG TAA-----
msa323014.2{343_COH1}	CTAGTATTAG TAA-----
msa323014.2{343_M732}	CTAGTATTAG TAA-----
msa323014.2{343_M781}	CTAGTATTAG TAAA-----
msa323014.2{343_2603}	CTAGTATTAG TAAAagaata tatacgtaat ggtgataaaa ctaatcaagc
msa323014.2{343_1169NT}	CTAGTATTAG TAA-----
msa323014.2{343_090}	CTAGTATTAG TAA-----
msa323014.2{343_CJB110}	CTAGTATTAG TAA-----
msa323014.2{343_H36B}	CTAGTATTAG TAA-----
msa323014.2{343_JM9130013}	GTAGTATTAG TAA-----
Consensus	***** * ***** * ***** * ***** * ***** * *****
	800
msa323014.2{343_18RS21}	-----
msa323014.2{343_A909}	-----
msa323014.2{343_COH1}	-----
msa323014.2{343_M732}	-----
msa323014.2{343_M781}	-----
msa323014.2{343_2603}	-----
msa323014.2{343_1169NT}	gataaaaaaa gtacaaaag aatttaatct caatagacaa gaactctatg
msa323014.2{343_090}	-----
msa323014.2{343_CJB110}	-----
msa323014.2{343_H36B}	-----
msa323014.2{343_JM9130013}	-----
Consensus	***** * ***** * ***** * ***** * ***** * *****
	801
msa323014.2{343_18RS21}	-----
msa323014.2{343_A909}	-----
msa323014.2{343_COH1}	-----
msa323014.2{343_M732}	-----
msa323014.2{343_M781}	-----
msa323014.2{343_2603}	-----
msa323014.2{343_1169NT}	-----
msa323014.2{343_090}	-----
msa323014.2{343_CJB110}	-----
msa323014.2{343_H36B}	-----
msa323014.2{343_JM9130013}	-----
Consensus	***** * ***** * ***** * ***** * ***** * *****
	850
msa323014.2{343_18RS21}	-----
msa323014.2{343_A909}	-----
msa323014.2{343_COH1}	-----
msa323014.2{343_M732}	-----
msa323014.2{343_M781}	-----
msa323014.2{343_2603}	-----
msa323014.2{343_1169NT}	-----
msa323014.2{343_090}	-----
msa323014.2{343_CJB110}	-----
msa323014.2{343_H36B}	-----
msa323014.2{343_JM9130013}	-----
Consensus	***** * ***** * ***** * ***** * ***** * *****
	851
msa323014.2{343_18RS21}	-----
msa323014.2{343_A909}	-----
msa323014.2{343_COH1}	-----
msa323014.2{343_M732}	-----
msa323014.2{343_M781}	-----
msa323014.2{343_2603}	-----
msa323014.2{343_1169NT}	-----
msa323014.2{343_090}	-----
msa323014.2{343_CJB110}	-----
msa323014.2{343_H36B}	-----
msa323014.2{343_JM9130013}	-----
Consensus	***** * ***** * ***** * ***** * ***** * *****
	867

SEQ ID NO. 7412

STRAIN 2603 frame: 1

MEMQVQSFKSNIHYGTLVLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLKHF
 DITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSI SDPGHDLVKAAIEGDI PV
 VSIPGASAGITALIASGLAPQPHIFYGFLPRKKQQITFFETKQDYPETQI FYESPFRVS
 DTLKHMKEIYGDQRQVVLVRELT KLYEEYQRGTISQLLEHIKVPLKGECLII VDGKRDTER
 RVKDSSQQDPLVLVKEYIANGDKTNQAIIKVAKEFNLNRQELYASFHD

SEQ ID NO. 7413

STRAIN 090 frame: 1

EMQVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLKFD
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSI SDPGHDLVKAAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKQQITFFETKQDYPETQI FYESPFRVSD
 TLKHMKEIYGDQRQVVLVRELT KLYEEYQRGTISQLLGHIEKVPLKGECLII VDGKRDTER
 VKDSSQQDPLVLV

SEQ ID NO. 7414

STRAIN A909 frame: 2

VQKSFKSNIHYGTLVLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLKFDIT
 KQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSI SDPGHDLVKAAIEGDI PV
 GASAGITALIASGLAPQPHIFYGFLPRKKQQITFFETKQDYPETQI FYESPFRVSD
 TLKHMKEIYGDQRQVVLVRELT KLYEEYQRGTISQLLGHIEKVPLKGECLII VDGKRDTER
 SSQQDPLVLV

SEQ ID NO. 7415

STRAIN H36B frame: 1

EMQVQKSFKSNTHYGTLYLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLKFD
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMPSI SDPGHDLVKAAIEGDI PVV
 SIPGASAGITALIASGLAPQPHIFYGFLPRKKQQITFFETKQDYPETQI FYESPFRVSD
 TLKHMKEIYGDQRQVVLVRELT KLYEEYQRGTISQLLGHIEKVPLKGECLII VDGKRDTER
 VKDSSQQDPLVLV

SEQ ID NO. 7416

Table 74: Comparative Sequences relating to SAG1572

STRAIN 18RS21 frame: 1
**EMQVQKSFKSNIHYGTLVLVPTPIGNLDDMTFRAIRILREVDFAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMP
 SI PGASAGITALIASGLAPQPHIFYGLPRKKQQITFFETKQDYPETQIIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRGTISQLLEHIEKVPLKGECLIIVDGKRDTER
 VKDSSQQDPLV**

SEQ ID NO. 7417

STRAIN M732 frame: 1
**EMQVQKSFKSNIHYGTLVLVPTPIGNLDDMTFRAIRILREVDFAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMP
 SI PGASAGITALIASGLAPQPHIFYGLPRKKQQITFFETKQDYPETQIIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRGTISQLLEHIEKVPLKGECLIIVDGKRDTER
 VKDSSQQDPLV**

SEQ ID NO. 7418

STRAIN COH1 frame: 1
**EMQVQKSFKSNIHYGTLVLVPTPIGNLDDMTFRAIRILREVDFAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMP
 SI PGASAGITALIASGLAPQPHIFYGLPRKKQQITFFETKQDYPETQIIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRGTISQLLEHIEKVPLKGECLIIVDGKRDTER
 VKDSSQQDPLV**

SEQ ID NO. 7419

STRAIN M781 frame: 3
**MQVQKSFKSNIHYGTLVLVPTPIGNLDDMTFRAIRILREVDFAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMP
 SI PGASAGITALIASGLAPQPHIFYGLPRKKQQITFFETKQDYPETQIIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRGTISQLLGHIIEKVPLKGECLIIVDGKRDTER
 KDSSQQDPLV**

SEQ ID NO. 7420

STRAIN CJB110 frame: 1
**EMQVQKSFKSNIHYGTLVLVPTPIGNLDDMTFRAIRILREVDFAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMP
 SI PGASAGITALIASGLAPQPHIFYGLPRKKQQITFFETKQDYPETQIIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRGTISQLLGHIIEKVPLKGECLIIVDGKRDTER
 VKDSSQQDPLV**

SEQ ID NO. 7421

STRAIN 1169NT frame: 3
**QVQKSFKSNTHYGTLVLVPTPIGNLDDMTFRAIRILREVDFAEDTRNTGLLLKHF
 TKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMP
 SI PGASAGITALIASGLAPQPHIFYGLPRKKQQITFFETKQDYPETQIIFYESPFRVSD
 KHMKEIYGDRQVVLVRELTKLYEYQRGTISQLLGHIIEKVPLKGECLIIVDGKRDTER
 DSSQQDPLV**

SEQ ID NO. 7422

STRAIN JM9130013 frame: 1
**EMQVQKSFKSNTHYGTLVLVPTPIGNLDDMTFRAIRILREVDFAEDTRNTGLLLKHF
 ITTKQISFHEHNAYDKISGLIDLLKEGKSLAQVSDAGMP
 SI PGASAGITALIASGLAPQPHIFYGLPRKKQQITFFETKQDYPETQIIFYESPFRVSD
 TLKHMKEIYGDRQVVLVRELTKLYEYQRGTISQLLGHIIEKVPLKGECLIIVDGKRDTER
 VKDSSQQDPVV**

msa324064.2{343_18RS21} msa324064.2{343_A909} msa324064.2{343_M781} msa324064.2{343_2603} msa324064.2{343_COH1} msa324064.2{343_M732} msa324064.2{343_1169NT} msa324064.2{343_090} msa324064.2{343_CJB110} msa324064.2{343_H36B} msa324064.2{343_JM9130013} Consensus	1 -emqVQKSFK SN1HYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT ~~~VQKSFK SN1HYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT --mqVQKSFK SN1HYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT memqVQKSFK SN1HYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT -emqVQKSFK SN1HYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT -emqVQKSFK SN1HYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT ---qVQKSFK SN1HYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT -emqVQKSFK SN1HYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT -emqVQKSFK SN1HYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT -emqVQKSFK SN1HYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT -emqVQKSFK SN1HYGTLYL VPTPIGNLDD MTFRAIRILR EVDFICAEDT ***** * ***** * ***** * ***** * ***** * *****	50
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msa324064.2{343_18RS21} msa324064.2{343_A909} msa324064.2{343_M781} msa324064.2{343_2603} msa324064.2{343_COH1} msa324064.2{343_M732} msa324064.2{343_1169NT} msa324064.2{343_090} msa324064.2{343_CJB110} msa324064.2{343_H36B} msa324064.2{343_JM9130013} Consensus	51 RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLLKEGKS LAQVSDAGMP RNTGLLLKHF DITTKQISFH EHNAYDKISG LIDLLKEGKS LAQVSDAGMP ***** * ***** * ***** * ***** * ***** - * *****	100
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Table 74: Comparative Sequences relating to SAG1572

msa324064.2{343_18RS21}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP	101
msa324064.2{343_A909}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP	
msa324064.2{343_M781}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP	
msa324064.2{343_2603}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP	
msa324064.2{343_COH1}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP	
msa324064.2{343_M732}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP	
msa324064.2{343_1169NT}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP	
msa324064.2{343_090}	SISDPGHDLV	KAAIEGgIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP	
msa324064.2{343_CJB110}	SISDPGHDLV	KAAIEGgIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP	
msa324064.2{343_H36B}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP	
msa324064.2{343_JM9130013}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP	QPHIFYGFLP	
Consensus	*****	*****	*****	*****	*****	
msa324064.2{343_18RS21}	RKkGQQITFFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE	151
msa324064.2{343_A909}	RKkGQQITFFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE	
msa324064.2{343_M781}	RKkGQQITFFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE	
msa324064.2{343_2603}	RKkGQQITFFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE	
msa324064.2{343_COH1}	RKkGQQITFFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE	
msa324064.2{343_M732}	RKkGQQITFFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE	
msa324064.2{343_1169NT}	RKkGQQITFFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE	
msa324064.2{343_090}	RKkGQQITFFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE	
msa324064.2{343_CJB110}	RKkGQQITFFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE	
msa324064.2{343_H36B}	RKkGQQITFFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE	
msa324064.2{343_JM9130013}	RKkGQQITFFF	ETKqDYPETQ	IFYESPFRVS	DTLKHMKEIY	GDRQVVLVRE	
Consensus	*****	*****	*****	*****	*****	
msa324064.2{343_18RS21}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDT	RVKDSSQQDP	201
msa324064.2{343_A909}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDT	RVKDSSQQDP	
msa324064.2{343_M781}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDT	RVKDSSQQDP	
msa324064.2{343_2603}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDT	RVKDSSQQDP	
msa324064.2{343_COH1}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDT	RVKDSSQQDP	
msa324064.2{343_M732}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDT	RVKDSSQQDP	
msa324064.2{343_1169NT}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDT	RVKDSSQQDP	
msa324064.2{343_090}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDT	RVKDSSQQDP	
msa324064.2{343_CJB110}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDT	RVKDSSQQDP	
msa324064.2{343_H36B}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDT	RVKDSSQQDP	
msa324064.2{343_JM9130013}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDT	RVKDSSQQDP	
Consensus	*****	*****	*****	*****	*****	
msa324064.2{343_18RS21}	251	-----	-----	-----	-----	289
msa324064.2{343_A909}	1VLV-----	-----	-----	-----	-----	
msa324064.2{343_M781}	1VLV-----	-----	-----	-----	-----	
msa324064.2{343_2603}	1VLVkeyian	gdkttnqaikk	vakefnlnrq	elyasfndl	-----	
msa324064.2{343_COH1}	1VLV-----	-----	-----	-----	-----	
msa324064.2{343_M732}	1VLV-----	-----	-----	-----	-----	
msa324064.2{343_1169NT}	1VLV-----	-----	-----	-----	-----	
msa324064.2{343_090}	1VLV-----	-----	-----	-----	-----	
msa324064.2{343_CJB110}	1VLV-----	-----	-----	-----	-----	
msa324064.2{343_H36B}	1VLV-----	-----	-----	-----	-----	
msa324064.2{343_JM9130013}	vVLV-----	-----	-----	-----	-----	
Consensus	*****	*****	*****	*****	*****	

Table 75: Comparative Sequences relating to SAG0671**SEQ ID NO. 7501****STRAIN 2603**

ATGAGCGTATACTGGTAGTGGAAATTAGGAATTATT
 TCTTCCTGGAAAGAATTATAGCGACATAAACAGCATCTTCGACTTAAAGAAGGA
 ATTCTAAACATTATATAAAATCAGCACTCTATTAGAAATCTTACAGGAACGATA
 ACTAGTGACCCAGGGTCTGAGCAATACAAGATGAGACACGTAATTAAATTGCT
 TTACCGCTTTGAAGAGGCTCTGAGGTAACTGGGGAAAGGTGCTGGTCAAAGT
 ATTCGCTGTGTTAGGGACCTCACTGGGGAAAGGTGCTGGTCAAAGTGCCTGAT
 CAATTGAAAGAAGGAGAGCGTCAGTAGATGCTAGTTATTAGAAAAAGCATCTGTTAC
 CATACTGCTGATGAATTGATGCTTATCATGATATTGTGGAGGCTTCGTATGTTATTICA
 ACCGCTGTTCTGCAAGTAATATGCCCTAATATTAGAAACACAATTACTCAAGATGGC
 GATTGTGATTAGCTATTGTGGTGGCTGTGAGGTTAAGTGTATTTCTAGCAGGC
 TTACACATCACTAGGAGCTTAATACAGAAATGECATGTCAGCCCTATTCTGAAA
 GGAATCATTTGGGTGGCTGGGGCTGGTTCTGTTCAAGAGATCAGTCCTTAGCT
 AAATATGGAAAATTATCGGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCT
 AAGCCAACAGGTGAAGGGGCGCAGATTGCAAGCAGCTAGTGAACAGCAGGTATT
 GACTACAGTGAGATTGACTATTAAACGGTACCGGTACAGGTACTCAACGTTATGATAAA
 ATGGAAAATTATGTGTTAGTGTGTTAGTGTGTTCTGCAACGATTGATCAGCTTACCAAG
 GGGCAACGGGTCAACTCTAGGGGCTGAGGTATTATGCAATTGATTAATTGTTAGCG
 GCAATAGAGGAACAGACTGACCAACTAAAGATGAGATTGGGATAGAAGGGTTTCCA
 GAAAATTGTCTTATCATCAAAGAGAAATACCCAAATGAAATGCTTAAATTTCG
 TTGCTTTGGTCAAATAATAGGGTCTTATGTCTTATGTCTTACAGTACCTCTAGAA
 ACATTACCTGCTAGAGAAAATCTTAAATGCTTATCTATCATCTGTTCTCATTCT
 AAGATGAACTTCTATAACCTTATGAAAAGTGTCTAGTAATTTCACGACTTGGAA
 GCATTACGCTTAAAGGGCTGACCAACCCAAACTGTCACACCCAGCACAAATTAGAAA
 ATGGATGATTTCACAAAGGTTGCTGCTAACACAGCTCAACACTAATAGAAAGCAAT
 ATTAATCTAAACAAAGATCTTAAAGTAGGAAATTGTTACACACTTCTGGA
 CCAGTTGAGGTGTTGAGGTATTGAAAGCAAACTCACACAGAAGGATATGCACATGTT
 TCTGCTTACGATTCGGTACAGTAATGAATGCAAGCAGCTGGTATGCTTCTATCATT
 TTAAATAACAGCTTCTGCTTACAGTAACTGAGGAAATAGTGGCCTGATGGTATA
 CAATATGCCAAAGRAATGATGGTAAACGATAATCTAGACTATGTGATTCTGTTCTGCT
 AACAGTGGACAGACATGAGTTTATGTGGTGGCAACAAITAAACTATGATAGTCACATG
 TTGTCGGTTCTGATTATGTTGAGCACAAGTCTCTCGTCAGCATTGGATAATTCT
 CCTATAATTATGGTACTGAGCTTAAACAAATTAAATAGGCTATAACACATTCAAGATGTGATG
 ACTATTATGATGCTGCGCTTAAACAAATTATGAGACTTACAGGACTAACACAAAGAT
 ATCAAAGGTTCTGTTGGATAGCGGAAGGAGCTTGTGATGGTATA
 GCGAATGCTGCTGTTGGAAAGAACCTGCTTCTGTCAGTTGGGATTTICA
 TCTAATGTCGCTGTTGGAAAGAACACTGAGTAAATGAGGATAGAAAAGGCTPAT
 TATTTAGTCCTATCTTATTGATCTTCGGTGGTATCTTGTCTTGTATTATTGAAAAAGG

SEQ ID NO. 7502**STRAIN 090**

ATGTTAGTGGAAAGGAAATTATCTCTTGGGAAAGAATTAT
 AGCGACATAAACAGCATCTCTGACTTAAAGAAGGAAATTCTAAACAA
 TTATATAAAATCACGACTCTATTAGAATCTTACAGGAAGCATAA
 CTAGTGACCCAGGGTCTGAGCAATACAAGATGAGACACGTAATT
 AAATTGCTTACCGCTTCTGGTAAAGAGGCTCTTCAAGTGTAA
 TTAAAGCTTATCATATAATTTGCTGTTAGGGACCTCACTGGGG
 GAAAGACTGCTGGTCAAATGCTTGTATCAAATTGAAAGAAGGAGAGCGT
 CAAGTAGATGCTAGTTATTGAAAGAATGCTGTTACCATATTGCTGA
 TGAATTGATGGCTTATCATGATATTGTTGAGCTCGTATGTTATTCTAA
 CCGGCTGTTCTGCAAGTAATACTGCGTAATTAGGAAACAAATTACTT
 CAAGATGGCATTGTAATTGACTATTGTTGGTGGCTGTGATGAGITAAG
 TGATAATTCTTACAGGCTTACATCACTAGGAGCTTAAATACAGAAA
 TGGCATGTCAGGCTTATTCTTCTGGAAAGGAATCAATTGGTGGAGGGC
 GCTGGTTTGTGTTCTGTCAAAGATCAGCTTCTAGCTAAATATGGAAA
 AATTATGGTGGCTTATTACTTCAGATGGTATCATATAACAGCACCTA
 AGCCAAACAGGTGAAGGGCGCAGATGCAAAGCAGCTAGTGAACCAA
 GCAGGTATTGACTACAGTGAGATTGACTATTAAACGGTACCGTACAGG
 TACTCAAGCTAATGAAAAATGAAAAAATATGTTGTTAAAGTTTCC
 CGACAACGACATTGATCAGGCTTACCAAGGGCAACAGGGCTACACTCTA
 GGGGCTGAGGTATTCTGAAATTGATTAATTGTTAGCGGAATAGAGGA
 ACAGACTGTACCGCAACTAAAGATGAGATTGGGATAGAAGGTTTCCAG
 AAAATTGCTTCTGTTGGTGGAAATATGTTGCTTATTGTCTATC
 ATTGAGTTGCTTCTGTTGAGGAAATATGTTGCTTATTGTCTATC
 TTAGATTCACTCTAGAAACATTACCTGCTAGAGAAAATCTAAATGG
 CTATCTTATCATCTGCTTCTCATTCTGCTTCTGCTTCTGCTT
 ACTATGAAAAAGTGTGCTAGTAATTCTCAAGACTTTGAGCATTACGCTT
 TAAAGGGCTAGACCAACCCAAACTGTCACCCAGCACAAATTAGGAAA
 TGATGTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT
 GAAAGCAATATTAACTTAAAGGAAATGCTTCTGCTTCTGCTTCTGCTT
 ATTACACACTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT
 AAATCACAACAGAAGGATATGCACATGTTCTGCTTCTGCTTCTGCTT
 ACAGTAATGAAATGCGACAGCTGCTGTTCTGCTTCTGCTTCTGCTT
 AGGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT
 AATATGCCAAAGGAAATGATGCGTAAACGATAATCTGACTATGTGATTCT
 GTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT
 AACTATGATGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT
 TCCTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT
 CAATTAAATATAGCCATAAAACATTCAACAGATGTGATGACTATTGTTGA
 TGCTGCGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT
 TCAAAGGTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT
 GATTTCTTAGCGAATTGCTGAGTATTATAATATGCCAAACCTTGCTT

Table 75: Comparative Sequences relating to SAG0671

TGGTCAGTTGGATTTCATCTAATGGTGTGGTAAGAACTGGACTATA
 CTGTTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCITATTG
 ATCTTTGGTGGATCTCTTGTCTATTGAAAAAAGG

SEQ ID NO. 7503

STRAIN A909

ATGTTAGTGGATAGGAATTATTCCTCTTGGGAAAGAATT
 ATAGCGAGCATAAACAGCCTCTCGACTTAAAGAAGGAATTCTAAA
 CATTATATAAAACAGCCTCTTGGACTTAAAGAAGGAATTCTTAA
 AACATGTCAGCCAGGGCTCTGAGCAATCAAAGATGAGACACGTAATT
 TTAATTTGGCTTACCGCTTGAAGAGGCTCTTGCTTCTCAGGGTGT
 ATTAAAGGCTTACAGGCTTGAAGAGGCTCTGCTTCTCAGGGTGT
 GGAAAGAGTGTGCTCAAATGCGCTGTATCAATTGAAAGAAGGAGAGC
 GTCAAGTAGAGTGTGCTAGTTTATAGAAAAGCATCTGTTACCATATTGCT
 GATGAAATTGAGGCTTATCATGATATTGAGGAGCTCTGATGTTATTTC
 AACCGCCCTGTTGCAAGTAATAATGCCGTAAATTAGGAACACAATTAC
 TTCAAGTGGCATTGTGATTAGCTTATTTGGCTGGCTGTGATGAGGTTA
 AGTGATATTCTTCTAGCAGGCTTACACTAGAGCTTAAATACAGA
 AAATGGCATGTCAGCCCTATTCTCTGGAAAAGGAATCAAATTGGGTGAGG
 GCCTGGTTTGTGCTTCTGCTCAAAGATCAGTCCTTAGCTAAATATGGA
 AAAATTATCGGTGGCTTATTACTTCAGATGGTTATCATATAACACCACC
 TAAGCCAACAGGTGAAGGGCCGACAGATTGCAAGCAGCTAGTGACTC
 AAGCAGGTTAGTACTACAGTGAGATTGACTTATTAACGGTCACGGTACA
 GGTACTCAAGCTTACAGTAAATGGAAAAAAATATGTTAGGTAAGGTTTT
 CCCGACAAACGACATTGATCACAGTACCAAGGGCAAACGGGTACACTC
 TAGGGGCTGCAGGTATTATGCAATTGATTAATTGTTAGCGGCAATAGAG
 GAACAGCTGACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTCC
 AGAAAATTGGCTTATCATAAAAGAGAAATACCCATAAAGAAATGCTT
 TAAATTTCTGTTGCTTGGGAAATAATAGTGGTGTCTTATGTC
 TCCTTAGATTACCTCTAGAAACATTACCTGCTAGAGAAAATCTAAAAT
 GGTATCTTATCATCTGTTGCTTCAAGAATGAAATCACTTCTA
 TAACCTATGAAAATTGCTAGTAAATTCAACGACTTGAAGCATTACGC
 TTAAAGGGCTAGACCAACCAAAACTGTCACCCAGCACAATTAGGAA
 ATGGATGATTTCACCAAAATGGCTGCGTAACAAACAGCTCAAGCCTAA
 TAGAAAGCAATTAAATCTAAAACAGATACTTCAAAAGTAGGAAATT
 GTATTTACAACACTTCTGGACCTGTTGAGGTTGTTGAAGGTATTGAAA
 GCAAATCACACAGAAGGATGCAACATGTTCTGCTTCAAGGATTCCCGT
 TTACAGTAAATGCAAGCAGCTGGTATGCTTCTATCATTTTAAAATA
 ACAGGTCTTATCTGTCATTGACAAATAGTGGAGCGCTTGTGTT
 ACAATACTGCAAGGAAATGAGCTGCAACGATAATCTAGACTTATGTT
 TTGTTCTGCTTACAGTGGACAGACATGAGTTTATGTTGCGCAACAA
 TAAACTATGATACTGCAAATGTTGCTGTTGTTGTTGTTGAGCACA
 AGTCCTCTCGTAAGCATTGATAATTCTCCCTAAATATTAGGTAGTA
 AACAAATTAAATATGCAACGAGCTTACAGATGTTGAGCTTATT
 GATGCTGGCTTCAAAATTATGAGCAGCTTGGACTAACATAAAAAGA
 TATCAAAGGTTCTGTTGGATGAGCGGAAGAAGGAGCTTAGTTGAGATT
 ATGATTTCTAGCGAACCTGCTGAGTATTATAATATGCAACACCTTGT
 TCTGGTCAAGTTGGATTCTCATTAATGGTGTGGTAAGAACTGGACTA
 TACTGTTAATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTT
 CGATCTCGTGGTATCTCTTGTCTATTGAAAAAAGG

SEQ ID NO. 7504

STRAIN H36B

ATGTTAGTGGATAGGAATTATTCCTCTTGGGAAAGAATTATAGCGA
 GCATAAACAGCCTCTCGACTTAAAGAAGGAATTCTAAACATTAT
 ATAAAAATCAGCCTCTTAAATGAAATCTTATACAGGAAGCATAACTAGT
 GACCCAGGGCTCTGAGCAATACAAGAGTGGAGACACGTAATTAAATT
 TGCTTCTACCGCTTGAAGAGGCTCTGCTTCTCAGGTGTAAATTAA
 AAAGCTTATCATATAATTGCTGTGTTAGGGACCTCCTTGGGGAAAG
 ACTGCTGTCAAATGCGCTTGATCAATTGAAAGAAGGAGGGCTCAAGT
 AGATGCTGTTATTAGAAAAGCATCTGTTACCATATTGCTGATGAAAT
 TGATGGCTTATCATGATATTGCTGGAGCTTGTGTTATTTCAACCGCC
 TGTCTGCAAGTAATAATGCCGTAAATTAGGAACACAATTCTCAAGA
 TGGCATTGCTGATGCTGTTAGCTTGTGCTGTGAGTTAGGTAAGT
 TTCTCTAGGGCTTACATCACTAGAGGCTTAAATACAGAAATGGCA
 TGTCAGCCCTATTCTCTGGAAAAGGAATCAAATTGGTGGAGGGCGCTGG
 TTGTTGTTGTTCTGCAAGGATCAGTCCTTAGCTAAATATGGAAAAATT
 TCGGGCTTATTACTTCAGATGGTTATCATATAACAGCACCTAACGCA
 ACAGGTGAAGGGCGCACAGATGCAAACGAGCTAGTGACTCAAGCAGG
 TATTGACTACAGTGAGATTGACTTATTAACGGTCACGGTACAGGTACTC
 AGAGCTAATGATAAAATGGAAAAAAATATGTTAGGTAAGGTTTCCCGACA
 ACGACATTGATCAGCACTACCAAGGGCAAACGGGTACACTCTAGGGC
 TGCAAGGTATTATGCAATTGATTAATTGTTAGCGGCAATAGAGGAACAGA
 CTGTCAGGCAACTAAAAATGAGATTGGGATAGAAGGTTTCCAGAAAAT
 TTGTTCTATCATCAAAGAGAAATACCCATAAAGAAATGCTTAAATT
 TCTGTTGCTTGGGAAATAATAGTGGTGTCTTATGTCATCTTATG
 ATTCAACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATGGCTATC
 TTATCATCTGCTGCTTCTCATTTCTAAGAATGAAATCACTTCTATACCTA
 TGAAGAAAATGCTGAGTAAATTCAACGACTTGAAGCATTACGCTTAAAG
 GGGCTAGACCAACCAAAACTGTCACCCAGCACAATTAGGAAAATGGAT
 GATTTTCCAAATGGTGTGGCTAACACAGCTCAAGCACAATAGAAAG
 CAATATTAACTCTAAAACAGATACTTCAAAAGTAGGAAATTGTTATT
 CAACACTTCTGGACCACTGAGGTTGAGGTTGAGGTAAGGAAAGCAAATC

Table 75: Comparative Sequences relating to SAG0671

ACAAACAGAAGGATATGCACATGTTCTGCTTCACGATTCCGTTTACAGT
 AATGAATGCAGCAGCTGGTATGCTTCTATCATTTAAAATAACAGGT
 CTITATCTGTCAATTTCGACAATAGTGAGCGCTTGATGGTATACAAT
 GCCAAGGAAATGATGCCAACATAATCTAGACTATGTGATTCTGTTTC
 TGCTAATCAGTGACAGACATGAGTTTATGGTGGCAACAAATTAAACT
 ATGATAGTCAAATGTTGCTGGTCTGATTATTGTCAGCACAAGTCCCTC
 TCTCGTCAAGCATTGACAATTCTCTATAATATTAGGTAGTAAACAAATT
 AAAATATAGCCATAAAACATTCAACAGATGTGATGACTATTGGATGCTG
 CGCTTCAAAATTATTATCAGACTTAGGACTAACATAAAAGATATCAA
 GGTTTGGATGGATGAGCGGAAGAAGGCAATTGAGTTCAAGATTATGATT
 CTAGCGAACCTGCTGAGTATTATAATATGCCAAACCTTGCTCTGGTC
 AGTTGGATTTCATCTAATGGTGTGAGAAGTGGACTATACTGTT
 AATGAAAGTATAGAAAAGGGCTATTATTAGTCCTATCTTATCGATCTT
 CGGTGGTATCTCTTGTATTATTGAAAAAGG

SEQ ID NO. 7505

STRAIN 18RS21

ATGTTAGTGGATAGGAATTATTCCTTCTGGAAAGAATTATAGC
 GAGCATAAACAGCATCTTCGACTTAAAGAAGGAATTCTAAACATT
 ATATAAAAATCACGACTCTATTAGAATCTTATACAGGAAGCATAACTA
 GTGACCCAGAGGTTCTGAGCAATACAAGATGAGACACGTAATTAA
 TTGCTTTACCGCTTTGAAGAGGCTCTGCTTCTCAGGTGTTAAATT
 AAAAGCTTATCATATAATTGCTGTGTGTTAGGGACCTCACTGGGGAA
 AGAGCTGGTCAAAATGCTTGTATCAATTGAGAAGGGAGACGTC
 GTAGATGCTAGTTATTAGAAAAGCATCTGTTACCCATAITGCTGATGA
 ATTGATGGCTTATCATGATATTGTTGGAGCTCGTATGTTATTCACCG
 CCTGTTCTGCAAGTAATAATGCCGAATTAGGAACCAAATTACTTCAA
 GATGGCGATTGTGATTAGCTATTGTTGGCTGTGATGAGTTAAGTGA
 ATTCTTCTAGCAGGCTTACATCACTAGAGGCTATTAAACAGAAATGG
 CATGTCAGCCCTATTCTCTGGAAAGGAATCAATTGGGTGAGGGCGCT
 GGTGTTGGTCTTATTACTTCAGATGGTATCATATAACAGCACCTAAC
 CAAACAGGTGAAGGGCGGCACAGATTGCAAGCAGCTAGTGACTCAAGCA
 GGATTGACTACAGTGAGATTGACTATTAAACGGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAAAAAAATATGTTATGTAAGGTTTCCC
 CAACGACATTGATCAGCAGTACCAAGGGCAACGGGTCTACTCTAGGG
 GCTGCGTATTATGAAATTGATTAAATTGTTAGCGCAATAGAGGAACA
 GACTGTACCGAACCTAAAGATGAGATTGGGATAGAAGGTTTCCAGAAA
 ATTGTTGCTATCATCAAAGAGAAATCCAATAAGAAATGCTTAAAT
 TTGCTTGTGCTTTGGTGAATAATAGTGGTGTCTATTGTCATCTT
 AGATTCAACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATGGCTA
 TCTTATCATCTGCTTCTCATTCTAAGATGATGAAATCACTTCTATAACC
 TATGAAAAGTTGCTAGTAATTCAACGACTTGAACGATTACGCTTAA
 AGGGCTAGGACCCCCAAACTGTCACCCAGCACATTAGGAAATAGG
 ATGATTTCACCAATGGTGTGCTTAACACAGCTAACGACTAAATAGAA
 AGCAATTAATCTAAAAAAACAAGATACTCAAAAGTAGGAATTGATT
 TACAACACTTCTGGACCGAGTTGGAGTTGTGAAGGTATTGAAAAGC
 TCAACACAGAAGGATATGCACATGTTCTGCTTACGATTCCCTTACA
 GTAAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTAAATAACAGG
 TCCTTATCTGCTATTGACAATAGTGAGCGCTTGATGGTATACAAT
 ATGCCAAGGAATGATGCGTAACGATAATCTAGACTATGTGATTCTGTT
 TCTGCTAATCAGTGACAGACATGAGTTTATGTTGGCGAACAAATTAA
 CTATGATAGTCAAATGTTGCTGTTCTGATTATTGTCAGCACAAGTCC
 TCTCTCGTCAAGCATGGATAATTCTCTTATAATTAGGTAGTAAACAA
 TTTAAATATAGCCATAAAACATTACAGATGTTGATGACTATTGATGC
 TCGCTTCAAAATTATTATCAGACTTAGGACTAACATAAAAGATATCA
 AAGGTTGGTGGAAATGAGCGGAAGAAGGAGCTTGTGAGTATTGAT
 TTCTTAGCGAACCTGCTGAGTATTATAATGCCAACCTTGCTTCTGG
 TCAGTTGGATTTCATCTAATGGTGTGAGAAGTGGACTATACTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCCTATCTTATCGATC
 TTGGTGGTATCTCTTGTATTATTGAAAAAGG

SEQ ID NO. 7506

STRAIN M732

ATGTTAGTGGATAGGAATTATTCCTTCTGGAAAGAATTATAG
 CGAGCATAAACAGCATCTTCGACTTAAAGAAGGAATTCTAAACATT
 TATATAAAAATCACGACTCTATTAGAATCTTATACAGGAAGCATAACT
 AGTGACCCAGAGGTTCTGAGCAATACAAGATGAGACACGTAATTAA
 ATTGCTTTACCGCTTTGAAGAGGCTCTGCTTCTCAGGTGTTAAATT
 TAAAAGCTTATCATATAATTGCTGTGTGTTAGGGACCTCACITGGGGAA
 AGAGCTGGTCAAAATGCTTGTATCAATTGAGAAGGGAGACGTC
 AGTAGATGCTAGTTATTAGAAAAGCATCTGTTACCATATTGCTGATG
 ATTGATGGCTTATCATGATATTGTTGGAGCTCGTATGTTATTCAACC
 GCCGTTCTGCAAGTAATAATGCCGTAATTAGGAACCAAATTACTICA
 AGATGGCGATTGTGATTAGCTATTGTTGGCTGTGATGAGTTAAGTG
 ATATTCTTGTGAGGCTTACATCACTAGGGACTATTAAACAGAAATG
 GCATGTCAGCCCTATTCTCTGGAAAAGGAATCAATTGGGTGAGGGCGC
 TGTTTGTGTTCTGCAAGATCAGTCTTGTGTTAATATGAAAAAA
 TTATCGGTGCTTATTACTTCAGTGGTTATCATATAACAGCACCTAAG
 CCAACAGGTGAAGGGCGGCACAGATTGCAAGCAGCTAGTGACTCAAGC
 AGGTGATTGACTACAGTGAGATTGACTATTAAACGGTCACGGTACAGGTA
 CTCAAGCTAATGATAAAATGAAAAAAATATGTTATGGTAAGTTTCCC
 AACACGACATTGATCAGCAGTACCAAGGGCAACGGGTCAACTCTAGG

Table 75: Comparative Sequences relating to SAG0671

GGCTGCAGGTATTATCGAATTGATTAATTGTTAGCGGCAATAGAGGAAC
 AGACTGTACCGACAATTTAAAGAGATTGGGATAGAAGGTTCCAGAAA
 AATTTGTCTATCATCAAAGAGAGAACATCCAATAAGAAATGCTTTAAA
 TTTTCTTGGGAAATAATAGTGGTCTTATTGTCTATCTT
 TAGATTCACTCTAGAACATACCTGCTAGAGAAAATCTAAAATGGCT
 ATCTTATCATCTGTTGCTTCCATTCTAAGAATGAATCCTTCTATAAC
 CTATGAAAAGGTGCTAGTAATTCAACGCTTGAACGCTTACGCTTAA
 AAGGGGCTAGACACCCAAAACCTGTCACCCAGCACAAATTAGGAAAATG
 GATGATTTCAAAATGGTGCCTAACACAGCTAACAGCAATAGA
 AACAAATTAACTAAAAAAACAGATACTTCAAAAGTAGGAATTGAT
 TTACAACACTTCTGGACAGCTGGAGTTGAGGTATTGAAAGGAA
 ATCACAAACAGAGGATATGCACATGTTCTGCTTCAAGATCCCCGTTAC
 AGTAATGAATGCAGCAGCTGGTATGCTTCTATCATTAAACAG
 GTCTTCTATCTGTCACAAATAGTGAGGCTTACGCTTACGTTA
 ATAGCCAAGGAAATGATGCGTAACCGATAATCTAGACTATGTTGATTCTG
 TTCTGCTAATCAGTGGACAGACATGAGTTTATGTTGAGGCAACAATTAA
 ACTATGATACTAAATGTTGCTGTTCTGATTATTGTTGAGCACAAGTC
 CTCCTCGTCAGCATTGATAATTCTCTTAAATAATTAGGTAGTAAACA
 ATTAAAATATAGCCATAAAACATTCACAGATGTGATGACTATTGATG
 CTGCGCTTAAATTATTATCAGACTTAGGACTAACATAAAAGATATC
 AAAGGTTTGGGATTTGAAATGACGGGAGAAGGAGTTAGTTCAGATTATG
 TTCTTAGGAACTTGTCTGAGTATTATAATGCTAACCTTGCTCTG
 GTCACTGTTGGATTTCATCTAATGGTCTGGTGAAGAACTGGACTAtaCT
 GTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCCCTATCTTATTGAT
 CTTGGTGGTATCTTTGCTATTATTGAAAAAGG

SEQ ID NO. 7507**STRAIN COH1**

ATGTTAGTGGAAATAGGAATTATTTCTTCTTGGGAAAGAATTATAGC
 GAGCCATAAAACAGCATCTCTCGACTTTAAAGAGGAATTCTAAACATT
 ATATAAAATCACGACTCTATTTAGAATCTTACAGGAGCATAACTA
 GTGACCCAGGGCTCTGAGCAATACAAAGATGAGACACGTAATTAAA
 TTTGCTTTACCGCTTTGAGAGGCTCTGCTTCTTCAGGTGTTAATT
 AAAAGCTTACATAATTTGCTGTTAGGGACCTCCTTGGGGAA
 AGAGTGTGCTTAAATGCCCTGTTATCAATTGAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTATTAGAAAAGCATCTGTTTACCATATTGCTGATG
 ATTGATGCTTATCATGATATTGTTGAGGCTTCTGTTATGTTATTCAACCG
 CCTTGTGCTTATCATGATATTGTTGAGGCTTCTGTTATGTTATTCAACCG
 CTTGCTTCTGCAAGTAAATGCCCATAATTAGGAACACATTACTTCAA
 GATGGCGATTGTTAGCTATTGTTGCTGTTGATGAGTTAACG
 TATTCTTCTGAGGCTTCACATCACTAGGAGCTTAAATACAGAAATGG
 CATGTCAGGCTTATCTGCAAAGATCAGTCTTCTGCTTAAATATGAAAAT
 GGTGTTGTTCTGCTTGTCAAAGATCAGTCTTCTGCTTAAATATGAAAAT
 TATCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAACG
 CAACAGGTAGGGGGCCACAGATTGCAAAACGAGCTAGTGACTAACGCA
 GGATTGACTACAGTGAGATTGACTATTTAACGGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAAAAAAATATGTTGAGGTTTTCTCGCA
 CAACGACATTGATCAGCACTAACGGGCAACGGGTCAACTCTAGGG
 GCTGAGGTTATGCAATTGTTAGGGTATGCGGCAATAGAGGAACA
 GACTGTACCAACAACTAAAATGAGATTGGGATAGAAGGTTTCCAGAAA
 ATTGTTGTTATCATCAAAGAGAGAACATCCAATAAGAAATGCTTTAAAT
 TTTGCTTCTGCTTGGGAAATAATAGTGGTCTTATTGTCATCTT
 AGATTCACTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATGCTT
 TCTTATCATCTGTTGCTTCCATTCTAAGAATGAATCCTTCTATAACC
 TAIGAAAAGTGTCTAGTATTCAACGACTTGAAGGATTTACGCTTTAA
 AGGGCTAGACCCAAAATGTCACCCAGCACAAATTAGGAAAATGG
 ATGATTTTTCCAAAATGCTGCGTAACACAGCTAACAGACTAATAGAA
 AGCAATATTAACTAAAAACAAAGACTTCAAAGTAAGGAAATTGATT
 TACAACACGACTTCTGGACCACTGAGGTTGAGGTTGAAGGTTAGGAA
 TCACAAACAGAAGGATATGCACTATGTTCTGCTTACGATTCCGTTACA
 GTAATGAATGCGCAGCTGGTATGCTTCTATCATTTTAAATAACAGG
 TCCCTTATCTGCTTCTGCAAAATGAGGGAGGGCTTGTAGGGTATACAAAT
 ATGCGCTTCAAGGAAATGATGCGTAACGATAATCTGACTATGTTGATTCTG
 TCTGCTAATCAGTGGACAGACATGAGTTTATGTTGCTGGCAACAATTAAA
 CTATGATGTTGCTGATAATTCTCTTAAATAATTAGGTAGTAAACA
 TTAAAATATAGCCATAAAACATTACAGATGTGATGACTATTGATG
 TGCGCTTCAAAATTATTATCAGACTTAGGACTAACCTAAAGATATCA
 AAGGTTTCTGTTGGAAATGAGGGAGAAGGAGCTTGTAGGTTGAGGTTATG
 TTCTTAGGCACTTGTCTGAGTATTATAATGCTAACCTTGCTCTGG
 TCAGTTGGATTTCATCTAATGGTCTGGTGAAGAACTGGACTATACIG
 TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCCCTATCTTATTGATC
 TTTGGTGGTATCTTTGCTATTATTGAAAAAGG

SEQ ID NO. 7508**STRAIN M781**

ATGTTAGTGGAAATAGGAATTATTTCTTCTTGGGAAAGAATTATAGC
 GAGCCATAAAACAGCATCTCTCGACTTTAAAGAGGAATTCTAAACATT
 ATATAAAATCACGACTCTATTAGAATCTTACAGGAGCATAACTA
 GTGACCCAGGGCTCTGAGCAATACAAAGATGAGACACGTAATTAAA
 TTTGCTTTACCGCTTTGAGAGGCTCTGCTTCTTCAGGTGTTAATT
 AAAAGCTTATCATATAATTGCTGTTAGGGACCTCCTTGGGGAA
 AGAGTGTGCTGCTTAAATGCTGTTATCAATTGAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTATTAGAAAAGCATCTGTTACCATATTGCTGATG

Table 75: Comparative Sequences relating to SAG0671

ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTTATGTTATTCACCCG
CCTGTTCTCGAAGTAATGCGCTAATATTAGGAACACAATTACTCCAA
GATGGCGATGTGATTIAGCTATTGTGGTGGCTGTGATGAGTTAACGTGA
TATTCTTACAGGCTTCACATCACTAGGAGCTATTATAACAGAAATGG
CATGTCAGGCCATTCTCTGAAAAGGAATCAATTGGGTGAGGGGGCT
GGTTTGTTCTCTGTCAGAGATCAGCTTCAGTAAATATGGAAAAT
TATCGTGGCTTATTAATCTCAGATGGTTATCATATAACAGCAGCTAACG
CAACAGGTGAGGGGCGGCACAGATTGCAAAGCAGCTAGTGAACAGCA
GGTATTGACTACAGTGAGATTGACTATTAATGGTCACCGTACAGGTAC
TCAAGCTATGAAATGGAAAATATGTGTTAGTGGTTCTCCCGA
CAACGACATTGATCAGCAGTACCAAGGGGAAACGGGTATACTCTAGGG
GCTGCAGGTATTATCGAAATTGATTAATTGTTAGCGCAATAGAGGAACA
GACTTGACCCAGCAACTAAAAATGAGATGGGATAGAGGTTCTCGAAA
ATTTTGTCTATCATCAAAAGAGAACATTAACCAATAAGAAATGCTTAAAT
TTTCGTTGCTTGTGGAAAATAATGTTGATCTTATGTCATCTT
AGATTCCACCTCTAGAAAATTCTACCTCTGCTAGAGAAAATCTTAAATGGCTA
TCTTATCATCTGCTTGTGCTTCTACCTCTAGAATGTAACCTTCTTATTAAC
TATGAAAATAGTGTGCTAGTATTTCTAACGACTTGTGAGCATTACGCTTAA
AGGGGCTAGACCACCCAAAATGTCACCCAGCACAAATTAGGAAAATGG
ATGATTCTTCCAAAATGGCTTGGCTAACACAGCTCAACGACTAAATGAA
AGCAATATTAACTCTAAAACAGATACTCTAACAGTAGGAAATTGTTATT
TACAAACACTTCTGGACCAGTTGAGGTGTTGAGGTATTGAAAACAAA
TCACAAACAGAAGGATATGCCACATGTTCTGCTTCACGATCTCCGTTTACA
GTAATGAAATGCGAGCTGGTATGCTTCTATCATTTTAAAATACAGG
TCTCTTATCTGCTATTGCGACAAAATAGTGGAGGCTTGTGATGTTACAT
ATGCCAAGGAATGATGCGTAACGATAATCTAGACTATGTGATTCTGTT
TCTGCTTAATCAGTGGACAGACATGAGTTTATGTTGTCACAACTTAA
CTATGAGTCAAAATGTTCTGCTTGTGATTATGTTGAGCTACAGCT
TCTCTGCTCAAGCACTGGATAATTCTCTATATAATTAGGTAGTAAACAA
TTAAAATATAGCCATAAAACATTACAGCATGTTGATGACTATTGTTGATG
TGGCCTTCAAAATTATGTTGAGCTTGTGAGCTAACATAAAAGATATCA
AAGGGTTCTGGGAATGCGGAAAGGCAAGGCACTTGTGAGCTTGTGAT
TTCTTAGCGAACTGTGCTGAGTATTATAATATGCCAAACCTGCTCTGG
TCAGTTGGATTTCTCATCTAATGGTCTGGTGAAGAACACTGGACTATACG
TTAAATGAAAGTAAAGGGCTATTATTTAGTCTCATCTTATTGATC
TCTGGTGTGATCTCTTGTCAATTGTTGAGG

SEQ ID NO. 7509

STRAIN CJB110

ATGTTAGTGGAAATAGGAATTATTCCTCTGGAAAGAATTATAGC
GAGCATAAAACAGCATCTTCGACTTAAAGAAGGGAAATTCTAACATT
ATATAAAAATCAGCCTCTTATTAAGAATCTTACAGGAAGCATACA
GTGACCCAGAGGTTCTGAGCAATAACAAAGATGAGCACGCTAATT
TTGCTTTACCGCTTGTGAAGAGGCTCTTGCTCTTCAGGGTTAATT
AAAAGCTTATCATATAATTGCTGCTGTGTTAGGGACCTACTGGGGAA
AGAGTGTCTGCCTAAATGGCTCTATCAATTGAGAAGGGAGACGGCTAA
GTAGATGCTAGTTATTAAGAAAAAGCATCTGTTACCATATTGCTGATGA
ATTGATGGCTTATCATGATATTGTTGGGGCTTCGTTGATTTCAACCC
CTCTGCTGCAAGTAATAATGCCCTAATTAGGAAACCAAATTACTCTAA
GATGGCGATTGTGATTAGCTATTGTTGGCTGTGATGAGTTAAAGTGA
TATTCTTCTTACGGCTTACATCACTACTAGGAGCTATTAAATCAGAACATTG
CATGTCAGGGCTTATTCTCTGGAAAGGAATCAATTGGTGTGGCGCT
GGTTTGTGTTCTGTCAAAGATCAGCTCTTAGCTAAATATGGAAAAAT
TATCGGTGGCTTATTACTCTAGATGGTTATCATATAACAGCACCTAACG
CAACAGGTGAAGGGGGCGCACAGTGGCAAAAGCAGCTAGTGTACTAACGCA
GGTTAGTACTACAGTGAGATTGACTATTAATGGTGTACGGTACAGGTAC
TCAAGCTAATGATAAAATGGAAAAAAATATGTATGGTAAGGTTTCCCGA
CAACGACATIGTACAGGACTTACAGGCAAAACGGCTCATCTCAGGG
GFTGCGAGGTATTATCGAATTGATTAAATTGTTAGCGCAATAGGAGAAC
GACTGTACAGCAACTAAAATGAGATTGGGATAGAAGGTTTCCAGAAA
ATTTTGTCTATCATAAAGAGGAATAACCCAATAAGGAATGCTTAAAT
TTTCGTTGCTTGTGGAATAATAGTGTATCTTATTGTCATCTTT
AGATTCACCTCTAGAAACATTACCTGCTAGAGAAAATCTAAATGGCTA
TCTTATCATCTGTTGCTTCAATTCTAAGAATGTAACCTTCTTATTAACC
TATGAAAATGTTGCTAGTATTCTAACAGACTTGTGAAGCATTACGCTTAA
AGGGGCTAGACCCCCAAACTGTCAACCCAGCACAATTAGGAAAATGG
ATGATTTTCCAAAATGGTGGCTAACACAGCTCAAGCCTAACTATAGAA
AGCAATATTATCTAAAACAAAGATACTCTAAAAGTAGGAATTGTT
TACACACTTTCTGGACCGATTGGTTGTGTTGAAGGTATTGAAACGAAA
TCACAACAGAAGGATATGCACATGTTCTGCTTCAGGATTCCTTACA
GTAATGTAATGAGCAGCTGGTATGTTCTATCATTTTAAAATACAGG
TCTTTATCTGTCATTCGACAAATAGTGGAGCCTGTTGATGGTATACAT
ATGCCAAGGAATATGCTGCAACGATACTAGACTATGTGATTCTGTT
TCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAACTAAA
CTATGATGATGCTAAATGTTGCTGTTCTGATTATTGTTGCTGACAGTCC
TCTCTGCTGCAACGATTGGATAATTCTCTCTATAAATTAGGCTAGTAACAA
TTAAAATATAGCCATAAAACATTACAGATGTGATGACTATTGTTGATGC
TGGCTTCAAAATTATTGCTAGACTTAGGACTAACATTAAGGATATCA
AAGGGTTCTGGAAATGAGCGGAAGAAGGCACTTGTGATGTTGAGGTT
TCTCTAGCGAACTTGTGCTGAGTATTATAATATGCCAAACCTGCTCTGG
TCAGTTGGAATTCTCATCTAATGGTGTGGTGAAGAACACTGGACTATACTG
TTAATGAAAGTATAGAAGGGCTTATTGTTGATCTTCTATCTTATTGCGATC
TTGGTGTGTTCTCTTCTGATTATTGAAAAAAGG

Table 75: Comparative Sequences relating to SAG0671**SEQ ID NO. 7510**

STRAIN 1169NT

ATGTTAGTGGAAATAGGAATTATTCCTTGGAAAGAATTATAG
 CGAGCATAAACAGCATCTTCGACTTAAAGAAGGAATTCTAAACATT
 TATAATAAAATCAGACTCTATTAGAACATCTATACAGGAAGCATAACT
 AGTGAACCCAGAGGTTCTGAGCAATACAAAGATGAGACACCGTAATT
 ATTTGCTTTACCGCTTTGAAGAGGCTCTGCTTCTCAGGTGTTAATT
 TAAAAGCTTATCATATAATTGCTGTGTTAGGGACCTCACTGGGGA
 AAAGAGTGTGGTCAAATGCCGTATCAATTGAAAGAAGGGAGCGTCA
 AGTAGATGGCTTATTAGAAAAGCATCTGTTTACCATATTGCTGATG
 AATTGATGGCTTATCATGATATTGTTGGAGCTTCGTATGTTATTCAACC
 GCCTGTTCTGCAAGTAATAATGCCGTAATTAGGAACACAATTACTCA
 AGATGGGATTGATTTAGCTATTGTTGGGCTGTGATGAGTTAAGTG
 ATATTCTTACAGGCTTACATCACTAGGAGCTTAAATACAGAAATG
 GCATGTCAGGCCATTCTTGGAAAGAATCAATTGGGTAGGGCGC
 TGTTTGTGTTCTGCAAGATCAGTCTTAGCTTAAATGGAAAAAA
 TTATCGGGCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAG
 CCAACAGGTGAAGGGCGCACAGATTGCAAAAGCAAGCTAGTGA
 AGCAGGTATTGACTACAGTGAGATTGACTATATAACGGTCACGGTACAGGTA
 CTCAGCAATGATAAAATGAAAAAAATATGTTAGTGAAGTTTCCCG
 ACAACAGCATTGATCAGCAGTACCAAGGGCAAACCGGTCAACTCTAGG
 GGCTGCAGGTATTATCGAATTGATTAATTGTTAGCGGCAATAGAGGAAC
 AGACTGTACCGCAACTAAATGAGATTGGGATAGAAGGTTTCCAGAA
 AATTGTTGCTATCATCAAAGAGAGAAATCCAATAAGAAATGTTAA
 TTTTCTGTTGCTTGGTGAATAATAGTGGTATCTATTGTCATCTT
 TAGATTCACTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATGGCT
 ATCTTATCATCTGCTTCCATTCTCAAGAATGAAATCACTTTCTATAAC
 CTATGAAAAGTGTCTAGTAAATTCAACCCACTTGAAGCAATTACGCTTAA
 AAGGGGCTAGACCCAAAATGTCACCCAGGCAAAATTAGGAAAATG
 GTGATTTTCCACCAAAATGGTGTCCAAACAGCTCAAGCATAATAGA
 AAGCAATTAAATCTAAAAAAACAAGATACTTCAAAGTAGGAAATTGAT
 TTACAACACTTCTGGACCAGTTGAGGTTGTGAAGGTTAGGAAAGCAA
 ATCACAAACAGAAGGATATGCACTGTTCTGCTTCAAGGATTCCCGTTAC
 AGTAATGATGTCAGCAGCTGGTATGCTTCTATCATTAAATAACAG
 GTTCTTCTGTCATTCGACAATAGTGGAGCGCTTGTGATGGTATA
 TATGCAAGGAAATGATGCGTAAAGATACTAGACTATGTTGATCTGTT
 TCTGCTTAATCTAGTGGAGCAGCATGAGTTTATGTTGCGCAACAAATTAA
 ACTATGATAGTCATGTTCTGGTTCTGATTATGTTCAAGCACAGTC
 CTCTCTGTCAGCATTGGATAATTCTCTATAATAATTAGGTAGTAAACA
 ATTAAAATATAGCCATAAAACATTACAGATGTGATGACTATTGTTGATG
 CTGCGCTTCAAAATTATTATCATGACTTAGGACTAAACCAATAAGATATC
 AAAGGTTCTGTTGGATGAGCGGAAGAAGGCAGTTAGTCAAGTATGA
 TTCTTACGCACTTGTCTGACTTATAATATGCAAACCTTCTGCTTCTG
 GTCAAGTTGGATTTCTAATGGTGTCTGGTAAGAAGCTGGACTTAACT
 GTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTTATTCGAT
 CTTGGTGTATCTTTGCTATTATTGAAAAAGG

SEQ ID NO. 7511

STRAIN JM9130013

ATGTTAGTGGAAATAGGAATTATTCCTTGGAAAGAATTATAGCGAG
 CATAAAACAGCATCTTCGACTTAAAGAAGGAATTCTAAACATTATA
 TAAAATCAGACTCTATTAGAACATCTATACAGGAAGCATAACTAGTG
 ACCCAGAGGTTCTGAGCAATACAAAGATGAGACACCGTAATTAAATT
 GCCTTACCGCTTGAAGAGGCTCTGCTTCAAGTGTAAATTAA
 AGCTTATCATATAATTGCTGTGTTAGGGACCTCACTGGGGAAAGA
 GTGCTGGTCAAATGCTTGTATCAAATTGAGAAGGAGAGCGTCAAGTA
 GATGCTGTTATTAGAAAAGCATCTGTTACCATATTGCTGATGAAAT
 GATGGCTTATCATGATATTGTTGGAGCTTGTATGTTATTCAACGGCT
 GTTCTGCAAGTAATAATGCCGTAATTAGGAACACAATTACTCAAGAT
 GCGGATTGTTAGCTTACATCACTAGGAGCTTAAATACAGAAATGGCAT
 GTCAAGCCATTCTCTGGAAAGGAATCAATTGGGTGAGGGCGCTGGT
 TTGTTGTTCTGTCAGTCTGCTAAAGATGACTTCTGCTAAATAGGAAAATTAT
 CGGTGGCTTATCATGATGGTTATCATATAACAGCACCTAAGCCAA
 CAGGTGAAGGGCGGCACAGATTGCAAAAGCAGCTAGTGA
 CTCAAGCAGGTT
 ATTGACTACAGTGAGATTGACTATATAACGGTCACGGTACAGGTACTCA
 AGCTAATGATAAAATGAAAAAAATATGTTAGTGAAGTTTCCCGACAA
 CGACATTGATCAGCAGTACCAAGGGCAAACGGGTCAACTCTAGGGCT
 GCAGGTATTATGCAATTGATTAATTGTTAGCGGCAATAGAGGAACAGAC
 TGTTACCGCAACTAAATGAGATTGGGATAGAAGGTTTCCAGAAAATT
 TTGCTATCATCAAAGAGGAAATACCCAAATAGAAATGTTAAATT
 TCGTTTGTCTTGGTGAATAATAGTGGTCTTATTGTCATCTTGA
 TTCACCTCTAGAAACATTACCTGCTAGAGAAAATCTTAAATGGCTATCT
 TATCATCTGCTGCTTCAATTCTAAGAACATCACTTCTATAACCTAT
 GAAAAGTGTCTAGTAAATTCAACGACTTGAAGCAATTGCTTAAAGG
 GGCTAGACCACCAAAACTGTCACCCAGACAATTAGGAAATGGATG
 ATTGTTCCAAAATGGTGTGCGTAACACAGCTCAAGCACAATAGAAAGC
 ATATTAATCTAAAAAAACAAGATACTTCAAAGTAGGAAATTGTTAC
 AACACTTCTGACCGACTTGGAGGTTGTGAAGGTTATTGAAAAGCAAATCA
 CAACAGAAGGATATGCACTGTTCTGCTTCAAGGATTCCCGTTACAGTA
 ATGAATGCGCAGCTGGTATGCTTCTATCATTTAAATAACAGGTC
 TTATCTGTCATTGCAAAATAGTGGAGCGCTTGTGATGGTATACAATATG

Table 75: Comparative Sequences relating to SAG0671

CCAAGGAAATGATCGTAAACGATAATCTAGACTATGTGATTCTTGTCT
 GCTAATCAGTGGCACAGACATGAGTTTATGTGGTGGCAACAATTAAACCA
 TGATAGTCAAATGTTGTCGGTCTGATTATGTGTTAGCACAAGTCCCTCT
 CTCGTCAGCATGGATAATTCTCTTATAATTAGTAGTAAACAAATTA
 AAATATAGCCATAAACACATTACAGATGTGACTATTGATGCTGC
 GCTTCAAAATTATATCAGACTTAGGACTAACCATAAAAGATATCAAAG
 GTTCCGTTGGATGAGCGGAAAGGAGCTAGTTCAGAATTATGATGTTTC
 TTAGCGAACATTGCTGAGTATAATGCAACCTGCTCTGGTCA
 GTTGGATTTCATCTAATGGTGTGGTGAAGAACTGGACTATACTGTTA
 ATGAAAGTATAGAAAAGGGCTATTATTTAGTCCTATCTTATTCGATCTTC
 GGTGGTATCTCTTGCTATTATGAAAAAAGG

PRETTY of: /biotmp/msa118688.2{*} April 9, 2003 02:55 ..

		1				50
msa118688.2{361_18RS21}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTCTT	TGGGAAAGAA	
msa118688.2{361_A909}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTCTT	TGGGAAAGAA	
msa118688.2{361_COH1}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTCTT	TGGGAAAGAA	
msa118688.2{361_H36B}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTCTT	TGGGAAAGAA	
msa118688.2{361_JM9130013}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTCTT	TGGGAAAGAA	
msa118688.2{361_M732}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTCTT	TGGGAAAGAA	
msa118688.2{GBS361_2603}	atgagcgat	ATGTTAGTGG	AATAGGAATT	ATTTCTCTT	TGGGAAAGAA	
msa118688.2{361_090}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTCTT	TGGGAAAGAA	
msa118688.2{361_1169NT}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTCTT	TGGGAAAGAA	
msa118688.2{361_CJB110}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTCTT	TGGGAAAGAA	
msa118688.2{361_M781}	-----	ATGTTAGTGG	AATAGGAATT	ATTTCTCTT	TGGGAAAGAA	
Consensus	*****	*****	*****	*****	*****	
		51				100
msa118688.2{361_18RS21}	TTATAGCGAG	CATAAACAGC	ATCTCTCGA	CTTAAAAGAA	GGAATTCTA	
msa118688.2{361_A909}	TTATAGCGAG	CATAAACAGC	ATCTCTCGA	CTTAAAAGAA	GGAATTCTA	
msa118688.2{361_COH1}	TTATAGCGAG	CATAAACAGC	ATCTCTCGA	CTTAAAAGAA	GGAATTCTA	
msa118688.2{361_H36B}	TTATAGCGAG	CATAAACAGC	ATCTCTCGA	CTTAAAAGAA	GGAATTCTA	
msa118688.2{361_JM9130013}	TTATAGCGAG	CATAAACAGC	ATCTCTCGA	CTTAAAAGAA	GGAATTCTA	
msa118688.2{361_M732}	TTATAGCGAG	CATAAACAGC	ATCTCTCGA	CTTAAAAGAA	GGAATTCTA	
msa118688.2{GBS361_2603}	TTATAGCGAG	CATAAACAGC	ATCTCTCGA	CTTAAAAGAA	GGAATTCTA	
msa118688.2{361_090}	TTATAGCGAG	CATAAACAGC	ATCTCTCGA	CTTAAAAGAA	GGAATTCTA	
msa118688.2{361_1169NT}	TTATAGCGAG	CATAAACAGC	ATCTCTCGA	CTTAAAAGAA	GGAATTCTA	
msa118688.2{361_CJB110}	TTATAGCGAG	CATAAACAGC	ATCTCTCGA	CTTAAAAGAA	GGAATTCTA	
msa118688.2{361_M781}	TTATAGCGAG	CATAAACAGC	ATCTCTCGA	CTTAAAAGAA	GGAATTCTA	
Consensus	*****	*****	*****	*****	*****	
		101				150
msa118688.2{361_18RS21}	AACATTATA	TAAAAATCAC	GACTCTATT	TAGAATCTTA	TACAGGAAGC	
msa118688.2{361_A909}	AACATTATA	TAAAAATCAC	GACTCTATT	TAGAATCTTA	TACAGGAAGC	
msa118688.2{361_COH1}	AACATTATA	TAAAAATCAC	GACTCTATT	TAGAATCTTA	TACAGGAAGC	
msa118688.2{361_H36B}	AACATTATA	TAAAAATCAC	GACTCTATT	TAGAATCTTA	TACAGGAAGC	
msa118688.2{361_JM9130013}	AACATTATA	TAAAAATCAC	GACTCTATT	TAGAATCTTA	TACAGGAAGC	
msa118688.2{361_M732}	AACATTATA	TAAAAATCAC	GACTCTATT	TAGAATCTTA	TACAGGAAGC	
msa118688.2{GBS361_2603}	AACATTATA	TAAAAATCAC	GACTCTATT	TAGAATCTTA	TACAGGAAGC	
msa118688.2{361_090}	AACATTATA	TAAAAATCAC	GACTCTATT	TAGAATCTTA	TACAGGAAGC	
msa118688.2{361_1169NT}	AACATTATA	TAAAAATCAC	GACTCTATT	TAGAATCTTA	TACAGGAAGC	
msa118688.2{361_CJB110}	AACATTATA	TAAAAATCAC	GACTCTATT	TAGAATCTTA	TACAGGAAGC	
msa118688.2{361_M781}	AACATTATA	TAAAAATCAC	GACTCTATT	TAGAATCTTA	TACAGGAAGC	
Consensus	*****	*****	*****	*****	*****	
		151				200
msa118688.2{361_18RS21}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTA	
msa118688.2{361_A909}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTA	
msa118688.2{361_COH1}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTA	
msa118688.2{361_H36B}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTA	
msa118688.2{361_JM9130013}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTA	
msa118688.2{361_M732}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTA	
msa118688.2{GBS361_2603}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTA	
msa118688.2{361_090}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTA	
msa118688.2{361_1169NT}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTA	
msa118688.2{361_CJB110}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTA	
msa118688.2{361_M781}	ATAACTAGTG	ACCCAGAGGT	TCCTGAGCAA	TACAAAGATG	AGACACGTA	
Consensus	*****	*****	*****	*****	*****	
		201				250
msa118688.2{361_18RS21}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG	
msa118688.2{361_A909}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG	
msa118688.2{361_COH1}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG	
msa118688.2{361_H36B}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG	
msa118688.2{361_JM9130013}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG	
msa118688.2{361_M732}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG	
msa118688.2{GBS361_2603}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG	
msa118688.2{361_090}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG	
msa118688.2{361_1169NT}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG	
msa118688.2{361_CJB110}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG	
msa118688.2{361_M781}	TTTTAAATTT	GCTTTTACCG	CTTTTGAAGA	GGCTCTTGCT	TCTTCAGGTG	
Consensus	*****	*****	*****	*****	*****	

Table 75: Comparative Sequences relating to SAG0671

		251			300	
msa118688.2{361_18RS21}	TAAATTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTAGG	GACCTCACIT	
msa118688.2{361_A909}	TAAATTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTAGG	GACCTCACIT	
msa118688.2{361_COH1}	TAAATTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTAGG	GACCTCACIT	
msa118688.2{361_H36B}	TAAATTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTAGG	GACCTCACIT	
msa118688.2{361_JM9130013}	TAAATTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTAGG	GACCTCACIT	
msa118688.2{361_M732}	TAAATTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTAGG	GACCTCACIT	
msa118688.2{GBS361_2603}	TAAATTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTAGG	GACCTCACIT	
msa118688.2{361_090}	TAAATTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTAGG	GACCTCACIT	
msa118688.2{361_1169NT}	TAAATTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTAGG	GACCTCACIT	
msa118688.2{361_CJB110}	TAAATTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTAGG	GACCTCACIT	
msa118688.2{361_M781}	TAAATTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTAGG	GACCTCACIT	
Consensus	*****	*****	*****	*****	*****	
		301			350	
msa118688.2{361_18RS21}	GGGGAAAGA	GTGCTGGTC	AAATGCCITG	TATCAATTG	AAGAAGGAGA	
msa118688.2{361_A909}	GGGGAAAGA	GTGCTGGTC	AAATGCCITG	TATCAATTG	AAGAAGGAGA	
msa118688.2{361_COH1}	GGGGAAAGA	GTGCTGGTC	AAATGCCITG	TATCAATTG	AAGAAGGAGA	
msa118688.2{361_H36B}	GGGGAAAGA	GTGCTGGTC	AAATGCCITG	TATCAATTG	AAGAAGGAGA	
msa118688.2{361_JM9130013}	GGGGAAAGA	GTGCTGGTC	AAATGCCITG	TATCAATTG	AAGAAGGAGA	
msa118688.2{361_M732}	GGGGAAAGA	GTGCTGGTC	AAATGCCITG	TATCAATTG	AAGAAGGAGA	
msa118688.2{GBS361_2603}	GGGGAAAGA	GTGCTGGTC	AAATGCCITG	TATCAATTG	AAGAAGGAGA	
msa118688.2{361_090}	GGGGAAAGA	GTGCTGGTC	AAATGCCITG	TATCAATTG	AAGAAGGAGA	
msa118688.2{361_1169NT}	GGGGAAAGA	GTGCTGGTC	AAATGCCITG	TATCAATTG	AAGAAGGAGA	
msa118688.2{361_CJB110}	GGGGAAAGA	GTGCTGGTC	AAATGCCITG	TATCAATTG	AAGAAGGAGA	
msa118688.2{361_M781}	GGGGAAAGA	GTGCTGGTC	AAATGCCITG	TATCAATTG	AAGAAGGAGA	
Consensus	*****	*****	*****	*****	*****	
		351			400	
msa118688.2{361_18RS21}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG	
msa118688.2{361_A909}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG	
msa118688.2{361_COH1}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG	
msa118688.2{361_H36B}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG	
msa118688.2{361_JM9130013}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG	
msa118688.2{361_M732}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG	
msa118688.2{GBS361_2603}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG	
msa118688.2{361_090}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG	
msa118688.2{361_1169NT}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG	
msa118688.2{361_CJB110}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG	
msa118688.2{361_M781}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG	
Consensus	*****	*****	*****	*****	*****	
		401			450	
msa118688.2{361_18RS21}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT	
msa118688.2{361_A909}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT	
msa118688.2{361_COH1}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT	
msa118688.2{361_H36B}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT	
msa118688.2{361_JM9130013}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT	
msa118688.2{361_M732}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT	
msa118688.2{GBS361_2603}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT	
msa118688.2{361_090}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT	
msa118688.2{361_1169NT}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT	
msa118688.2{361_CJB110}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT	
msa118688.2{361_M781}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT	
Consensus	*****	*****	*****	*****	*****	
		451			500	
msa118688.2{361_18RS21}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT	
msa118688.2{361_A909}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT	
msa118688.2{361_COH1}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT	
msa118688.2{361_H36B}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT	
msa118688.2{361_JM9130013}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT	
msa118688.2{361_M732}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT	
msa118688.2{GBS361_2603}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT	
msa118688.2{361_090}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT	
msa118688.2{361_1169NT}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT	
msa118688.2{361_CJB110}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT	
msa118688.2{361_M781}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT	
Consensus	*****	*****	*****	*****	*****	
		501			550	
msa118688.2{361_18RS21}	ACTTCAAGAT	GGCGATTGTC	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT	
msa118688.2{361_A909}	ACTTCAAGAT	GGCGATTGTC	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT	
msa118688.2{361_COH1}	ACTTCAAGAT	GGCGATTGTC	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT	
msa118688.2{361_H36B}	ACTTCAAGAT	GGCGATTGTC	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT	
msa118688.2{361_JM9130013}	ACTTCAAGAT	GGCGATTGTC	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT	
msa118688.2{361_M732}	ACTTCAAGAT	GGCGATTGTC	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT	
msa118688.2{GBS361_2603}	ACTTCAAGAT	GGCGATTGTC	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT	
msa118688.2{361_090}	ACTTCAAGAT	GGCGATTGTC	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT	
msa118688.2{361_1169NT}	ACTTCAAGAT	GGCGATTGTC	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT	
msa118688.2{361_CJB110}	ACTTCAAGAT	GGCGATTGTC	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT	
msa118688.2{361_M781}	ACTTCAAGAT	GGCGATTGTC	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT	

Table 75: Comparative Sequences relating to SAG0671

Consensus	*****	*****	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	551	TAAGTGTAT	TTCCTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA	600
msa118688.2{361_A909}		TAAGTGTAT	TTCCTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA	
msa118688.2{361_COH1}		TAAGTGTAT	TTCCTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA	
msa118688.2{361_H36B}		TAAGTGTAT	TTCCTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA	
msa118688.2{361_JM9130013}		TAAGTGTAT	TTCCTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA	
msa118688.2{361_M732}		TAAGTGTAT	TTCCTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA	
msa118688.2{GBS361_2603}		TAAGTGTAT	TTCCTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA	
msa118688.2{361_090}		TAAGTGTAT	TTCCTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA	
msa118688.2{361_1169NT}		TAAGTGTAT	TTCCTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA	
msa118688.2{361_CJB110}		TAAGTGTAT	TTCCTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA	
msa118688.2{361_M781}		TAAGTGTAT	TTCCTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA	
Consensus	*****	*****	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	601	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTGGGTGA	650
msa118688.2{361_A909}		GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTGGGTGA	
msa118688.2{361_COH1}		GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTGGGTGA	
msa118688.2{361_H36B}		GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTGGGTGA	
msa118688.2{361_JM9130013}		GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTGGGTGA	
msa118688.2{361_M732}		GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTGGGTGA	
msa118688.2{GBS361_2603}		GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTGGGTGA	
msa118688.2{361_090}		GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTGGGTGA	
msa118688.2{361_1169NT}		GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTGGGTGA	
msa118688.2{361_CJB110}		GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTGGGTGA	
msa118688.2{361_M781}		GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTGGGTGA	
Consensus	*****	*****	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	651	GGCGCCTGGT	TTTGTGTTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG	700
msa118688.2{361_A909}		GGCGCCTGGT	TTTGTGTTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG	
msa118688.2{361_COH1}		GGCGCCTGGT	TTTGTGTTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG	
msa118688.2{361_H36B}		GGCGCCTGGT	TTTGTGTTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG	
msa118688.2{361_JM9130013}		GGCGCCTGGT	TTTGTGTTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG	
msa118688.2{361_M732}		GGCGCCTGGT	TTTGTGTTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG	
msa118688.2{GBS361_2603}		GGCGCCTGGT	TTTGTGTTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG	
msa118688.2{361_090}		GGCGCCTGGT	TTTGTGTTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG	
msa118688.2{361_1169NT}		GGCGCCTGGT	TTTGTGTTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG	
msa118688.2{361_CJB110}		GGCGCCTGGT	TTTGTGTTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG	
msa118688.2{361_M781}		GGCGCCTGGT	TTTGTGTTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG	
Consensus	*****	*****	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	701	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA	750
msa118688.2{361_A909}		GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA	
msa118688.2{361_COH1}		GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA	
msa118688.2{361_H36B}		GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA	
msa118688.2{361_JM9130013}		GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA	
msa118688.2{361_M732}		GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA	
msa118688.2{GBS361_2603}		GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA	
msa118688.2{361_090}		GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA	
msa118688.2{361_1169NT}		GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA	
msa118688.2{361_CJB110}		GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA	
msa118688.2{361_M781}		GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA	
Consensus	*****	*****	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	751	CCTAACGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC	800
msa118688.2{361_A909}		CCTAACGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC	
msa118688.2{361_COH1}		CCTAACGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC	
msa118688.2{361_H36B}		CCTAACGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC	
msa118688.2{361_JM9130013}		CCTAACGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC	
msa118688.2{361_M732}		CCTAACGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC	
msa118688.2{GBS361_2603}		CCTAACGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC	
msa118688.2{361_090}		CCTAACGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC	
msa118688.2{361_1169NT}		CCTAACGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC	
msa118688.2{361_CJB110}		CCTAACGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC	
msa118688.2{361_M781}		CCTAACGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC	
Consensus	*****	*****	*****	*****	*****	*****	*****
msa118688.2{361_18RS21}	801	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA	850
msa118688.2{361_A909}		TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA	
msa118688.2{361_COH1}		TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA	
msa118688.2{361_H36B}		TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA	
msa118688.2{361_JM9130013}		TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA	
msa118688.2{361_M732}		TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA	
msa118688.2{GBS361_2603}		TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA	
msa118688.2{361_090}		TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA	
msa118688.2{361_1169NT}		TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA	
msa118688.2{361_CJB110}		TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA	

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_M781}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAt	GGTCACGGTA
Consensus *****					
	851				900
msa118688.2{361_18RS21}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_A909}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_COH1}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_H36B}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_JM9130013}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_M732}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{GBS361_2603}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_090}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_1169NT}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_CJB110}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_M781}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
Consensus *****					
	901				950
msa118688.2{361_18RS21}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCCAA	CGGGTCATAC
msa118688.2{361_A909}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCCAA	CGGGTCATAC
msa118688.2{361_COH1}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCCAA	CGGGTCATAC
msa118688.2{361_H36B}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCCAA	CGGGTCATAC
msa118688.2{361_JM9130013}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCCAA	CGGGTCATAC
msa118688.2{361_M732}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCCAA	CGGGTCATAC
msa118688.2{GBS361_2603}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCCAA	CGGGTCATAC
msa118688.2{361_090}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCCAA	CGGGTCATAC
msa118688.2{361_1169NT}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCCAA	CGGGTCATAC
msa118688.2{361_CJB110}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCCAA	CGGGTCATAC
msa118688.2{361_M781}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCCAA	CGGGTCATAC
Consensus *****					
	951				1000
msa118688.2{361_18RS21}	TCTAGGGGCT	GCAGGTATTCA	TCGAATTGAT	TAATTGTTTA	CGGGCAATAG
msa118688.2{361_A909}	TCTAGGGGCT	GCAGGTATTCA	TCGAATTGAT	TAATTGTTTA	CGGGCAATAG
msa118688.2{361_COH1}	TCTAGGGGCT	GCAGGTATTCA	TCGAATTGAT	TAATTGTTTA	CGGGCAATAG
msa118688.2{361_H36B}	TCTAGGGGCT	GCAGGTATTCA	TCGAATTGAT	TAATTGTTTA	CGGGCAATAG
msa118688.2{361_JM9130013}	TCTAGGGGCT	GCAGGTATTCA	TCGAATTGAT	TAATTGTTTA	CGGGCAATAG
msa118688.2{361_M732}	TCTAGGGGCT	GCAGGTATTCA	TCGAATTGAT	TAATTGTTTA	CGGGCAATAG
msa118688.2{GBS361_2603}	TCTAGGGGCT	GCAGGTATTCA	TCGAATTGAT	TAATTGTTTA	CGGGCAATAG
msa118688.2{361_090}	TCTAGGGGCT	GCAGGTATTCA	TCGAATTGAT	TAATTGTTTA	CGGGCAATAG
msa118688.2{361_1169NT}	TCTAGGGGCT	GCAGGTATTCA	TCGAATTGAT	TAATTGTTTA	CGGGCAATAG
msa118688.2{361_CJB110}	TCTAGGGGCT	GCAGGTATTCA	TCGAATTGAT	TAATTGTTTA	CGGGCAATAG
msa118688.2{361_M781}	TCTAGGGGCT	GCAGGTATTCA	TCGAATTGAT	TAATTGTTTA	CGGGCAATAG
Consensus *****					
	1001				1050
msa118688.2{361_18RS21}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_A909}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_COH1}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_H36B}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_JM9130013}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_M732}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{GBS361_2603}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_090}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_1169NT}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_CJB110}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_M781}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
Consensus *****					
	1051				1100
msa118688.2{361_18RS21}	CCAGAAAATT	TTGCTCATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_A909}	CCAGAAAATT	TTGCTCATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_COH1}	CCAGAAAATT	TTGCTCATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_H36B}	CCAGAAAATT	TTGCTCATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_JM9130013}	CCAGAAAATT	TTGCTCATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_M732}	CCAGAAAATT	TTGCTCATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{GBS361_2603}	CCAGAAAATT	TTGCTCATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_090}	CCAGAAAATT	TTGCTCATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_1169NT}	CCAGAAAATT	TTGCTCATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_CJB110}	CCAGAAAATT	TTGCTCATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_M781}	CCAGAAAATT	TTGCTCATCA	TCAAAAGAGA	GAATACCCAA	TAAGAAATGC
Consensus *****					
	1101				1150
msa118688.2{361_18RS21}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	9TCTTATTGT
msa118688.2{361_A909}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	9TCTTATTGT
msa118688.2{361_COH1}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	9TCTTATTGT
msa118688.2{361_H36B}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	9TCTTATTGT
msa118688.2{361_JM9130013}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	9TCTTATTGT
msa118688.2{361_M732}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	9TCTTATTGT
msa118688.2{GBS361_2603}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	9TCTTATTGT
msa118688.2{361_090}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	9TCTTATTGT
msa118688.2{361_1169NT}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	9TCTTATTGT

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_CJB110}	TTTAAATTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	aTCTTATTGT	
msa118688.2{361_M781}	TTTAAATTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	aTCTTATTGT	
Consensus	*****	*****	*****	*****	*****	*****
						1200
msa118688.2{361_18RS21}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA	
msa118688.2{361_A909}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA	
msa118688.2{361_COH1}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA	
msa118688.2{361_H36B}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA	
msa118688.2{361_JM9130013}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA	
msa118688.2{361_M732}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA	
msa118688.2{GBS361_2603}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA	
msa118688.2{361_090}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA	
msa118688.2{361_1169NT}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA	
msa118688.2{361_CJB110}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA	
msa118688.2{361_M781}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA	
Consensus	*****	*****	*****	*****	*****	*****
						1250
msa118688.2{361_18RS21}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC	
msa118688.2{361_A909}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC	
msa118688.2{361_COH1}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC	
msa118688.2{361_H36B}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC	
msa118688.2{361_JM9130013}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC	
msa118688.2{361_M732}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC	
msa118688.2{GBS361_2603}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC	
msa118688.2{361_090}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC	
msa118688.2{361_1169NT}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC	
msa118688.2{361_CJB110}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC	
msa118688.2{361_M781}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC	
Consensus	*****	*****	*****	*****	*****	*****
						1300
msa118688.2{361_18RS21}	TATAACCTAT	GAAAAAGTTG	CTAGTAATT	CAACGACTTT	GAAGCATTAC	
msa118688.2{361_A909}	TATAACCTAT	GAAAAAGTTG	CTAGTAATT	CAACGACTTT	GAAGCATTAC	
msa118688.2{361_COH1}	TATAACCTAT	GAAAAAGTTG	CTAGTAATT	CAACGACTTT	GAAGCATTAC	
msa118688.2{361_H36B}	TATAACCTAT	GAAAAAGTTG	CTAGTAATT	CAACGACTTT	GAAGCATTAC	
msa118688.2{361_JM9130013}	TATAACCTAT	GAAAAAGTTG	CTAGTAATT	CAACGACTTT	GAAGCATTAC	
msa118688.2{361_M732}	TATAACCTAT	GAAAAAGTTG	CTAGTAATT	CAACGACTTT	GAAGCATTAC	
msa118688.2{GBS361_2603}	TATAACCTAT	GAAAAAGTTG	CTAGTAATT	CAACGACTTT	GAAGCATTAC	
msa118688.2{361_090}	TATAACCTAT	GAAAAAGTTG	CTAGTAATT	CAACGACTTT	GAAGCATTAC	
msa118688.2{361_1169NT}	TATAACCTAT	GAAAAAGTTG	CTAGTAATT	CAACGACTTT	GAAGCATTAC	
msa118688.2{361_CJB110}	TATAACCTAT	GAAAAAGTTG	CTAGTAATT	CAACGACTTT	GAAGCATTAC	
msa118688.2{361_M781}	TATAACCTAT	GAAAAAGTTG	CTAGTAATT	CAACGACTTT	GAAGCATTAC	
Consensus	*****	*****	*****	*****	*****	*****
						1350
msa118688.2{361_18RS21}	GCTTTAAAGG	GGCTAGACCA	CCCAAACCTG	TCAACCAGC	ACAATTAGG	
msa118688.2{361_A909}	GCTTTAAAGG	GGCTAGACCA	CCCAAACCTG	TCAACCAGC	ACAATTAGG	
msa118688.2{361_COH1}	GCTTTAAAGG	GGCTAGACCA	CCCAAACCTG	TCAACCAGC	ACAATTAGG	
msa118688.2{361_H36B}	GCTTTAAAGG	GGCTAGACCA	CCCAAACCTG	TCAACCAGC	ACAATTAGG	
msa118688.2{361_JM9130013}	GCTTTAAAGG	GGCTAGACCA	CCCAAACCTG	TCAACCAGC	ACAATTAGG	
msa118688.2{361_M732}	GCTTTAAAGG	GGCTAGACCA	CCCAAACCTG	TCAACCAGC	ACAATTAGG	
msa118688.2{GBS361_2603}	GCTTTAAAGG	GGCTAGACCA	CCCAAACCTG	TCAACCAGC	ACAATTAGG	
msa118688.2{361_090}	GCTTTAAAGG	GGCTAGACCA	CCCAAACCTG	TCAACCAGC	ACAATTAGG	
msa118688.2{361_1169NT}	GCTTTAAAGG	GGCTAGACCA	CCCAAACCTG	TCAACCAGC	ACAATTAGG	
msa118688.2{361_CJB110}	GCTTTAAAGG	GGCTAGACCA	CCCAAACCTG	TCAACCAGC	ACAATTAGG	
msa118688.2{361_M781}	GCTTTAAAGG	GGCTAGACCA	CCCAAACCTG	TCAACCAGC	ACAATTAGG	
Consensus	*****	*****	*****	*****	*****	*****
						1400
msa118688.2{361_18RS21}	AAAATGGATG	ATTTTCCAA	AATGGTTGCC	GTAACAAACAG	CTCAAGCACT	
msa118688.2{361_A909}	AAAATGGATG	ATTTTCCAA	AATGGTTGCC	GTAACAAACAG	CTCAAGCACT	
msa118688.2{361_COH1}	AAAATGGATG	ATTTTCCAA	AATGGTTGCC	GTAACAAACAG	CTCAAGCACT	
msa118688.2{361_H36B}	AAAATGGATG	ATTTTCCAA	AATGGTTGCC	GTAACAAACAG	CTCAAGCACT	
msa118688.2{361_JM9130013}	AAAATGGATG	ATTTTCCAA	AATGGTTGCC	GTAACAAACAG	CTCAAGCACT	
msa118688.2{361_M732}	AAAATGGATG	ATTTTCCAA	AATGGTTGCC	GTAACAAACAG	CTCAAGCACT	
msa118688.2{GBS361_2603}	AAAATGGATG	ATTTTCCAA	AATGGTTGCC	GTAACAAACAG	CTCAAGCACT	
msa118688.2{361_090}	AAAATGGATG	ATTTTCCAA	AATGGTTGCC	GTAACAAACAG	CTCAAGCACT	
msa118688.2{361_1169NT}	AAAATGGATG	ATTTTCCAA	AATGGTTGCC	GTAACAAACAG	CTCAAGCACT	
msa118688.2{361_CJB110}	AAAATGGATG	ATTTTCCAA	AATGGTTGCC	GTAACAAACAG	CTCAAGCACT	
msa118688.2{361_M781}	AAAATGGATG	ATTTTCCAA	AATGGTTGCC	GTAACAAACAG	CTCAAGCACT	
Consensus	*****	*****	*****	*****	*****	*****
						1450
msa118688.2{361_18RS21}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA	
msa118688.2{361_A909}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA	
msa118688.2{361_COH1}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA	
msa118688.2{361_H36B}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA	
msa118688.2{361_JM9130013}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA	
msa118688.2{361_M732}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA	
msa118688.2{GBS361_2603}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA	
msa118688.2{361_090}	AATAGAAAGC	AATATTAATC	TAAAAAAACA	AGATACTTCA	AAAGTAGGAA	

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_1169NT}	AATAGAAAAGC	AATATTAATC	AAAAAAAACA	AGATACTTC	AAAGTAGGAA
msa118688.2{361_CJB110}	AATAGAAAAGC	AATATTAATC	AAAAAAAACA	AGATACTTC	AAAGTAGGAA
msa118688.2{361_M781}	AATAGAAAAGC	AATATTAATC	AAAAAAAACA	AGATACTTC	AAAGTAGGAA
Consensus	*****	*****	*****	*****	*****
	1451				1500
msa118688.2{361_18RS21}	TTGTATTAC	AAACACTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_A909}	TTGTATTAC	AAACACTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_COH1}	TTGTATTAC	AAACACTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_H36B}	TTGTATTAC	AAACACTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_JM9130013}	TTGTATTAC	AAACACTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_M732}	TTGTATTAC	AAACACTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{GBS361_2603}	TTGTATTAC	AAACACTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_090}	TTGTATTAC	AAACACTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_1169NT}	TTGTATTAC	AAACACTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_CJB110}	TTGTATTAC	AAACACTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_M781}	TTGTATTAC	AAACACTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
Consensus	*****	*****	*****	*****	*****
	1501				1550
msa118688.2{361_18RS21}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCIGCTT	CACGATTCCC
msa118688.2{361_A909}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCIGCTT	CACGATTCCC
msa118688.2{361_COH1}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCIGCTT	CACGATTCCC
msa118688.2{361_H36B}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCIGCTT	CACGATTCCC
msa118688.2{361_JM9130013}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCIGCTT	CACGATTCCC
msa118688.2{361_M732}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCIGCTT	CACGATTCCC
msa118688.2{GBS361_2603}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCIGCTT	CACGATTCCC
msa118688.2{361_090}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCIGCTT	CACGATTCCC
msa118688.2{361_1169NT}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCIGCTT	CACGATTCCC
msa118688.2{361_CJB110}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCIGCTT	CACGATTCCC
msa118688.2{361_M781}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCIGCTT	CACGATTCCC
Consensus	*****	*****	*****	*****	*****
	1551				1600
msa118688.2{361_18RS21}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC	ATTTTTAAAA
msa118688.2{361_A909}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC	ATTTTTAAAA
msa118688.2{361_COH1}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC	ATTTTTAAAA
msa118688.2{361_H36B}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC	ATTTTTAAAA
msa118688.2{361_JM9130013}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC	ATTTTTAAAA
msa118688.2{361_M732}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC	ATTTTTAAAA
msa118688.2{GBS361_2603}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC	ATTTTTAAAA
msa118688.2{361_090}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC	ATTTTTAAAA
msa118688.2{361_1169NT}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC	ATTTTTAAAA
msa118688.2{361_CJB110}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC	ATTTTTAAAA
msa118688.2{361_M781}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTTCTATC	ATTTTTAAAA
Consensus	*****	*****	*****	*****	*****
	1601				1650
msa118688.2{361_18RS21}	TAACAGGTCC	TTTATCTGTC	ATTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_A909}	TAACAGGTCC	TTTATCTGTC	ATTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_COH1}	TAACAGGTCC	TTTATCTGTC	ATTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_H36B}	TAACAGGTCC	TTTATCTGTC	ATTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_JM9130013}	TAACAGGTCC	TTTATCTGTC	ATTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_M732}	TAACAGGTCC	TTTATCTGTC	ATTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{GBS361_2603}	TAACAGGTCC	TTTATCTGTC	ATTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_090}	TAACAGGTCC	TTTATCTGTC	ATTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_1169NT}	TAACAGGTCC	TTTATCTGTC	ATTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_CJB110}	TAACAGGTCC	TTTATCTGTC	ATTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_M781}	TAACAGGTCC	TTTATCTGTC	ATTCGACAA	ATAGTGGAGC	GCTTGATGGT
Consensus	*****	*****	*****	*****	*****
	1651				1700
msa118688.2{361_18RS21}	ATACAATATG	CCAAGGAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_A909}	ATACAATATG	CCAAGGAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_COH1}	ATACAATATG	CCAAGGAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_H36B}	ATACAATATG	CCAAGGAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_JM9130013}	ATACAATATG	CCAAGGAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_M732}	ATACAATATG	CCAAGGAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{GBS361_2603}	ATACAATATG	CCAAGGAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_090}	ATACAATATG	CCAAGGAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_1169NT}	ATACAATATG	CCAAGGAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_CJB110}	ATACAATATG	CCAAGGAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_M781}	ATACAATATG	CCAAGGAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
Consensus	*****	*****	*****	*****	*****
	1701				1750
msa118688.2{361_18RS21}	TCTTGTTC	GCTAACATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_A909}	TCTTGTTC	GCTAACATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_COH1}	TCTTGTTC	GCTAACATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_H36B}	TCTTGTTC	GCTAACATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_JM9130013}	TCTTGTTC	GCTAACATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_M732}	TCTTGTTC	GCTAACATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{GBS361_2603}	TCTTGTTC	GCTAACATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_090}	TCTTGTTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_1169NT}	TCTTGTTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_CJB110}	TCTTGTTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_M781}	TCTTGTTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
Consensus	*****	*****	*****	*****	*****
	1751				1800
msa118688.2{361_18RS21}	AATTAAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_A909}	AATTAAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_COH1}	AATTAAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_H36B}	AATTAAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_JM9130013}	AATTAAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_M732}	AATTAAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{GBS361_2603}	AATTAAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_090}	AATTAAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_1169NT}	AATTAAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_CJB110}	AATTAAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA
msa118688.2{361_M781}	AATTAAACTA	TGATAGTCAA	ATGTTTGTGCG	GTTCTGATTA	TTGTTTCAGCA
Consensus	*****	*****	*****	*****	*****
	1801				1850
msa118688.2{361_18RS21}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_A909}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_COH1}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_H36B}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_JM9130013}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_M732}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{GBS361_2603}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_090}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_1169NT}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_CJB110}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_M781}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
Consensus	*****	*****	*****	*****	*****
	1851				1900
msa118688.2{361_18RS21}	TAACACAATTA	AAATATAGCC	ATAAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_A909}	TAACACAATTA	AAATATAGCC	ATAAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_COH1}	TAACACAATTA	AAATATAGCC	ATAAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_H36B}	TAACACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_JM9130013}	TAACACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_M732}	TAACACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{GBS361_2603}	TAACACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_090}	TAACACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_1169NT}	TAACACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_CJB110}	TAACACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_M781}	TAACACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
Consensus	*****	*****	*****	*****	*****
	1901				1950
msa118688.2{361_18RS21}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTGGACT	AACCATAAAA
msa118688.2{361_A909}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTGGACT	AACCATAAAA
msa118688.2{361_COH1}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTGGACT	AACCATAAAA
msa118688.2{361_H36B}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTGGACT	AACCATAAAA
msa118688.2{361_JM9130013}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTGGACT	AACCATAAAA
msa118688.2{361_M732}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTGGACT	AACCATAAAA
msa118688.2{GBS361_2603}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTGGACT	AACCATAAAA
msa118688.2{361_090}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTGGACT	AACCATAAAA
msa118688.2{361_1169NT}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTGGACT	AACCATAAAA
msa118688.2{361_CJB110}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTGGACT	AACCATAAAA
msa118688.2{361_M781}	TTGATGCTGC	GCTTCAAAAT	TTATTATCAG	ACTTGGACT	AACCATAAAA
Consensus	*****	*****	*****	*****	*****
	1951				2000
msa118688.2{361_18RS21}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_A909}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_COH1}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_H36B}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_JM9130013}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_M732}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{GBS361_2603}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_090}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_1169NT}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_CJB110}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_M781}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
Consensus	*****	*****	*****	*****	*****
	2001				2050
msa118688.2{361_18RS21}	TTATGATTTG	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_A909}	TTATGATTTG	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_COH1}	TTATGATTTG	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_H36B}	TTATGATTTG	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_JM9130013}	TTATGATTTG	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_M732}	TTATGATTTG	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{GBS361_2603}	TTATGATTTTC TTAGCGAACT TGTCTGAGTA TTATAATATG CCAAAACCTTG	
msa118688.2{361_090}	TTATGATTTTC TTAGCGAACT TGTCTGAGTA TTATAATATG CCAAAACCTTG	
msa118688.2{361_1169NT}	TTATGATTTTC TTAGCGAACT TGTCTGAGTA TTATAATATG CCAAAACCTTG	
msa118688.2{361_CJB110}	TTATGATTTTC TTAGCGAACT TGTCTGAGTA TTATAATATG CCAAAACCTTG	
msa118688.2{361_M781}	TTATGATTTTC TTAGCGAACT TGTCTGAGTA TTATAATATG CCAAAACCTTG	
Consensus	*****	*****
	2051	2100
msa118688.2{361_18RS21}	CTTCTGGTCA GTTTGGATTTCATCTAAATG GTGCTGGTGA AGAACCTGGAC	
msa118688.2{361_A909}	CTTCTGGTCA GTTTGGATTTCATCTAAATG GTGCTGGTGA AGAACCTGGAC	
msa118688.2{361_COH1}	CTTCTGGTCA GTTTGGATTTCATCTAAATG GTGCTGGTGA AGAACCTGGAC	
msa118688.2{361_H36B}	CTTCTGGTCA GTTTGGATTTCATCTAAATG GTGCTGGTGA AGAACCTGGAC	
msa118688.2{361_JM9130013}	CTTCTGGTCA GTTTGGATTTCATCTAAATG GTGCTGGTGA AGAACCTGGAC	
msa118688.2{361_M732}	CTTCTGGTCA GTTTGGATTTCATCTAAATG GTGCTGGTGA AGAACCTGGAC	
msa118688.2{GBS361_2603}	CTTCTGGTCA GTTTGGATTTCATCTAAATG GTGCTGGTGA AGAACCTGGAC	
msa118688.2{361_090}	CTTCTGGTCA GTTTGGATTTCATCTAAATG GTGCTGGTGA AGAACCTGGAC	
msa118688.2{361_1169NT}	CTTCTGGTCA GTTTGGATTTCATCTAAATG GTGCTGGTGA AGAACCTGGAC	
msa118688.2{361_CJB110}	CTTCTGGTCA GTTTGGATTTCATCTAAATG GTGCTGGTGA AGAACCTGGAC	
msa118688.2{361_M781}	CTTCTGGTCA GTTTGGATTTCATCTAAATG GTGCTGGTGA AGAACCTGGAC	
Consensus	*****	*****
	2101	2150
msa118688.2{361_18RS21}	TACTCTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA	
msa118688.2{361_A909}	TACTCTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA	
msa118688.2{361_COH1}	TACTCTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA	
msa118688.2{361_H36B}	TACTCTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA	
msa118688.2{361_JM9130013}	TACTCTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA	
msa118688.2{361_M732}	TACTCTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA	
msa118688.2{GBS361_2603}	TACTCTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA	
msa118688.2{361_090}	TACTCTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA	
msa118688.2{361_1169NT}	TACTCTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA	
msa118688.2{361_CJB110}	TACTCTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA	
msa118688.2{361_M781}	TACTCTGTTA ATGAAAGTAT AGAAAAGGGC TATTATTTAG TCCTATCTTA	
Consensus	*****	*****
	2151	2193
msa118688.2{361_18RS21}	TTCGATCTTC GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG	
msa118688.2{361_A909}	TTCGATCTTC GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG	
msa118688.2{361_COH1}	TTCGATCTTC GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG	
msa118688.2{361_H36B}	TTCGATCTTC GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG	
msa118688.2{361_JM9130013}	TTCGATCTTC GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG	
msa118688.2{361_M732}	TTCGATCTTC GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG	
msa118688.2{GBS361_2603}	TTCGATCTTC GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG	
msa118688.2{361_090}	TTCGATCTTC GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG	
msa118688.2{361_1169NT}	TTCGATCTTC GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG	
msa118688.2{361_CJB110}	TTCGATCTTC GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG	
msa118688.2{361_M781}	TTCGATCTTC GGTGGTATCT CTTTTGCTAT TATTGAAAAA AGG	
Consensus	*****	***

SEQ ID NO. 7512

STRAIN 2603 frame: 1

MSVYVGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPVEVPEQ
 YKDETTRNFKAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGSAGQNLYQFEEGERQV
 DASLLEKASVYHIADELMAYHDIVGASVVI STACSA SNNNAVILGTQLLDQGDCDLAICGG
 CDELSDIISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQS LAKY GKII GGL
 ITSDGYHITAPKPTGE GAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNM YGKF PTT
 FPTTTLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEI GIEGFENFVYHQKR
 EYPIRNALNFSFAFGGNNSVLLSSLDSPLETLPARENLKMAILSSV ASISKNESLSITY
 EKVASNFNDFEALR FKGARPPKTVNP AQFRKMDDFSKMVAVTTAQALIESNINLKKQDTS
 KVGI VFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAGMLSII FKITGPLSV
 ISTNSGALDGIOYAKEMMRNLDYVILVSANQWTDMSFMWWQQLNYDSQM FVGSDYCSA
 QVLSRQALDN SPII LGSKQLKYSHTFTDVMTIFDAALQNL LSDLGLTI KDI KGFWNER
 KKA VSSYDFFLANLSEYYNMPLASGQFGFSSNGAGEE LDYTVNESIEKGYYLVL SYSI FGG
 GISFAI IEKR

SEQ ID NO. 7513

STRAIN 090 frame: 3

VSGIGIISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPVEVPEQYKDE
 TRNFKAFTAFEEALASSGVNLKAYHNIAVCLGTSLGGSAGQNLYQFEEGERQV
 DASLLEKASVYHIADELMAYHDIVGASVVI STACSA SNNNAVILGTQLLDQGDCDLAICGG
 CDELSDIISLAGFTSLGAINTEMACQPYSSGKGINLGEGAGFVVLVKDQS LAKY GKII GGL
 GYHITAPKPTGE GAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNM YGKF PTT
 TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEI GIEGFENFVYHQKR
 EYNALNFSFAFGGNNSVLLSSLDSPLETLPARENLKMAILSSV ASISKNESLSITY
 EKVASNFNDFEALR FKGARPPKTVNP AQFRKMDDFSKMVAVTTAQALIESNINLKKQDTS
 KVGI VFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAGMLSII FKITGPLSV
 ISTNSGALDGIOYAKEMMRNLDYVILVSANQWTDMSFMWWQQLNYDSQM FVGSDYCSA
 QVLSRQALDN SPII LGSKQLKYSHTFTDVMTIFDAALQNL LSDLGLTI KDI KGFWNER
 KKA VSSYDFFLANLSEYYNMPLASGQFGFSSNGAGEE LDYTVNESIEKGYYLVL SYSI FGG
 GISFAI IEKR

SEQ ID NO. 7514

STRAIN A909 frame: 3

Table 75: Comparative Sequences relating to SAG0671

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTACASASNNAVILGTQOLLQDGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACOPYSSGKGINLGEGAGFVVVLVKDQSLAKYKIIIGGLITSD
 GHITAPKPTGEAAQIAKQLVTQAGIDSEIDYINGHTGTQANDKMEKNMYGKFPPPT
 TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTPATKNEIGIEGFPEVFVHQKREYPI
 RNALNFSFAFGNNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGARPPKTVMPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFFKITGPLSVISTN
 SGALDGQYAKEMMRNDNLDYVILVSANQWTDMMSFMWWQQLNYDSQMFVGSDYCSAQVLS
 RQALDNSPIILGSKQLKYSHKTFDVMTIFDAALQNLLSDLGLTIKDIKGFWNERKKAV
 SSDYDFFLANLSEYYNMPNLASQFGFSSNGAGEELDYTVNESIEKGYYLVLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7515

STRAIN H36B frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTACASASNNAVILGTQOLLQDGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACOPYSSGKGINLGEGAGFVVVLVKDQSLAKYKIIIGGLITSD
 GHITAPKPTGEAAQIAKQLVTQAGIDSEIDYINGHTGTQANDKMEKNMYGKFPPPT
 TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTPATKNEIGIEGFPEVFVHQKREYPI
 RNALNFSFAFGNNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGARPPKTVMPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFFKITGPLSVISTN
 SGALDGQYAKEMMRNDNLDYVILVSANQWTDMMSFMWWQQLNYDSQMFVGSDYCSAQVLS
 RQALDNSPIILGSKQLKYSHKTFDVMTIFDAALQNLLSDLGLTIKDIKGFWNERKKAV
 SSDYDFFLANLSEYYNMPNLASQFGFSSNGAGEELDYTVNESIEKGYYLVLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7516

STRAIN 18RS21 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTACASASNNAVILGTQOLLQDGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACOPYSSGKGINLGEGAGFVVVLVKDQSLAKYKIIIGGLITSD
 GHITAPKPTGEAAQIAKQLVTQAGIDSEIDYINGHTGTQANDKMEKNMYGKFPPPT
 TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTPATKNEIGIEGFPEVFVHQKREYPI
 RNALNFSFAFGNNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGARPPKTVMPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFFKITGPLSVISTN
 SGALDGQYAKEMMRNDNLDYVILVSANQWTDMMSFMWWQQLNYDSQMFVGSDYCSAQVLS
 RQALDNSPIILGSKQLKYSHKTFDVMTIFDAALQNLLSDLGLTIKDIKGFWNERKKAV
 SSDYDFFLANLSEYYNMPNLASQFGFSSNGAGEELDYTVNESIEKGYYLVLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7517

STRAIN M732 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTACASASNNAVILGTQOLLQDGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACOPYSSGKGINLGEGAGFVVVLVKDQSLAKYKIIIGGLITSD
 GHITAPKPTGEAAQIAKQLVTQAGIDSEIDYINGHTGTQANDKMEKNMYGKFPPPT
 TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTPATKNEIGIEGFPEVFVHQKREYPI
 RNALNFSFAFGNNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGARPPKTVMPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFFKITGPLSVISTN
 SGALDGQYAKEMMRNDNLDYVILVSANQWTDMMSFMWWQQLNYDSQMFVGSDYCSAQVLS
 RQALDNSPIILGSKQLKYSHKTFDVMTIFDAALQNLLSDLGLTIKDIKGFWNERKKAV
 SSDYDFFLANLSEYYNMPNLASQFGFSSNGAGEELDYTVNESIEKGYYLVLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7518

STRAIN COH1 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTS LGGKSAGQNALYQFEEGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTACASASNNAVILGTQOLLQDGDCDLAICGGCDEL
 SDISLAGFTSLGAINTEMACOPYSSGKGINLGEGAGFVVVLVKDQSLAKYKIIIGGLITSD
 GHITAPKPTGEAAQIAKQLVTQAGIDSEIDYINGHTGTQANDKMEKNMYGKFPPPT
 TLISSTKGQTGHTLGAAGIIELINCLAAIEEQTPATKNEIGIEGFPEVFVHQKREYPI
 RNALNFSFAFGNNNSGVLLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGARPPKTVMPAQFRKMDDFSKMVAVTTAQALIESNINLKKQDTSKVGI
 VFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIIFFKITGPLSVISTN
 SGALDGQYAKEMMRNDNLDYVILVSANQWTDMMSFMWWQQLNYDSQMFVGSDYCSAQVLS
 RQALDNSPIILGSKQLKYSHKTFDVMTIFDAALQNLLSDLGLTIKDIKGFWNERKKAV
 SSDYDFFLANLSEYYNMPNLASQFGFSSNGAGEELDYTVNESIEKGYYLVLVLSYSIFGGIS
 FAIEKR

SEQ ID NO. 7519

STRAIN M781 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITS DPEVPEQYKDE
 TRNFKFAFTAFEEALASSGVNLKAYHNIAVCLGTS LGGKSAGQNALYQFEEGERQVDASL

Table 75: Comparative Sequences relating to SAG0671

LEKASVYHIADELMAYHDIVGASYVISTACASASNNAVILGTQLLQDGDCDLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGGINLGEAGFVVVLKDQSLAKYGKI IGGLITSD
 GYHITAPKPTGEAAQIAKQLVTQAGIDYSEIDIYINGHGTGTQANDKMEKNMYGKFPPPT
 TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTPATKNEIGIEGFPEVFYHQKREYPI
 RNALNFSFAFGGNNSGILLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGARPPKTVPNAQFRKMDDFSKMVAVTAAQALIESNINLKKQDTSKVGI
 VFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIOYAKEMMRNDNLDVILVSANQWTDMSFMWQQLNYDSQMVFVGSDYCSAQVLS
 RQALDN SPI ILGSKQLKYSHKFTDVMTI FDAALQNLSSDLGLTI KDIKGFWNERKKA
 SSDYDFLANLSEYYNMPNLASQFGFSSNGAGEELDYTVNESIEKGYYVLVLSYSIFGGIS
 FAII EKR

SEQ ID NO. 7520

STRAIN CJB110 frame: 3
 VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPPEVPEQYKDE
 TRNFKFAFTAAFEALASSGVNLKAYHNIAVCLGTSLLGGKSAGQNALLYQFEEGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTACASASNNAVILGTQLLQDGDCDLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGGINLGEAGFVVVLKDQSLAKYGKI IGGLITSD
 GYHITAPKPTGEAAQIAKQLVTQAGIDYSEIDIYINGHGTGTQANDKMEKNMYGKFPPPT
 TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTPATKNEIGIEGFPEVFYHQKREYPI
 RNALNFSFAFGGNNSGILLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGARPPKTVPNAQFRKMDDFSKMVAVTAAQALIESNINLKKQDTSKVGI
 VFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIOYAKEMMRNDNLDVILVSANQWTDMSFMWQQLNYDSQMVFVGSDYCSAQVLS
 RQALDN SPI ILGSKQLKYSHKFTDVMTI FDAALQNLSSDLGLTI KDIKGFWNERKKA
 SSDYDFLANLSEYYNMPNLASQFGFSSNGAGEELDYTVNESIEKGYYVLVLSYSIFGGIS
 FAII EKR

SEQ ID NO. 7521

STRAIN 1169NT frame: 3
 VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPPEVPEQYKDE
 TRNFKFAFTAAFEALASSGVNLKAYHNIAVCLGTSLLGGKSAGQNALLYQFEEGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTACASASNNAVILGTQLLQDGDCDLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGGINLGEAGFVVVLKDQSLAKYGKI IGGLITSD
 GYHITAPKPTGEAAQIAKQLVTQAGIDYSEIDIYINGHGTGTQANDKMEKNMYGKFPPPT
 TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTPATKNEIGIEGFPEVFYHQKREYPI
 RNALNFSFAFGGNNSGILLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGARPPKTVPNAQFRKMDDFSKMVAVTAAQALIESNINLKKQDTSKVGI
 VFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIOYAKEMMRNDNLDVILVSANQWTDMSFMWQQLNYDSQMVFVGSDYCSAQVLS
 RQALDN SPI ILGSKQLKYSHKFTDVMTI FDAALQNLSSDLGLTI KDIKGFWNERKKA
 SSDYDFLANLSEYYNMPNLASQFGFSSNGAGEELDYTVNESIEKGYYVLVLSYSIFGGIS
 FAII EKR

SEQ ID NO. 7522

STRAIN JM9130013 frame: 3
 VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILESYTGSITSDPPEVPEQYKDE
 TRNFKFAFTAAFEALASSGVNLKAYHNIAVCLGTSLLGGKSAGQNALLYQFEEGERQVDASL
 LEKASVYHIADELMAYHDIVGASYVISTACASASNNAVILGTQLLQDGDCDLAI CGGCDEL
 SDISLAGFTSLGAINTEMACQPYSSGKGGINLGEAGFVVVLKDQSLAKYGKI IGGLITSD
 GYHITAPKPTGEAAQIAKQLVTQAGIDYSEIDIYINGHGTGTQANDKMEKNMYGKFPPPT
 TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTPATKNEIGIEGFPEVFYHQKREYPI
 RNALNFSFAFGGNNSGILLSSLDSPLETLPARENLKMAILSSVASISKNESLSITYEKVA
 SNFNDFEALRFKGARPPKTVPNAQFRKMDDFSKMVAVTAAQALIESNINLKKQDTSKVGI
 VFTTSLGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSII FKITGPLSVISTN
 SGALDGIOYAKEMMRNDNLDVILVSANQWTDMSFMWQQLNYDSQMVFVGSDYCSAQVLS
 RQALDN SPI ILGSKQLKYSHKFTDVMTI FDAALQNLSSDLGLTI KDIKGFWNERKKA
 SSDYDFLANLSEYYNMPNLASQFGFSSNGAGEELDYTVNESIEKGYYVLVLSYSIFGGIS
 FAII EKR

PRETTY of: /biotmp/msa118713.2{*} April 9, 2003 02:54 ..

	1	50
msa118713.2{361_090}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS	
msa118713.2{361_1169NT}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS	
msa118713.2{361_CJB110}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS	
msa118713.2{361_M781}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS	
msa118713.2{361_18RS21}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS	
msa118713.2{361_A909}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS	
msa118713.2{361_COH1}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS	
msa118713.2{361_H36B}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS	
msa118713.2{361_JM9130013}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS	
msa118713.2{361_M732}	----VSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS	
msa118713.2{GBS361_2603}	msv yVSGIGI ISSLGKNYSE HKQHLFDLKE GISKHLYKNH DSILESYTGS	
Consensus	*****	*****
	51	100
msa118713.2{361_090}	ITSDPEVPEQ YKDETTRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTS	
msa118713.2{361_1169NT}	ITSDPEVPEQ YKDETTRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTS	
msa118713.2{361_CJB110}	ITSDPEVPEQ YKDETTRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTS	
msa118713.2{361_M781}	ITSDPEVPEQ YKDETTRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTS	
msa118713.2{361_18RS21}	ITSDPEVPEQ YKDETTRNFKF AFTAFEEALA SSGVNLKAYH NIAVCLGTS	

Table 75: Comparative Sequences relating to SAG0671

msa118713.2{361_A909}	ITSDPEVPEQ	YKDET RNFKF	AFTAFEEA ALA	SSGVNLKAYH	NIAVCLG TSL
msa118713.2{361_COH1}	ITSDPEVPEQ	YKDET RNFKF	AFTAFEEA ALA	SSGVNLKAYH	NIAVCLG TSL
msa118713.2{361_H36B}	ITSDPEVPEQ	YKDET RNFKF	AFTAFEEA ALA	SSGVNLKAYH	NIAVCLG TSL
msa118713.2{361_JM9130013}	ITSDPEVPEQ	YKDET RNFKF	AFTAFEEA ALA	SSGVNLKAYH	NIAVCLG TSL
msa118713.2{361_M732}	ITSDPEVPEQ	YKDET RNFKF	AFTAFEEA ALA	SSGVNLKAYH	NIAVCLG TSL
msa118713.2{GBS361_2603}	ITSDPEVPEQ	YKDET RNFKF	AFTAFEEA ALA	SSGVNLKAYH	NIAVCLG TSL
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	101	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY HDIVGASYVI
msa118713.2{361_1169NT}		GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY HDIVGASYVI
msa118713.2{361_CJB110}		GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY HDIVGASYVI
msa118713.2{361_M781}		GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY HDIVGASYVI
msa118713.2{361_18RS21}		GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY HDIVGASYVI
msa118713.2{361_A909}		GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY HDIVGASYVI
msa118713.2{361_COH1}		GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY HDIVGASYVI
msa118713.2{361_H36B}		GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY HDIVGASYVI
msa118713.2{361_JM9130013}		GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY HDIVGASYVI
msa118713.2{361_M732}		GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY HDIVGASYVI
msa118713.2{GBS361_2603}		GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY HDIVGASYVI
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	151	STAC SASNN A	VILGTQLLQD	GDCDLAICGG	CDELSDISLA GFTSLGA INT
msa118713.2{361_1169NT}		STAC SASNN A	VILGTQLLQD	GDCDLAICGG	CDELSDISLA GFTSLGA INT
msa118713.2{361_CJB110}		STAC SASNN A	VILGTQLLQD	GDCDLAICGG	CDELSDISLA GFTSLGA INT
msa118713.2{361_M781}		STAC SASNN A	VILGTQLLQD	GDCDLAICGG	CDELSDISLA GFTSLGA INT
msa118713.2{361_18RS21}		STAC SASNN A	VILGTQLLQD	GDCDLAICGG	CDELSDISLA GFTSLGA INT
msa118713.2{361_A909}		STAC SASNN A	VILGTQLLQD	GDCDLAICGG	CDELSDISLA GFTSLGA INT
msa118713.2{361_COH1}		STAC SASNN A	VILGTQLLQD	GDCDLAICGG	CDELSDISLA GFTSLGA INT
msa118713.2{361_H36B}		STAC SASNN A	VILGTQLLQD	GDCDLAICGG	CDELSDISLA GFTSLGA INT
msa118713.2{361_JM9130013}		STAC SASNN A	VILGTQLLQD	GDCDLAICGG	CDELSDISLA GFTSLGA INT
msa118713.2{361_M732}		STAC SASNN A	VILGTQLLQD	GDCDLAICGG	CDELSDISLA GFTSLGA INT
msa118713.2{GBS361_2603}		STAC SASNN A	VILGTQLLQD	GDCDLAICGG	CDELSDISLA GFTSLGA INT
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	201	EMACQPYSSG	KGINLGEGAG	FVVLVKDQSL	AKYGKIIIGGL ITSDGYHITA
msa118713.2{361_1169NT}		EMACQPYSSG	KGINLGEGAG	FVVLVKDQSL	AKYGKIIIGGL ITSDGYHITA
msa118713.2{361_CJB110}		EMACQPYSSG	KGINLGEGAG	FVVLVKDQSL	AKYGKIIIGGL ITSDGYHITA
msa118713.2{361_M781}		EMACQPYSSG	KGINLGEGAG	FVVLVKDQSL	AKYGKIIIGGL ITSDGYHITA
msa118713.2{361_18RS21}		EMACQPYSSG	KGINLGEGAG	FVVLVKDQSL	AKYGKIIIGGL ITSDGYHITA
msa118713.2{361_A909}		EMACQPYSSG	KGINLGEGAG	FVVLVKDQSL	AKYGKIIIGGL ITSDGYHITA
msa118713.2{361_COH1}		EMACQPYSSG	KGINLGEGAG	FVVLVKDQSL	AKYGKIIIGGL ITSDGYHITA
msa118713.2{361_H36B}		EMACQPYSSG	KGINLGEGAG	FVVLVKDQSL	AKYGKIIIGGL ITSDGYHITA
msa118713.2{361_JM9130013}		EMACQPYSSG	KGINLGEGAG	FVVLVKDQSL	AKYGKIIIGGL ITSDGYHITA
msa118713.2{361_M732}		EMACQPYSSG	KGINLGEGAG	FVVLVKDQSL	AKYGKIIIGGL ITSDGYHITA
msa118713.2{GBS361_2603}		EMACQPYSSG	KGINLGEGAG	FVVLVKDQSL	AKYGKIIIGGL ITSDGYHITA
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	251	PKPTGE GAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND KMEKNMYGKF
msa118713.2{361_1169NT}		PKPTGE GAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND KMEKNMYGKF
msa118713.2{361_CJB110}		PKPTGE GAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND KMEKNMYGKF
msa118713.2{361_M781}		PKPTGE GAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND KMEKNMYGKF
msa118713.2{361_18RS21}		PKPTGE GAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND KMEKNMYGKF
msa118713.2{361_A909}		PKPTGE GAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND KMEKNMYGKF
msa118713.2{361_COH1}		PKPTGE GAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND KMEKNMYGKF
msa118713.2{361_H36B}		PKPTGE GAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND KMEKNMYGKF
msa118713.2{361_JM9130013}		PKPTGE GAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND KMEKNMYGKF
msa118713.2{361_M732}		PKPTGE GAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND KMEKNMYGKF
msa118713.2{GBS361_2603}		PKPTGE GAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND KMEKNMYGKF
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	301	FPTTTLIS ST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA TKNEIGIEGF
msa118713.2{361_1169NT}		FPTTTLIS ST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA TKNEIGIEGF
msa118713.2{361_CJB110}		FPTTTLIS ST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA TKNEIGIEGF
msa118713.2{361_M781}		FPTTTLIS ST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA TKNEIGIEGF
msa118713.2{361_18RS21}		FPTTTLIS ST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA TKNEIGIEGF
msa118713.2{361_A909}		FPTTTLIS ST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA TKNEIGIEGF
msa118713.2{361_COH1}		FPTTTLIS ST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA TKNEIGIEGF
msa118713.2{361_H36B}		FPTTTLIS ST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA TKNEIGIEGF
msa118713.2{361_JM9130013}		FPTTTLIS ST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA TKNEIGIEGF
msa118713.2{361_M732}		FPTTTLIS ST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA TKNEIGIEGF
msa118713.2{GBS361_2603}		FPTTTLIS ST	KGQTGHTLGA	AGIIELINCL	AAIEEQTVPA TKNEIGIEGF
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	351	PENFVYHQ KR	EYPIRNALNF	SFAFGGNNSG	I LSSLDSP ETL PARENLK
msa118713.2{361_1169NT}		PENFVYHQ KR	EYPIRNALNF	SFAFGGNNSG	I LSSLDSP ETL PARENLK
msa118713.2{361_CJB110}		PENFVYHQ KR	EYPIRNALNF	SFAFGGNNSG	I LSSLDSP ETL PARENLK
msa118713.2{361_M781}		PENFVYHQ KR	EYPIRNALNF	SFAFGGNNSG	I LSSLDSP ETL PARENLK

Table 75: Comparative Sequences relating to SAG0671

msa118713.2{361_18RS21}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK
msa118713.2{361_A909}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK
msa118713.2{361_COH1}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK
msa118713.2{361_H36B}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK
msa118713.2{361_JM9130013}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK
msa118713.2{361_M732}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK
msa118713.2{GBS361_2603}	PENFVYHQKR	EYPIRNALNF	SFAFGGNNSG	VLLSSLDSP	ETLPARENLK
Consensus	*****	*****	*****	-*****	*****
	401				450
msa118713.2{361_090}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVPNAQFR
msa118713.2{361_1169NT}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVPNAQFR
msa118713.2{361_CJB110}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVPNAQFR
msa118713.2{361_M781}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVPNAQFR
msa118713.2{361_18RS21}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVPNAQFR
msa118713.2{361_A909}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVPNAQFR
msa118713.2{361_COH1}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVPNAQFR
msa118713.2{361_H36B}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVPNAQFR
msa118713.2{361_JM9130013}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVPNAQFR
msa118713.2{361_M732}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVPNAQFR
msa118713.2{GBS361_2603}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKGARP	PKTVPNAQFR
Consensus	*****	*****	*****	*****	*****
	451				500
msa118713.2{361_090}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_1169NT}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_CJB110}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_M781}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_18RS21}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_A909}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_COH1}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_H36B}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_JM9130013}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_M732}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{GBS361_2603}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
Consensus	*****	*****	*****	*****	*****
	501				550
msa118713.2{361_090}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_1169NT}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_CJB110}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_M781}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_18RS21}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_A909}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_COH1}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_H36B}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_JM9130013}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_M732}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{GBS361_2603}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
Consensus	*****	*****	*****	*****	*****
	551				600
msa118713.2{361_090}	IQYAKEMMRN	DNLDDYVILVS	ANQWTDMSFM	WWQQLNYSQ	MFVGSODYCSA
msa118713.2{361_1169NT}	IQYAKEMMRN	DNLDDYVILVS	ANQWTDMSFM	WWQQLNYSQ	MFVGSODYCSA
msa118713.2{361_CJB110}	IQYAKEMMRN	DNLDDYVILVS	ANQWTDMSFM	WWQQLNYSQ	MFVGSODYCSA
msa118713.2{361_M781}	IQYAKEMMRN	DNLDDYVILVS	ANQWTDMSFM	WWQQLNYSQ	MFVGSODYCSA
msa118713.2{361_18RS21}	IQYAKEMMRN	DNLDDYVILVS	ANQWTDMSFM	WWQQLNYSQ	MFVGSODYCSA
msa118713.2{361_A909}	IQYAKEMMRN	DNLDDYVILVS	ANQWTDMSFM	WWQQLNYSQ	MFVGSODYCSA
msa118713.2{361_COH1}	IQYAKEMMRN	DNLDDYVILVS	ANQWTDMSFM	WWQQLNYSQ	MFVGSODYCSA
msa118713.2{361_H36B}	IQYAKEMMRN	DNLDDYVILVS	ANQWTDMSFM	WWQQLNYSQ	MFVGSODYCSA
msa118713.2{361_JM9130013}	IQYAKEMMRN	DNLDDYVILVS	ANQWTDMSFM	WWQQLNYSQ	MFVGSODYCSA
msa118713.2{361_M732}	IQYAKEMMRN	DNLDDYVILVS	ANQWTDMSFM	WWQQLNYSQ	MFVGSODYCSA
msa118713.2{GBS361_2603}	IQYAKEMMRN	DNLDDYVILVS	ANQWTDMSFM	WWQQLNYSQ	MFVGSODYCSA
Consensus	*****	*****	*****	*****	*****
	601				650
msa118713.2{361_090}	OVLSRQALDN	SPIIILGSKQL	KYSHKTFDTV	MTIFDAALQN	LSDLGTLIK
msa118713.2{361_1169NT}	OVLSRQALDN	SPIIILGSKQL	KYSHKTFDTV	MTIFDAALQN	LSDLGTLIK
msa118713.2{361_CJB110}	OVLSRQALDN	SPIIILGSKQL	KYSHKTFDTV	MTIFDAALQN	LSDLGTLIK
msa118713.2{361_M781}	OVLSRQALDN	SPIIILGSKQL	KYSHKTFDTV	MTIFDAALQN	LSDLGTLIK
msa118713.2{361_18RS21}	OVLSRQALDN	SPIIILGSKQL	KYSHKTFDTV	MTIFDAALQN	LSDLGTLIK
msa118713.2{361_A909}	OVLSRQALDN	SPIIILGSKQL	KYSHKTFDTV	MTIFDAALQN	LSDLGTLIK
msa118713.2{361_COH1}	OVLSRQALDN	SPIIILGSKQL	KYSHKTFDTV	MTIFDAALQN	LSDLGTLIK
msa118713.2{361_H36B}	OVLSRQALDN	SPIIILGSKQL	KYSHKTFDTV	MTIFDAALQN	LSDLGTLIK
msa118713.2{361_JM9130013}	OVLSRQALDN	SPIIILGSKQL	KYSHKTFDTV	MTIFDAALQN	LSDLGTLIK
msa118713.2{361_M732}	OVLSRQALDN	SPIIILGSKQL	KYSHKTFDTV	MTIFDAALQN	LSDLGTLIK
msa118713.2{GBS361_2603}	OVLSRQALDN	SPIIILGSKQL	KYSHKTFDTV	MTIFDAALQN	LSDLGTLIK
Consensus	*****	*****	*****	*****	*****
	651				700
msa118713.2{361_090}	DIKGFWNNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_1169NT}	DIKGFWNNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_CJB110}	DIKGFWNNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD

Table 75: Comparative Sequences relating to SAG0671

msa118713.2{361_M781}	DIKGFWNNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_18RS21}	DIKGFWNNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_A909}	DIKGFWNNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_COH1}	DIKGFWNNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_H36B}	DIKGFWNNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_JM9130013}	DIKGFWNNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_M732}	DIKGFWNNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
msa118713.2{GBS361_2603}	DIKGFWNNER	KKAVSSDYDF	LANLSEYYNM	PNLASGQFGF	SSNGAGEELD
Consensus	*****	*****	*****	*****	*****
			701	731	
msa118713.2{361_090}	YTVNESIEKG	YYLVLSYSIF	GGISFAIIEK	R	
msa118713.2{361_1169NT}	YTVNESIEKG	YYLVLSYSIF	GGISFAIIEK	R	
msa118713.2{361_CJB110}	YTVNESIEKG	YYLVLSYSIF	GGISFAIIEK	R	
msa118713.2{361_M781}	YTVNESIEKG	YYLVLSYSIF	GGISFAIIEK	R	
msa118713.2{361_18RS21}	YTVNESIEKG	YYLVLSYSIF	GGISFAIIEK	R	
msa118713.2{361_A909}	YTVNESIEKG	YYLVLSYSIF	GGISFAIIEK	R	
msa118713.2{361_COH1}	YTVNESIEKG	YYLVLSYSIF	GGISFAIIEK	R	
msa118713.2{361_H36B}	YTVNESIEKG	YYLVLSYSIF	GGISFAIIEK	R	
msa118713.2{361_JM9130013}	YTVNESIEKG	YYLVLSYSIF	GGISFAIIEK	R	
msa118713.2{361_M732}	YTVNESIEKG	YYLVLSYSIF	GGISFAIIEK	R	
msa118713.2{GBS361_2603}	YTVNESIEKG	YYLVLSYSIF	GGISFAIIEK	R	
Consensus	*****	*****	*****	*	

Table 76: Comparative Sequences relating to SAG0260**SEQ ID NO. 7601****STRAIN 2603**

ATGAAAAAAAGTCATCGATTAAAAAAACTACAAAAAGCATATGCCCTAGAAACCGTTTA
 AATAATATTAAATTGGAGGTGTTAAAGGCAGAATAATTGGATTAATAGGACCCCTGGA
 GCAGGGAAATCTACCTTGATTAAAACCTATGCCCTGAGGAAACA
 GCTCTTGTCTTGATACTCAAATGCCAGATCGTAATATTGGCTATAATG
 GCTCAATCTGATGCCCTTACCGAGTCTTAACCTGCTTAGAAAATTATTCTTGGA
 AAAATGAAAGGTATTCAAAAACGAACTGAAATTAAACAGCAGATAACTCATATTCTAAAGTA
 GTAGATCTAGAAAACCGTAAATTGTCTCAGGTTACTCAGGAGGTATGAAAAGA
 CGGCTTCTGAGCCATGCCCTACTGGAAACCCCACAGGTTTAATCTAGATGAACT
 ACCGGTGGAAATTGATCCATCCCTGAGGAGAAAATCTGCAAGAGCTAATTAAATTAAAG
 GATGAAGGACATTCTATTTATTACAAACCCACGTTATGGATGAAGCAAGATTAAACAGT
 AAGGGTGCACTACTATTACGTGAAACATTATTGCTTGTACTCCATTACATTAAAAA
 AAACAATTAAATGTGAGTACTATTGAGGAAGTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7602**STRAIN 090**

ATTTAAAAAAACTACAAAAAGCATATGCCCTAGAAACTGTTTAAATAAT
 ATTAATTGGAGGTGTTAAAGGCAGAATAATTGGATTAATAGGACCCCTC
 TGAGCAGGGAAATCTACCTTGATTAAAACCTATGCCCTGAGGAAAAG
 CAGATAAGGGAAACGCTCTTGTCTTGATACTCAAATGCCAGATCGTAAT
 ATTAAATCAAATTGGCTATATGGCTCAATCTGCTTATACGAATC
 TTAACTGCTTAGAAAATTATTCTTGAGGAAATTGAAAGGTATTC
 AAAAACGAACTCATACGAGATAACTCATATTCTAAAGTAGTAGAT
 CTAGAAAACCAACTTGATAAATTGTCTCAGGTTACTCAGGAGGTATGAA
 AGAGCGCTTCTCTAGGCCATGCCCTACTTGGAACCCACAGGTTTA
 TCTCTAGATGAAACCTACCGTGGAAATTGATCATCCCTGAGGAGAAAATC
 TGCAAGAGCTAATTAAATTAAAGGATGAAGGAGCTTATCTTATTAC
 AACCCACGTTATGGATGAAGCAGAATTAAACAGTAAGGTGCACTACTAT
 TACGTGAAACATTATTGCTTGTACTCCATTACATTAAAAAAACAA
 TTAAATGTGAGTACTATTGAGGAAGTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7603**STRAIN A909**

AAAAAAAGTCATCGATTAAAAAAACTACAAAAAGCATATGCCCTCA
 GAAACCGTTTAAATAATATTAAATTGGAGGTGTTAAAGGCAGAATAAT
 TGATTAATAGGACCCCTGAGCAGGGAAATCTACCTTGATTAACCTA
 TGCTTGCGATGAAAAGCAGATAAGGGAAACAGCTCTTGTCTTGATACT
 CAAATGCCAGATCATAATATTAAATCAAATTGGCTATATGGCTCAATC
 TGATGCTTACCGAGTCTTAACCTGCTTAGAAAATTATTCTTGT
 GAAAATGAAAGGTATTCAAAAACGAACTCATATTAAACAGCAGATAACTCAT
 ATTCTAAAGTAGTAGATCTGAAACCAACTTGATAAATTGTCTCAGG
 TTACTCAGGAGGTATGAAAAGCAGGCTTCTCTAGCCCATGCCCTACTTG
 GAAACCCACAGGTTTAATCTCTAGATGAAACCTACCGTTGAAATTGATCCA
 TCTCTGAGGAGAAAATCTGCAAGAGCTAATTAAATTAAAGGATGAAGG
 AGGTTCTATCTTATTACACCCACGTTATGGATGAAGCAGAATTAAACAA
 GTAAGGTGCACTACTATTACGTGAAACATTATTGCTTGTACTCTCA
 TTACATTAAAAAAACAAATTAAATGTGAGTACTATTGAGGAAGTTCTT
 AAAAGCTGAAGGAGAA

SEQ ID NO. 7604**STRAIN H36B**

AAAAAAAGTCATTGATTAAAAAAACTACAAAAAGCATATGCC
 TCAGAAACCGTTTAAATAATATTAAATTGGAGGTGTTAAAGGCAGAAT
 AATTGGATTAATAGGACCCCTGAGCAGGGAAATCTACCTTGATTAACCT
 CTATGCTTGGCGATGAAAAGCAGATAAGGGAAACAGCTCTTGTCTTGAT
 ACTCAAATGCCAGATCGTAATATTAAATCAAATTGGCTATATGGCTCA
 ATCTGATGCCCTTACCGAGTCTTAACCTGCTTAGAAAATTATTCTT
 TTGGAAAATGAAAGGTATTCAAAAACGAACTTGATAAATTGTCTC
 CATATTCTAAAGTAGTAGATCTGAAACCAACTTGATAAATTGTCTC
 AGGTTACTCAGGAGCTATGAAAAGCAGGCTTCTCTAGCCATGCCCTAC
 TTGGAAACCCACAGGTTTAATCTCTAGATGAAACCTACCGTTGAAATTGAT
 CCATCTTGAGGAGAAAATCTGCAAGAGCTAATTAAATTAAAGGATGA
 AGGACGTTCTATCTTATTACACCCACGTTATGGATGAAGCAGAATTAA
 CAAGTAAGGTGCACTACTATTACGTGAAACATTATTGCTTGTACTCT
 CCATTACATTAAAAAAACAAATTAAATGTGAGTACTATTGAGGAAGTTT
 CTAAAGCTGAAGGAGAA

SEQ ID NO. 7605**STRAIN 18RS21**

GATTTAAAAAAACTACAAAAAGCATATGCCCTAGAAACCGTTTAAATAA
 TATTAATTGGAGGTGTTAAAGGCAGAATAATTGGATTAATAGGACCC
 CTGGAGCAGGGAAATCTACCTGATTAAAACCTATGCCCTGAGGAAAA
 GCAGATAAGGGAAACAGCTCTTGTCTTGATACTCAAATGCCAGATCGTA
 TATTAAATCAAATTGGCTATATGGCTCAATCTGATGCCCTTACCGAGT
 CTITAACCTGCTTAGAAAATTATTCTTGAGGAAATGAAAGGTATT
 CAAAACGAACTGAAATTAAACGAGATAACTCATATTCTAAAGTAGT
 TCTAGAAAACCAACTTGATAAATTGTCTCAGGTTACTCAGGAGGTATG
 AAAGACGGCTTCTCTAGCCATGCCCTACTTGGAACCCACAGGTTA
 ATCCCTAGATGAAACCTACCGTTGGAATTGATCCATCCCTGAGGAGAAAAT
 CTGGCAAGAGCTAATTAAATTAAAGGATGAAGGACATTCTATCTTATT
 AACCCACGTTATGGATGAAGCAGAATTAAACAGTAAGGTGCACTACTA

Table 76: Comparative Sequences relating to SAG0260

TTACGTGGAAACATTATTGCCTTGATACTCCATTACATTAAAAAAACA
ATTAATGTGAGTACTATTGAGGAAGTTCTAAAAGCTGAAGGAGAA

SEQ ID NO. 7606

STRAIN M732

AAAAAAGTCATCGATTTAAAAAAACTACAAAAGCATAACGCCCA
GAAACTGTTTAAATAATATTAAATTGGAGGTGTTAAAGGAGAAATAAT
TGGATTAAAGGACCTCTGGAGCAGGGAAATCTACCTTGATTAAAAC
TGCCTGCGATGGAAAAGCAGATAAGGGAACAGCTCTTGTCTTGATACT
CAAATGCCAGATCGTAAATTTAAATCAATTGGCTATATGGCTCAATC
TGATGCCCTACACGAGTCITTAACTGGCTTAGAAAATTATTCTTG
GAAAATGAAAGTATTCAAAAACGAGATAACGGAACAGCTCAT
ATTCTCAAAAGTAGATCTAGAAAACCCAACTTGATAAAATTGTCTCAGG
TTACTCAGGAGGTATGAAAAGACGGCTTCTAGCCATGCCCTACTTG
GAAACCCCACAGTTTAATCTAGATGAACCTACCGTTGAAATTGATCCA
TCCCTGAGGAGAAAATCTGGCAAGAGCTAATTAAATTAAAGGATGAAGG
ACGTTCTATCTTATTACAACCCACGTTATGGATGAAGCAGAAATTAAACAA
GTAAGGTTGCACTATTACGTGAAACATTATTGCCCTTGATACTCCA
TTACATTTAAAAAAACAATTAAATGTGAGTACTATTGAGGAAGTTTCTT
AAAAGCTGAAGGAGAA

SEQ ID NO. 7607

STRAIN COH1

AAAAAAGTCATCGATTTAAAAAAACTACAAAAGCATAACGCCCAAGAA
ACIGTTTAAATAATATTAAATTGGAGGTGTTAAAGGAGAAATAATTGG
ATTAAATAGGACCTCTGGAGCAGGGAAATCTACCTTGATTAAAACATG
TGGCATGGAAAAGCAGATAAGGGAACAGCTCTTGTCTTGATACTCAA
ATGCCAGATCGTAAATTTAAATCAAATTGGCTATATGGCTCAATCTGA
TGCCTACACGAGTCITTAACTGGCTAGAAAATTAAATTCTTGAA
AAATGAAAGTATTCAAAAACGAGATAACGGAACAGCTACCTCATATT
TCTAAAGTAGATCTAGAAAACCAACTTGATAAAATTGTCTCAGGTTA
CTCAGGAGGTATGAAAAGACGGCTTCTAGCCATGCCCTACTTGAA
ACCCCAAGTTAAATCTAGATGAACCTACCGTTGGAAATTGATCCATC
TTGAGGAGAAAATCTGGCAAGAGCTAATTAAATTAAAGGATGAAGGAGC
TTCTATCTTATTACAACCCACGTTATGGATGAAGCAGAAATTAAAGTA
AGTTGCACTACTATTACGTGAAACATTATTGCCCTTGATACTCCATT
CATTAAAAAAACAATTAAATGTGAGTACTATTGAGGAAG

SEQ ID NO. 7608

STRAIN M781

AAAAAAGTCATCGATTTAAAAAAACTACAAAAGCATAAC
GCCTCAGAAACIGTTTAAATAATATTAAATTGGAGGTGTTAAAGGAGA
AAATAATTGGATTAAATAGGACCTCTGGAGCAGGGAAATCTACCTTGATT
AAACTATGCTGGCATGGAAAAGCAGATAAGGGAACAGCTCTTGTCT
GATACTCAAATGCCAGATCGTAAATTTAAATCAAATTGGCTATATGGC
TCAATCTGATGCCCTACACGAGTCITTAACTGGCTAGAAAATTATT
TCTTGGAAAATGAAAGGTATTCAAAAACGAGATAACGGAACAGCAGATA
ACTCATATTCTAAAGTAGATCTAGAAAACCAACTTGATAAAATTGT
CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTCTAGCCATGCC
TACTTGGAAACCCCACAGTTAAATCTAGATGAACCTACCGTTGGAAATT
GATCCATCCTGGAGGAGAAAATCTGGCAAGAGCTAATTAAATTAAAGGA
TGAAGGACGTTCTATCTTATTACAACCCACGTTATGGATGAAGCAGAA
TAACAAGTAAGGTTGCACTACTATTACGTGAAACATTATTGCCCTTGAT
ACTCCATTACATTAAAAAAACAATTAAATGTGAGTACTATTGAGGAAGT
TTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7609

STRAIN CJB110

AAAAAAGTCATCGATTTAAAAAAACTACAAAAGCATAAC
CCTCAGAAACIGTTTAAATAATATTAAATTGGAGGTGTTAAAGGCGAA
AAATAATTGGATTAAATAGGACCTCTGGAGCAGGGAAATCTACCTTGATT
AAACTATGCTGGCATGGAAAAGCAGATAAGGGAACAGCTCTTGTCT
ATACTCAAATGCCAGATCGTAAATTTAAATCAAATTGGCTATATGGC
CAATCTGATGCCCTACGAAATCTTAACTGCCCTAGAAAATTATT
CTTGGAAAATGAAAGGTATTCAAAAACGAGATAACGGAACAGCAGATA
CTCATATTCTAAAGTAGATCTAGAAAACCAACTTGATAAAATTGT
TCAGGTTACTCAGGAGGTATGAAAAGACGGCTTCTAGCCATGCC
ACTTGGAAACCCCACAGTTAAATCTAGATGAACCTACCGTTGGAAATTG
ATCCATCCTGGAGGAGAAAATCTGGCAAGAGCTAATTAAATTAAAGGAT
GAAGGAGCTCTATCTTATTACAACCCACGTTATGGATGAAGCAGAA
AACAAAGTAAGGTTGCACTACTATTACGTGAAACATTATTGCCCTTGATA
CTCCATTACATTAAAAAAACAATTAAATGTGAGTACTATTGAGGAAGT
TTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7610

STRAIN 1169NT

AAAAAAGTCATCGATTTAAAAAAACTACAAAAGCATAAC
GCCTCAGAAACIGTTTAAATAATATTAAATTGGAGGTGTTAAAGGCGA
AAATAATTGGATTAAATAGGACCTCTGGAGCAGGGAAATCTACCTTGATT
AAACTATGCTGGCATGGAAAAGCAGATAAGGGAACAGCTCTTGTCT
GATACTCAAATGCCAGATCGTAAATTTAAATCAAATTGGCTATATGGC
TCAATCTGATGCCCTACGAAATCTTAACTGCC

Table 76: Comparative Sequences relating to SAG0260

TCTTTGGAAAAATGAAAGGTATTCAAAAACACTGAATTAAAACAGCAGATA
 ACTCATATTTCTAAAGTAGTATGAGTCTAGAAAACCAACTTGATAAATTGTT
 CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTCTCTAGCCATCGCCC
 TACTTGGAAACCCACAGTTTAATCTAGATGAACCTACCGTTGGAATT
 GATCCATCCTGAGGAGAAAATCTGGCAAGAGCTAATTAAATTAAAGGA
 TGAAAGGACGTTCTATCTTATTACAACCCACGTTATGGATGAAGCAGAAAT
 TAACAAGTAAGGTGACTACTATTACGTGGAAACATTATTGCCCTTGAT
 ACTCCATTACATTAAAAAACAAATTAAATGTGAGTACTATTGAGGAAGT
 TTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7611

STRAIN JM9130013

AAAAAAAGTCATCGATTAAAAAAACTACAAAAAGCATATGCC
 TCAGAAACCGTTTAAATAATATAATTGGAGGTGTTAAAGGCAGAAAT
 AATTGGATTAATAGGACCCTCTGGAGCAGGGAAATCTACCTTGATTTAA
 CTATGCTGGCATGGAAAAACAGATAAGGAAACAGCTTGTGTTCTGAT
 ACTCAAATGCCAGCTGAATATTAAATCTAACTGGCTATATGGCTCA
 ATCTGATGCCCTATACGAGTCCTTAACGCTTAGAAAATTATTCTT
 TTGGAAAATGAAAGGTATTCAAAAACAGTAAACAGCAGATAACT
 CATATTCTAAAGTAGTATGAGTCTAGGAAACCAACTTGATAAATTGTC
 AGGTTACTCAGGAGGTATGAAAGACGGCTTCTAGCCATGCCCTAC
 TTGGAAACCCACAGTTTAATCCTAGATGAACCTACCGTTGGAATTGAT
 CCATCTTGAGGAGAAAATCTGGCAAGGCTAATTAAATTAAAGGATGA
 AGGACGTTCTATTTATTACAACCCACGTTATGGATGAAGCAGAAATTAA
 CAAGTAAGGTGCACTACTATTACGTGGAAACATTATTGCCCTTGATACT
 CCTTAAAGCTGAAGGAGAA

PRETTY of: /biotmp/msa134270.2{*} April 10, 2003 02:14 ..

		50
msa134270.2{391_COH1}	---aaaaaaag	tcatcgATTT AAAAAAACPA CAAAAAGCAT AcGCCTCAGA
msa134270.2{391_M732}	---aaaaaaag	tcatcgATTT AAAAAAACPA CAAAAAGCAT AcGCCTCAGA
msa134270.2{391_M781}	---aaaaaaag	tcatcgATTT AAAAAAACPA CAAAAAGCAT AcGCCTCAGA
msa134270.2{391_090}	-----ATT	AAAAAAACPA CAAAAAGCAT AtGCCTCAGA
msa134270.2{391_CJB110}	-----aaaaaaag	tcatcgATTT AAAAAAACPA CAAAAAGCAT AtGCCTCAGA
msa134270.2{391_1169NT}	-----aaaaaaag	tcatcgATTT AAAAAAACPA CAAAAAGCAT AcGCCTCAGA
msa134270.2{391_18RS21}	-----	-----gATT AAAAAAACPA CAAAAAGCAT AtGCCTCAGA
msa134270.2{391_2603}	atgaaaaaaag	tcatcgATTT AAAAAAACPA CAAAAAGCAT AtGCCTCAGA
msa134270.2{391_A909}	-----aaaaaaag	tcatcgATTT AAAAAAACPA CAAAAAGCAT AtGCCTCAGA
msa134270.2{391_JM9130013}	-----aaaaaaag	tcatcgATTT AAAAAAACPA CAAAAAGCAT AtGCCTCAGA
msa134270.2{391_H36B}	-----aaaaaaag	tcatcgATTT AAAAAAACPA CAAAAAGCAT AtGCCTCAGA
Consensus	*****	*****
		100
msa134270.2{391_COH1}	AACTGTTTA	AATAATATTA ATTTGGAGGT GTTAAAGGAA GAAATAATTG
msa134270.2{391_M732}	AACTGTTTA	AATAATATTA ATTTGGAGGT GTTAAAGGAA GAAATAATTG
msa134270.2{391_M781}	AACTGTTTA	AATAATATTA ATTTGGAGGT GTTAAAGGAA GAAATAATTG
msa134270.2{391_090}	AACTGTTTA	AATAATATTA ATTTGGAGGT GTTAAAGGAA GAAATAATTG
msa134270.2{391_CJB110}	AACTGTTTA	AATAATATTA ATTTGGAGGT GTTAAAGGc GAAATAATTG
msa134270.2{391_1169NT}	AACTGTTTA	AATAATATTA ATTTGGAGGT GTTAAAGGc GAAATAATTG
msa134270.2{391_18RS21}	AACCGTTTA	AATAATATTA ATTTGGAGGT GTTAAAGGc GAAATAATTG
msa134270.2{391_2603}	AACCGTTTA	AATAATATTA ATTTGGAGGT GTTAAAGGc GAAATAATTG
msa134270.2{391_A909}	AACCGTTTA	AATAATATTA ATTTGGAGGT GTTAAAGGc GAAATAATTG
msa134270.2{391_JM9130013}	AACCGTTTA	AATAATATTA ATTTGGAGGT GTTAAAGGc GAAATAATTG
msa134270.2{391_H36B}	ACCGTTTA	AATAATATTA ATTTGGAGGT GTTAAAGGc GAAATAATTG
Consensus	*****	*****
		150
msa134270.2{391_COH1}	GATTAATAGG	ACCCCTCTGGA GCAGGGAAAT CTACCTGAT TAAAACATATG
msa134270.2{391_M732}	GATTAATAGG	ACCCCTCTGGA GCAGGGAAAT CTACCTGAT TAAAACATATG
msa134270.2{391_M781}	GATTAATAGG	ACCCCTCTGGA GCAGGGAAAT CTACCTGAT TAAAACATATG
msa134270.2{391_090}	GATTAATAGG	ACCCCTCTGGA GCAGGGAAAT CTACCTGAT TAAAACATATG
msa134270.2{391_CJB110}	GATTAATAGG	ACCCCTCTGGA GCAGGGAAAT CTACCTGAT TAAAACATATG
msa134270.2{391_1169NT}	GATTAATAGG	ACCCCTCTGGA GCAGGGAAAT CTACCTGAT TAAAACATATG
msa134270.2{391_18RS21}	GATTAATAGG	ACCCCTCTGGA GCAGGGAAAT CTACCTGAT TAAAACATATG
msa134270.2{391_2603}	GATTAATAGG	ACCCCTCTGGA GCAGGGAAAT CTACCTGAT TAAAACATATG
msa134270.2{391_A909}	GATTAATAGG	ACCCCTCTGGA GCAGGGAAAT CTACCTGAT TAAAACATATG
msa134270.2{391_JM9130013}	GATTAATAGG	ACCCCTCTGGA GCAGGGAAAT CTACCTGAT TAAAACATATG
msa134270.2{391_H36B}	GATTAATAGG	ACCCCTCTGGA GCAGGGAAAT CTACCTGAT TAAAACATATG
Consensus	*****	*****
		200
msa134270.2{391_COH1}	CTTGGCATGG	AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
msa134270.2{391_M732}	CTTGGCATGG	AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
msa134270.2{391_M781}	CTTGGCATGG	AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
msa134270.2{391_090}	CTTGGCATGG	AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
msa134270.2{391_CJB110}	CTTGGCATGG	AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
msa134270.2{391_1169NT}	CTTGGCATGG	AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
msa134270.2{391_18RS21}	CTTGGCATGG	AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
msa134270.2{391_2603}	CTTGGCATGG	AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA
msa134270.2{391_A909}	CTTGGCATGG	AAAAAGCAGA TAAGGGAACA GCTCTTGTTC TTGATACTCA

Table 76: Comparative Sequences relating to SAG0260

msa134270.2{391_JM9130013}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAAACA	GCTCTTGTC	TTGATACTCA
msa134270.2{391_H36B}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAAACA	GCTCTTGTC	TTGATACTCA
Consensus	*****	*****	*****	*****	*****
	201				250
msa134270.2{391_COH1}	AATGCCAGAT	CgTAATATT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_M732}	AATGCCAGAT	CgTAATATT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_M781}	AATGCCAGAT	CgTAATATT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_090}	AATGCCAGAT	CgTAATATT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_CJB110}	AATGCCAGAT	CgTAATATT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_1169NT}	AATGCCAGAT	CgTAATATT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_18RS21}	AATGCCAGAT	CgTAATATT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_2603}	AATGCCAGAT	CgTAATATT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_A909}	AATGCCAGAT	CgTAATATT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_JM9130013}	AATGCCAGAT	CgTAATATT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_H36B}	AATGCCAGAT	CgTAATATT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
Consensus	*****	*****	*****	*****	*****
	251				300
msa134270.2{391_COH1}	ATGCCTTAcA	CGAgCTTTA	ACTGgCTTAG	AAAATTATT	ATTCTTTGGA
msa134270.2{391_M732}	ATGCCTTAcA	CGAgCTTTA	ACTGgCTTAG	AAAATTATT	ATTCTTTGGA
msa134270.2{391_M781}	ATGCCTTAcA	CGAgCTTTA	ACTGgCTTAG	AAAATTATT	ATTCTTTGGA
msa134270.2{391_090}	ATGCCTTAtA	CGAatCTTTA	ACTGcCTTAG	AAAATTATT	ATTCTTTGGA
msa134270.2{391_CJB110}	ATGCCTTAtA	CGAatCTTTA	ACTGcCTTAG	AAAATTATT	ATTCTTTGGA
msa134270.2{391_1169NT}	ATGCCTTAtA	CGAatCTTTA	ACTGcCTTAG	AAAATTATT	ATTCTTTGGA
msa134270.2{391_18RS21}	ATGCCTTAtA	CGAgCTTTA	ACTGgCTTAG	AAAATTATT	ATTCTTTGGA
msa134270.2{391_2603}	ATGCCTTAtA	CGAgCTTTA	ACTGgCTTAG	AAAATTATT	ATTCTTTGGA
msa134270.2{391_A909}	ATGCCTTAtA	CGAgCTTTA	ACTGgCTTAG	AAAATTATT	ATTCTTTGGA
msa134270.2{391_JM9130013}	ATGCCTTAtA	CGAgCTTTA	ACTGgCTTAG	AAAATTATT	ATTCTTTGGA
msa134270.2{391_H36B}	ATGCCTTAtA	CGAgCTTTA	ACTGgCTTAG	AAAATTATT	ATTCTTTGGA
Consensus	*****	*****	*****	*****	*****
	301				350
msa134270.2{391_COH1}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_M732}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_M781}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_090}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_CJB110}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_1169NT}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_18RS21}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_2603}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_A909}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_JM9130013}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
msa134270.2{391_H36B}	AAAATGAAAG	GTATTCAAAA	AACTGAATTA	AAACAGCAGA	TAACTCATAT
Consensus	*****	*****	*****	*****	*****
	351				400
msa134270.2{391_COH1}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATT	GTCTCAGGTT
msa134270.2{391_M732}	TTCTAAAGTA	GTAGATCTAG	AAAACCACT	TGATAAATT	GTCTCAGGTT
msa134270.2{391_M781}	TTCTAAAGTA	GTAGATCTAG	AAAACCACT	TGATAAATT	GTCTCAGGTT
msa134270.2{391_090}	TTCTAAAGTA	GTAGATCTAG	AAAACCACT	TGATAAATT	GTCTCAGGTT
msa134270.2{391_CJB110}	TTCTAAAGTA	GTAGATCTAG	AAAACCACT	TGATAAATT	GTCTCAGGTT
msa134270.2{391_1169NT}	TTCTAAAGTA	GTAGATCTAG	AAAACCACT	TGATAAATT	GTCTCAGGTT
msa134270.2{391_18RS21}	TTCTAAAGTA	GTAGATCTAG	AAAACCACT	TGATAAATT	GTCTCAGGTT
msa134270.2{391_2603}	TTCTAAAGTA	GTAGATCTAG	AAAACCACT	TGATAAATT	GTCTCAGGTT
msa134270.2{391_A909}	TTCTAAAGTA	GTAGATCTAG	AAAACCACT	TGATAAATT	GTCTCAGGTT
msa134270.2{391_JM9130013}	TTCTAAAGTA	GTAGATCTAG	AAAACCACT	TGATAAATT	GTCTCAGGTT
msa134270.2{391_H36B}	TTCTAAAGTA	GTAGATCTAG	AAAACCACT	TGATAAATT	GTCTCAGGTT
Consensus	*****	*****	*****	*****	*****
	401				450
msa134270.2{391_COH1}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGG
msa134270.2{391_M732}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGG
msa134270.2{391_M781}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGG
msa134270.2{391_090}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGG
msa134270.2{391_CJB110}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGG
msa134270.2{391_1169NT}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGG
msa134270.2{391_18RS21}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGG
msa134270.2{391_2603}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGG
msa134270.2{391_A909}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGG
msa134270.2{391_JM9130013}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGG
msa134270.2{391_H36B}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGG
Consensus	*****	*****	*****	*****	*****
	451				500
msa134270.2{391_COH1}	AACCCCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_M732}	AACCCCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_M781}	AACCCCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_090}	AACCCCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_CJB110}	AACCCCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_1169NT}	AACCCCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_18RS21}	AACCCCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_2603}	AACCCCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC

Table 76: Comparative Sequences relating to SAG0260

msa134270.2{391_A909}	AACCCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC	
msa134270.2{391_JM9130013}	ACCCCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC	
msa134270.2{391_H36B}	ACCCCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC	
Consensus	*****	*****	*****	*****	*****	
						501
msa134270.2{391_COH1}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC	550
msa134270.2{391_M732}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC	
msa134270.2{391_M781}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC	
msa134270.2{391_090}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC	
msa134270.2{391_CJB110}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC	
msa134270.2{391_1169NT}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC	
msa134270.2{391_18RS21}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC	
msa134270.2{391_2603}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC	
msa134270.2{391_A909}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC	
msa134270.2{391_JM9130013}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC	
msa134270.2{391_H36B}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC	
Consensus	*****	*****	*****	*****	*****	
						551
msa134270.2{391_COH1}	GTTCCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT	600
msa134270.2{391_M732}	GTTCCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT	
msa134270.2{391_M781}	GTTCCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT	
msa134270.2{391_090}	GTTCCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT	
msa134270.2{391_CJB110}	GTTCCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT	
msa134270.2{391_1169NT}	GTTCCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT	
msa134270.2{391_18RS21}	ATTCCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT	
msa134270.2{391_2603}	ATTCCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT	
msa134270.2{391_A909}	GTTCCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT	
msa134270.2{391_JM9130013}	GTTCCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT	
msa134270.2{391_H36B}	GTTCCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT	
Consensus	*****	*****	*****	*****	*****	
						601
msa134270.2{391_COH1}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCCTTG	ATACTCCATT	650
msa134270.2{391_M732}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCCTTG	ATACTCCATT	
msa134270.2{391_M781}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCCTTG	ATACTCCATT	
msa134270.2{391_090}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCCTTG	ATACTCCATT	
msa134270.2{391_CJB110}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCCTTG	ATACTCCATT	
msa134270.2{391_1169NT}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCCTTG	ATACTCCATT	
msa134270.2{391_18RS21}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCCTTG	ATACTCCATT	
msa134270.2{391_2603}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCCTTG	ATACTCCATT	
msa134270.2{391_A909}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCCTTG	ATACTCCATT	
msa134270.2{391_JM9130013}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCCTTG	ATACTCCATT	
msa134270.2{391_H36B}	AAGGTTGCAC	TACTATTACG	TGGAAACATT	ATTGCCCTTG	ATACTCCATT	
Consensus	*****	*****	*****	*****	*****	
						651
msa134270.2{391_COH1}	ACATTTAAAA	AAACAATTAA	ATGTGAGTAC	TATTGAGGAA	G-----	700
msa134270.2{391_M732}	ACATTTAAAA	AAACAATTAA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA	
msa134270.2{391_M781}	ACATTTAAAA	AAACAATTAA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA	
msa134270.2{391_090}	ACATTTAAAA	AAACAATTAA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA	
msa134270.2{391_CJB110}	ACATTTAAAA	AAACAATTAA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA	
msa134270.2{391_1169NT}	ACATTTAAAA	AAACAATTAA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA	
msa134270.2{391_18RS21}	ACATTTAAAA	AAACAATTAA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA	
msa134270.2{391_2603}	ACATTTAAAA	AAACAATTAA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA	
msa134270.2{391_A909}	ACATTTAAAA	AAACAATTAA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA	
msa134270.2{391_JM9130013}	ACATTTAAAA	AAACAATTAA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA	
msa134270.2{391_H36B}	ACATTTAAAA	AAACAATTAA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA	
Consensus	*****	*****	*****	*****	*****	
						652
msa134270.2{391_COH1}	-----	-----	-----	-----	-----	701
msa134270.2{391_M732}	AAGCTGAAGG	AGAA				714
msa134270.2{391_M781}	AAGCTGAAGG	AGAA				
msa134270.2{391_090}	AAGCTGAAGG	AGAA				
msa134270.2{391_CJB110}	AAGCTGAAGG	AGAA				
msa134270.2{391_1169NT}	AAGCTGAAGG	AGAA				
msa134270.2{391_18RS21}	AAGCTGAAGG	AGAA				
msa134270.2{391_2603}	AAGCTGAAGG	AGAA				
msa134270.2{391_A909}	AAGCTGAAGG	AGAA				
msa134270.2{391_JM9130013}	AAGCTGAAGG	AGAA				
msa134270.2{391_H36B}	AAGCTGAAGG	AGAA				
Consensus	*****	*****	*****	*****	*****	

SEQ ID NO. 7612

STRAIN 2603 frame: 1

KKVIDLKKLQKAYASETVLNNINLEVFKEIIGLIGPSGAGKSTLIKTMLGMEADKGTA
 LVLDTQMPDRNILNQIGYMAQS DALYESLTGLENLFFGKMKGIQKTELKQOITHISKVV
 DLENQLDKFVSGYSGGMKRRRLSLAIALLCNPTVLILDEPTVGDPSLRRKIWQELNIKD
 EGHSIFITTHVMDEAEELSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7613

Table 76: Comparative Sequences relating to SAG0260

STRAIN 090 frame: 3
LKKLQKAYASETVLNNINLEVFKGEEIGLIGPSGAGKSTLIKTMILGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELQQI
THISKVV
DLENQLDKFVSGYSGGMKRRSLAIAALLGNPTVLI
LDEPTVGIDPSLRRKIWQELINKDEGRSI
FITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7614**STRAIN A909 frame: 1**

KKVIDLKLQKAYASETVLNNINLEVFKGEEIGLIGPSGAGKSTLIKTMILGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALYESLTGLENLFFGKMKGIQKTELQQI
THISKVV
DLENQLDKFVSGYSGGMKRRSLAIAALLGNPTVLI
LDEPTVGIDPSLRRKIWQELINKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7615**STRAIN H36B frame: 1**

KKVIDLKLQKAYASETVLNNINLEVFKGEEIGLIGPSGAGKSTLIKTMILGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALYESLTGLENLFFGKMKGIQKTELQQI
THISKVV
DLENQLDKFVSGYSGGMKRRSLAIAALLGNPTVLI
LDEPTVGIDPSLRRKIWQELINKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7616**STRAIN 18RS21 frame: 1**

DLKKLQKAYASETVLNNINLEVFKGEEIGLIGPSGAGKSTLIKTMILGMEKADKGTA
TQMPDRNILNQIGYMAQSDALYESLTGLENLFFGKMKGIQKTELQQI
THISKVV
DLENQLDKFVSGYSGGMKRRSLAIAALLGNPTVLI
LDEPTVGIDPSLRRKIWQELINKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7617**STRAIN M732 frame: 1**

KKVIDLKLQKAYASETVLNNINLEVFKGEEIGLIGPSGAGKSTLIKTMILGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALHESLTGLENLFFGKMKGIQKTELQQI
THISKVV
DLENQLDKFVSGYSGGMKRRSLAIAALLGNPTVLI
LDEPTVGIDPSLRRKIWQELINKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7618**STRAIN COH1 frame: 1**

KKVIDLKLQKAYASETVLNNINLEVFKGEEIGLIGPSGAGKSTLIKTMILGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALHESLTGLENLFFGKMKGIQKTELQQI
THISKVV
DLENQLDKFVSGYSGGMKRRSLAIAALLGNPTVLI
LDEPTVGIDPSLRRKIWQELINKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7619**STRAIN M781 frame: 1**

KKVIDLKLQKAYASETVLNNINLEVFKGEEIGLIGPSGAGKSTLIKTMILGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALHESLTGLENLFFGKMKGIQKTELQQI
THISKVV
DLENQLDKFVSGYSGGMKRRSLAIAALLGNPTVLI
LDEPTVGIDPSLRRKIWQELINKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7620**STRAIN CJB110 frame: 1**

KKVIDLKLQKAYASETVLNNINLEVFKGEEIGLIGPSGAGKSTLIKTMILGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELQQI
THISKVV
DLENQLDKFVSGYSGGMKRRSLAIAALLGNPTVLI
LDEPTVGIDPSLRRKIWQELINKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7621**STRAIN 1169NT frame: 1**

KKVIDLKLQKAYASETVLNNINLEVFKGEEIGLIGPSGAGKSTLIKTMILGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELQQI
THISKVV
DLENQLDKFVSGYSGGMKRRSLAIAALLGNPTVLI
LDEPTVGIDPSLRRKIWQELINKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

SEQ ID NO. 7622**STRAIN JM9130013 frame: 1**

KKVIDLKLQKAYASETVLNNINLEVFKGEEIGLIGPSGAGKSTLIKTMILGMEKADKGTA
LVLDTQMPDRNILNQIGYMAQSDALYESLTGLENLFFGKMKGIQKTELQQI
THISKVV
DLENQLDKFVSGYSGGMKRRSLAIAALLGNPTVLI
LDEPTVGIDPSLRRKIWQELINKD
EGRSIFITTHVMDEAELTSKVALLLRGNIIAFDTPLHLKKQFNV

PRETTY of: /biotmp/msa134470.2{*} April 10, 2003 02:16 ..

1	50
msa134470.2{391_090}	----LKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTM
msa134470.2{391_1169NT}	KKVIDLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTM
msa134470.2{391_CJB110}	KKVIDLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTM
msa134470.2{391_COH1}	KKVIDLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTM
msa134470.2{391_M732}	KKVIDLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTM
msa134470.2{391_M781}	KKVIDLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTM
msa134470.2{391_18RS21}	----DLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTM
msa134470.2{391_2603}	KKVIDLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTM
msa134470.2{391_H36B}	KKVIDLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTM
msa134470.2{391_JM9130013}	KKVIDLKKLQ KAYASETVLN NINLEVFKGE IIGLIGPSGA GKSTLIKTM

Table 76: Comparative Sequences relating to SAG0260

msa134470.2{391_A909}	KKVIDLKKLQ	KAYASETVLN	NINLEVFKGE	IIGLIGPSGA	GKSTLIKTML
Consensus *****					
msa134470.2{391_090}	51 GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALYESLT	aLENLLFFGK
msa134470.2{391_1169NT}	MGEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALYESLT	aLENLLFFGK
msa134470.2{391_CJB110}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALYESLT	aLENLLFFGK
msa134470.2{391_COH1}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALYESLT	aLENLLFFGK
msa134470.2{391_M732}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALYESLT	gLENLLFFGK
msa134470.2{391_M781}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALYESLT	gLENLLFFGK
msa134470.2{391_18RS21}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALYESLT	gLENLLFFGK
msa134470.2{391_2603}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALYESLT	gLENLLFFGK
msa134470.2{391_H36B}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALYESLT	gLENLLFFGK
msa134470.2{391_JM9130013}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALYESLT	gLENLLFFGK
msa134470.2{391_A909}	GMEKADKGTA	LVLDTQMPDr	NILNQIGYMA	QSDALYESLT	gLENLLFFGK
Consensus *****					
msa134470.2{391_090}	101 MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_1169NT}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_CJB110}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_COH1}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_M732}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_M781}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_18RS21}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_2603}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_H36B}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_JM9130013}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
msa134470.2{391_A909}	MKGIQKTELK	QQITHISKVV	DLENQLDKFV	SGYSGGMKRR	LSLAIALLGN
Consensus *****					
msa134470.2{391_090}	151 PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_1169NT}	PTVLLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_CJB110}	PTVLLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_COH1}	PTVLLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_M732}	PTVLLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_M781}	PTVLLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_18RS21}	PTVLLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_2603}	PTVLLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_H36B}	PTVLLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_JM9130013}	PTVLLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_A909}	PTVLLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
Consensus *****					
msa134470.2{391_090}	201 VALLLRGNII	AFDTPLHLKK	QFNV		224
msa134470.2{391_1169NT}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_CJB110}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_COH1}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_M732}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_M781}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_18RS21}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_2603}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_H36B}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_JM9130013}	VALLLRGNII	AFDTPLHLKK	QFNV		
msa134470.2{391_A909}	VALLLRGNII	AFDTPLHLKK	QFNV		
Consensus *****					

Table 77: Comparative Sequences relating to SAG2059**SEQ ID NO. 7701****STRAIN 2603**

TTGCCCTATGTTGTCGTGGTTAGTTAGAGGGTGGCGGAATGAGAGGTCTTATACT
 GCTGGAGTTTAGATGCTTCTAGATGCAGGAATAAAATAGATGGTATCGTATCTGTC
 TCTGCTGGTGCATTGTTGGTITAATTGATCTAGACAACGAGAGAGGGCTTGCGA
 TACATAAAAAGTATTATCCCACCCCTAAATATAGTGGCTAAGGTCACTGGTTTCGAACA
 GGGAAATTGTTAATAAAAGATTCACTTATTAGAAGTCTATGAAATTGGATGTATT
 GACGATGAAGCATTTAAAAAATCAAGTATTGATTTACGTAGTTGCTACAGAGATGACA
 TCTGGTAAACCTGAATAATTAAATGAGTGGTTAGAACAATGAAAATTGAGT
 GCTAGTTGAGCATACCACTAGTCTCAAAGATGGTGTGGCAGGGGAAAAAGTACTTA
 GATGGTGGTTATCTGATAGTCTCCCGTTGATTTGCCGTGTTAGGATTGACAAG
 TTGATTGTTGTCGTGACTAGGCCGCTCAATTATCAGAAAAGCCTCAAGTGGACGATTG
 TATAAAACTCTGTATAGGAATAATCTCTAATTGTTGAAAGACAGCCTCGAATCGGTACCAA
 CAGTATAATAATAGTCTGAAAGGTCTGAGCCTTGAACAGGCCATCTATTGCA
 ATTAGACCAGTAAAGAGCTGGTATTGGCCGTTAGAGAAGAATCCGATAAACTTGAT
 AGTATTGTTACGCTTGGTATGAAAGATGCTAAAGTGTGATGCCCTGAGCTGAATAGTTAT
 CTAATGAAA

SEQ ID NO. 7702**STRAIN 090**

CCTATGTTGTCGTGGTTAGTTTAG
 AGGGTGGCGGAATGAGAGGTCTTATACTGCTGGAGTTTAGATGCTTT
 CTAGATGCAGGAATAAAATAGATGGTATCGTATCTGCTCTGCTGGTGC
 ATTGTTGGTGTAAATTGATCTAGACAACGAGAGAGGGCTTGCGAT
 ACAATAAAAAGTATTATCCCACCCCTAAATATAGTGGCTAAGGTCACTGG
 TTTGCAACAGGGAAATTGTTGATAATAAAAGATTCACTTATTATGAGTTCC
 TATGAAATTGGATGTTGACAAAGATGAAATTGAGTATTGAGCTAGTT
 ATTTTACGCTAGTGTCTCACAGAGATGACATCTGTTAACCTGAATATT
 AAAATTGATAGTGTGTTGACAAAGATGAAATTGAGTATTGAGCTAGTT
 ATACCGTAGTGTCTCAAAAGATGGTTGATTTGCCGTGTTAGGATT
 ATGGTGTGTTATCTGATAGTATTCCCGTTGATTTGCCGTGTTAGGATT
 TGACAAGTTGATTGTTGACTAGGCCGCTCAATTATCAGAAAAGC
 CTTCAAGTGGCAGTATTGATAAAACTCTGTATAGGAAATATCCTAATT
 GTAAACAGCAGCTCGAACCGTACCAACAGTATAATAATAGCCTTGAAA
 GGTGATGAGCCTGAAAAAACAGGCATCTATTGCAATTAGCCAAGTA
 AGAGCTGGTATTGGCCGCTTAGAGAAGAATCCGATAAACTTGATAGT
 ATTATCAGCTTGGTATGAAAGATGCTAAAGTGGATGCCCTGAGCTGAA
 TAGTTATCTAATGAAA

SEQ ID NO. 7703**STRAIN A909**

CCTATGTTGTCGTGGTTAGTTAGAG
 GGTGGCGGAATGAGAGGTCTTATACTGCTGGAGTTTAGATGCTTT
 AGATGCAGGAATAAAAGTAGATGGTATCATATCTGCTCTGCTGGTGC
 TGTTGGTGTAAATTGATCTAGACAACGAGAGAGGGCTTGCGATAC
 AATAAAAAGTATTATCCCACCCCTAAATATAGTGGCTAAGGTCACTGG
 TCGAACAGGGAAATTGTTGATAATAAAAGATTCACTTATTATGAGTTCC
 TGAAATTGGATGTTGACGATTGAGCTAAGTATTGAGCTAGTT
 TTTACGCTAGTGTCTCACAGAGATGACATCTGTTAACCTGAGTATT
 AATTGATAGTGTGTTGAAACATGAAATTGAGCTAGTTACGTGCTAGTT
 TACAGTAGTCTCAAAGATGGTTGTTGGCAGGGAAAAGTACTTAGAT
 GGTTGGTTATCTGATAGTATTCCCGTTGATTTGCCGTGTTAGGATT
 TGACAAGTTGATTGTTGACTAGGCCGCTCAATTATCAGAAAAGC
 CTTCAAGTGGCAGTATTGATAAAACTCTGTATAGGAAATATCCTAATT
 GTAAACAGCAGCTCGAACCGTACCAACAGTATAATAATAGCCTTGAAA
 GGTGATGAGCCTGAAAAAACAGGCATCTATTGCAATTAGCCAAGTA
 AGAGCTGGTATTGGCCGCTTAGAGAAGAATCCGATAAACTTGATAGT
 ATTATCAGCTTGGTATGAAAGATGCTAAAGTGGATGCCCTGAGCTGAA
 TAGTTATCTAATGAAA

SEQ ID NO. 7704**STRAIN H36B**

CCTATGTTGTCGTGGTTAGTTAG
 AGGGTGGCGGAATGAGAGGTCTTATACTGCTGGAGTTTAGATGCTTT
 CTAGATGCAGGAATAAAAGTAGATGGTATCATATCTGCTCTGCTGGTGC
 ATTGTTGGTGTAAATTGATCTAGACAACGAGAGAGGGCTTGCGAT
 ACAATAAAAAGTATTATCCCACCCCTAAATATAGTGGCTAAGGTCACTGG
 CTTGCAAGCAGGAAATTGTTGATAATAAAAGATTCACTTATTATGAGTTCC
 TATGAAATTGGATGTTGACGATGAAACATTAAAAATCAAGTATTG
 ATTGTTACGCTAGTGTCTCACAGAGATGACATCTGTTAACCTGAGTATT
 AAAATTGATAGTGTGTTGAAACAAATGAAATTTACGTGCTAGTT
 ATTACCAAGTAGTCTCAAAGATGGTTGTTGGCAGGGAAAAGTACTTAG
 ATGGTGGTTATCTGATAGTATTCCCGTTGATTTGCCGTGTTAGGAA
 TTGACAAGTTGATGTTGACTAGGCCGCTCAATTATCAGAAAAGA
 GCCCTCAAGTGGCAGATTGATAAAACTCTGTATAGGAAATATCCTAATT
 TTGTAAGACAGCCTCGAACCGTACCAACAGTATAATAATAGCCTTGAA
 AAGGTGATGAGCCTGAAAAAACAGGCATCTATTGCAATTAGCCAAG
 TAAGAGCTGGTATTGGCCGCTTAGAGAAGAATCCGATAAACTTGATAGT
 GTATTATCAGCTTGGTATGAAAGATGCTAAAGTGGATGCCCTGAGCTGAA
 ATAAGTTATCTAATGAAA

SEQ ID NO. 7705

Table 77: Comparative Sequences relating to SAG2059

STRAIN 18RS21

CCTATGTTGTCGTGGTTAGTTAGAGG
 GTGGCGGAATGAGAGGTCTTACTGCTGGAGTTAGATGCTTTCTA
 GATCAGGAATAAAAATAGATGGTATCGTATCTGCTCTGCTGGTGCATT
 GTTCTGTTAATTGTAATAGACAACGAGAGGGCTTGCATACA
 ATAAAAAGTATTATCCACCTAAATATGAGTCTAAGGTATGGTT
 CGAACAGGAATTTCGTTAATAGACAACCTTACCTTATGAGTCTAAGGTCTAT
 GAAATTGGATGATTGACGATGAAGCATTTAAAATCAAGTATTGATT
 TTACGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTAAA
 ATTGATAGTGTGAAACAAATGGAAATTCTACCGTAGTTTCAAGCATT
 ACCAGTAGTCTCAAAGATGGTGTGATTGGCAGGGAAAAGTACTTAGATG
 GTGGTTATCTGATAGTATTCCCGTTGATTGCCCCGTGGTTAGGATT
 GACAAGTTGATGTTGTGACTAGGCCGCTCAATTATGAGTCTAAGAAAAGCC
 TTCAAGTGGACGATTGATAAAACTCTGATAGGAATATCTTAATTG
 TAAAGACAGCCTCGAATCGTACCAACAGTATAATAAGTCTTGAAAG
 GTCATGAGCCTGAAAAAACAGGCGATCTTGCATTAGACCGAGTAA
 GAGCTTGGTATGGCCGCTAGAGAAGAATCCGATAAACCTGATAGTA
 TTATCAGCTGGTATGAAAGATGCTAAAGTGTGATGCCGAGCTGAAT
 AGTTATCTAATGAAA

SEQ ID NO. 7706

STRAIN M732

CCTATGTTGTCGTGGTTAGTTAGA
 GGTTGGCGGAATGAGAGGTCTTACTGCTGGAGTTAGATGCTTTCTC
 TAGATGCAAGGAATAAAAATAGATGGTATCGTATCTGCTCTGCGGGTGC
 TTGTTGGTGTAAATTGTAATCTAGACAACGAGAGGGCTTGCATA
 CAATAAAAAGTATTATCCACCTGAATATGAGTCTAAGATCATGGC
 TTGCAACAGGAATTGTTGTAATAAAAGATTCACTTATTATGAAGTTCT
 ATGAAATTGGATGTTGACGATGAAGCATTAAAATCAAGTATTG
 TTGTTACGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTA
 AAATTGATAGTGTGTTGAAACATTTACGTTGCTAGTT
 TTACCACTGCTCAAAGATGGTGTGATTGGCAGGGAAAAGTACTT
 TGTTGTTATCTGATAGTATTCCCGTTGATTGCCCCGTGGTTAGGAT
 TTGACAAGTTGATGTTGTGACTAGGCCGCTCAATTATCAGAAA
 CCTCAAGTGGCAGATTGATAAAACTCTGATAGGAATATCTTAATT
 TGAAAGACAGCCTCGAATCGTACCAACAGTATAATAAGTCTTGAA
 AGTCATGAGCCTGAAAAAACAGGCGATCTTGCATTAGACCGAGT
 AAGAGCTTGGTATGGCCGCTAGAGAAGAATCCGATAAACCTGATAG
 TAATTATCAGCTGGTATGAAATATGCTAAAGTGTGATGCCGAGCTGA
 ATAGTTATCTAATGAAA

SEQ ID NO. 7707

STRAIN COH1

CCTATGTTGTCGTGGTTAGTTA
 GAGGGGTGGCGGAATGAGAGGTCTTACTGCTGGAGTTAGATGCTTT
 TCTAGATGCAAGGAATAAAAATAGATGGTATCGTATCTGCTCTGCGGGTG
 CATTGTTGGTGTAAATTGTAATCTAGACAACGAGAGGGCTTGC
 TACAATAAAAAGTATTATCCACCTGAATATGAGTCTAAGATCATG
 GCTTCAACAGGAATTGTTGTAATAAAAGATTCACTTATTATGAAGTTCT
 CTATGAAATTGGATGTTGACGATGAAGCATTAAAATCAAGTATT
 GATTGTTACGTTGCTACAGAGATGACATCTGGTAAACCTGAATATT
 TAAAATTGATAGTGTGTTGTAACAAATGGAAATTGTTACGTTGCTAGTT
 CATTACCACTGCTCAAAGATGGTGTGATTGGCAGGGAAAAGTACTTA
 GATGGGTTATCTGATAGTATTCCCGTTGATTGCCCCGTGGTTAGG
 ATTGACAAGTTGATGTTGTGACTAGGCCGCTCAATTATCAGAAA
 AGCCCTCAAGTGGACGATTGATAAAACTCTGATAGGAATATCTTAAT
 TTGTAAGAACAGCCTCGAATCGTACCAACAGTATAATAAGTCTTG
 AAAGGTCAATGCCGTTAGAGAAGAATCCGATAAACCTGATAG
 GAAAGAGCTTGGTATGGCCGCTAGAGAAGAATCCGATAAACCTGAT
 AGTATTATCAGCTGGTATGAAATATGCTAAAGTGTGATGCCGAGCT
 GAATAGTTATCTAATGAAA

SEQ ID NO. 7708

STRAIN M781

CCTATGTTGTCGTGGTTAGTTAG
 AGGGTGGCGGAATGAGAGGTCTTACTGCTGGAGTTAGATGCTTT
 CTAGATGCAAGGAATAAAAATAGATGGTATCGTATCTGCTCTGCGGGTG
 ATTGTTGGTGTAAATTGTAATCTAGACAACGAGAGGGCTTGC
 ACAATAAAAAGTATTATCCACCTGAATATGAGTCTAAGATCATGG
 CTTGCAACAGGAATTGTTGTAATAAAAGATTCACTTATTATGAAGTTCC
 TATGAAATTGGATGTTGACGATGAAGCATTAAAATCAAGTATTG
 ATTGTTACGTTGCTACAGAGATGACATCTGGTAAACCTGAATATT
 AAAATTGATAGTGTGTTGTAACAAATGGAAATTGTTACGTTGCTAGTT
 ATTACCACTGCTCAAAGATGGTGTGACTAGGCCGCTCAATTATCAGAAA
 TTGACAAGTTGATGTTGTGACTAGGCCGCTCAATTATCAGAAA
 GCCTTCAAGTGGACGATTGATAAAACTCTGATAGGAATATCTTAATT
 TTGTAAGAACAGCCTCGAATCCGTAACAGTATAATAAGTCTTGAA
 AAGGTCAATGCCGTTAGAGAAGAATCCGATAAACCTGATAG
 TAAGAGCTTGGTATGGCCGCTAGAGAAGAATCCGATAAACCTGATAG
 GTATTATCAGCTGGTATGAAATATGCTAAAGTGTGATGCCGAGCTG
 ATAAGTTATCTAATGAAA

Table 77: Comparative Sequences relating to SAG2059**SEQ ID NO. 7709**

STRAIN CJB110

CCTATGTTGTCGTGGTTAGTTTA
 CCTAGATGCAGGAATAAAAATAGATGCTATCGTATCTGTCCTGCTGGTG
 CATTGTTGGTAAATTTGATCTAGACAAACGAGAGAGGGCCTTGC
 TACAATAAAAAGTATTTATCCACCTAAATATAGTCAAGGTCAATG
 GTTCAAGCAGGGAAATTGTTAATAAGATTCACCTATTATGAAGGTC
 CTATGAAATTGGATGATTTGACGATGAAGCATTAAAAATCAAGTATT
 GATTTTACGTAGTGGCTACAGAGATGACATCTGTAACCTGAATATT
 TAAGGATGATGTTGACAAAGATGGAAATTTCAGTGTAGTTCTAG
 CATTACCGTAGTCTCAAAGATGGTGGATTGGCAGGGAAAAGTACTTA
 GATGGGGTTATCTGATAGTATTCCCGTGAATTGCCCCTCAATTATCAGAAA
 ATTTGAAAGTCAAGTGGTGGATTGATGACTAGGCCGCTCAATTATCAGAAA
 AGCCTTCAAGTGGCAGATTGATAAAAACCTGTATAGGAAATATCCTAAT
 TTGTAAGAACAGCCTGATGAAAGAACAGGGATCTATTGCAATTAGACCGA
 GTAAGAGCTTGGTATTGGCCGCTTAGAGAAGAATCCGGATAAAACTTGAT
 AGTATTATCAGCTGGTATGAAAGATGCTAAAGTGTGATGCCCTGAGCT
 GAATAGTTATCTAATGAAA

SEQ ID NO. 7710

STRAIN 1169NT

CCTATGTTGTCGTGGTTAGTTTAGAGGGTG
 GCGGAATGAGGGCTTTATAGTCTGAGGTTAGATGCTTTCTAGAT
 GCAGGAATAAAAATAGATGGTATCGTATCTGCTGGGTCATTGTT
 TGTTGTTAATTGATCTAGACAAACGAGAGAGGGCCTTGCATAACAATA
 AAAAGTATTATCCACCTAAATATAGTCAAGATCATGGCTTCGA
 ACAGGGAAATTGTTAATAAGATTCACCTATTATGAAGGTCCTATGAA
 ATTGGATGATTTGACGATGAAGCATTAAAAATCAAGTATTGATT
 ACGCAGTTGCTACAGAGATGACATCTGTAACCTGAATATTAAAAATT
 GATAGTGTCTTGAACAAATGAAATTTCAGTGTAGTTCACTTAC
 AGTAGTCTCAAAGATGGTGTAGGGAGAAAAGTACTTAGATGGTG
 GTTTATCTGATAGTATCCCGTGAATTGGCCGCTGGTTAGGATTGAC
 AAGTTGATGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAGCCTTC
 AAGTGGACGATTGATATAAAACTGTATAGGAAATATCCTAATTGTA
 AGACAGCCTGAACTGGTACCAACAGTATAATAATAGCCTGAAAAGGTC
 ATGAGGCTTGGATGAAAGACAGGGATCTATTGCAATTAGGGAGTAAAAG
 CTGGTTATTGTCGGCTTAGAGAAGAATCCGGATAAAACTGTAGTATT
 ATCAGCTGGTATGAAAGATGCTAAAGTGTGATGCCCTGAGCTGAATAGT
 TATCTAATGAAA

SEQ ID NO. 7711

STRAIN JM9130013

CCTATGTTGTCGTGGTTAGTTAGAG
 GGTGGCGGAATGAGGGCTTTATAGTCTGAGGAGTTAGATGCTTTCT
 AGATGCAGGAATAAAAAGTAGATGGTATCATATCTGTCCTGCTGGTGCA
 ATGTTGGTGTAAATTGATCTAGACAAACGAGAGAGGGCCTTGC
 ATAATAAAAGTATTATCCACCTAAATATAGTCAAGTATTGAT
 TCGAACAGGGAAATTGTTAATAAGATTCACCTATTATGAAGGTC
 TGAAATTGGATGATTTGACGATGAAGCATTAAAAATCAAGTATT
 TTACGAGTGTCTACAGAGATGACATCTGGTAAACCTGAGTATT
 AATTGATAGTGTGTTGAACAAATGAAATTTCAGTGTAGTTCA
 TACCACTAGTCTCAAAGATGGTGTGGCAGGGAAAAGTACTTAGAT
 GGTGGTTATCTGATAGTATTCCCGTGGATTGGCCGCTGGTTAGGATT
 TGACAAGTTGATGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAGC
 CTTCAAGTGGACGATTGATATAAAACTGTATAGGAAATATCCTAATT
 GTAAAGACAGCCTGCAACCGTACCAACAGTATAATAATAGCCTGAAAAA
 GTCATGAGCCTTGAACAGGGCAGTCTATTGCAATTAGACCAAGTA
 AGAGCTGGTTATGGCCGCTTAGAGAAGAATCCGGATAAAACTTGATAGT
 ATTATCAGCTGGTATGAAAGATGCTAAAGTGGATGCCCTGAGCTGAA
 TAGTTATCTAATGAAA

PRETTY of: /biotmp/msa47199.2{*} February 19, 2003 05:51 ..

1	50
msa47199.2{394_A909}	---CCTATGT TGTCTGGTGG TTTAGTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_H36B}	---CCTATGT TGTCTGGTGG TTTAGTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_JM9130013}	---CCTATGT TGTCTGGTGG TTTAGTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_090}	---CCTATGT TGTCTGGTGG TTTAGTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_18RS21}	---CCTATGT TGTCTGGTGG TTTAGTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_2603}	ttgcctatgt TGTCTGGTGG TTTAGTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_CJB110}	---CCTATGT TGTCTGGTGG TTTAGTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_COH1}	---CCTATGT TGTCTGGTGG TTTAGTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_M732}	---CCTATGT TGTCTGGTGG TTTAGTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_M781}	---CCTATGT TGTCTGGTGG TTTAGTTTA GAGGGTGGCG GAATGAGAGG
msa47199.2{394_1169NT}	---CCTATGT TGTCTGGTGG TTTAGTTTA GAGGGTGGCG GAATGAGAGG
Consensus	***** * ***** * ***** * ***** * ***** * *****
51	100
msa47199.2{394_A909}	TCTTTATACT GCTGGAGTT TAGATGCTTT TCTAGATGCA GGAATAAAAG
msa47199.2{394_H36B}	TCTTTATACT GCTGGAGTT TAGATGCTTT TCTAGATGCA GGAATAAAAG
msa47199.2{394_JM9130013}	TCTTTATACT GCTGGAGTT TAGATGCTTT TCTAGATGCA GGAATAAAAG

Table 77: Comparative Sequences relating to SAG2059

msa47199.2{394_090}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_18RS21}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_2603}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_CJB110}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_COH1}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_M732}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_M781}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_1169NT}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
Consensus	*****	*****	*****	*****	*****
	101				150
msa47199.2{394_A909}	TAGATGGTAT	CaTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATT
msa47199.2{394_H36B}	TAGATGGTAT	CaTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATT
msa47199.2{394_JM9130013}	TAGATGGTAT	CaTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATT
msa47199.2{394_090}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATT
msa47199.2{394_18RS21}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATT
msa47199.2{394_2603}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATT
msa47199.2{394_CJB110}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATT
msa47199.2{394_COH1}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATT
msa47199.2{394_M732}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATT
msa47199.2{394_M781}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATT
msa47199.2{394_1169NT}	TAGATGGTAT	CgTATCTGTC	TCTGCTGGTG	CATTGTTTGG	TGTTAATT
Consensus	*****	*****	*****	*****	*****
	151				200
msa47199.2{394_A909}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATT
msa47199.2{394_H36B}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATT
msa47199.2{394_JM9130013}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATT
msa47199.2{394_090}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATT
msa47199.2{394_18RS21}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATT
msa47199.2{394_2603}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATT
msa47199.2{394_CJB110}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATT
msa47199.2{394_COH1}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATT
msa47199.2{394_M732}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATT
msa47199.2{394_M781}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATT
msa47199.2{394_1169NT}	GTATCTAGAC	AACGAGAGAG	GGCTTTGCGA	TACAATAAAA	AGTATT
Consensus	*****	*****	*****	*****	*****
	201				250
msa47199.2{394_A909}	CCACCCtaAA	TATATGAGTC	TAAGgTCATG	GtTTCGAACA	GGGAATT
msa47199.2{394_H36B}	CCACCCtaAA	TATATGAGTC	TAAGgTCATG	GtTTCGAACA	GGGAATT
msa47199.2{394_JM9130013}	CCACCCtaAA	TATATGAGTC	TAAGgTCATG	GtTTCGAACA	GGGAATT
msa47199.2{394_090}	CCACCCtaAA	TATATGAGTC	TAAGgTCATG	GtTTCGAACA	GGGAATT
msa47199.2{394_18RS21}	CCACCCtaAA	TATATGAGTC	TAAGgTCATG	GtTTCGAACA	GGGAATT
msa47199.2{394_2603}	CCACCCtaAA	TATATGAGTC	TAAGgTCATG	GtTTCGAACA	GGGAATT
msa47199.2{394_CJB110}	CCACCCtaAA	TATATGAGTC	TAAGgTCATG	GtTTCGAACA	GGGAATT
msa47199.2{394_COH1}	CCACCCtaAA	TATATGAGTC	TAAGgTCATG	GtTTCGAACA	GGGAATT
msa47199.2{394_M732}	CCACCCtaAA	TATATGAGTC	TAAGgTCATG	GtTTCGAACA	GGGAATT
msa47199.2{394_M781}	CCACCCtaAA	TATATGAGTC	TAAGgTCATG	GtTTCGAACA	GGGAATT
msa47199.2{394_1169NT}	CCACCCtaAA	TATATGAGTC	TAAGgTCATG	GtTTCGAACA	GGGAATT
Consensus	*****	*****	*****	*****	*****
	251				300
msa47199.2{394_A909}	TTAATAAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATT
msa47199.2{394_H36B}	TTAATAAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATT
msa47199.2{394_JM9130013}	TTAATAAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATT
msa47199.2{394_090}	TTAATAAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATT
msa47199.2{394_18RS21}	TTAATAAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATT
msa47199.2{394_2603}	TTAATAAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATT
msa47199.2{394_CJB110}	TTAATAAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATT
msa47199.2{394_COH1}	TTAATAAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATT
msa47199.2{394_M732}	TTAATAAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATT
msa47199.2{394_M781}	TTAATAAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATT
msa47199.2{394_1169NT}	TTAATAAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATT
Consensus	*****	*****	*****	*****	*****
	301				350
msa47199.2{394_A909}	GACGGATGAAG	CATTTAAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_H36B}	GACGGATGAAG	CATTTAAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_JM9130013}	GACGGATGAAG	CATTTAAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_090}	GACGGATGAAG	CATTTAAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_18RS21}	GACGGATGAAG	CATTTAAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_2603}	GACGGATGAAG	CATTTAAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_CJB110}	GACGGATGAAG	CATTTAAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_COH1}	GACGGATGAAG	CATTTAAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_M732}	GACGGATGAAG	CATTTAAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_M781}	GACGGATGAAG	CATTTAAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
msa47199.2{394_1169NT}	GACGGATGAAG	CATTTAAAAAA	ATCAAGTATT	GATTTTTACG	cAGTTGCTAC
Consensus	*****	*****	*****	*****	*****
	351				400
msa47199.2{394_A909}	AGAGATGACA	TCTGGTAAAC	CTGAGTATT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_H36B}	AGAGATGACA	TCTGGTAAAC	CTGAGTATT	TAAAATTGAT	AGTGTtTTTG

Table 77: Comparative Sequences relating to SAG2059

msa47199.2{394_JM9130013}	AGAGATGACA	TCTGGTAAAC	CTGAGTATT	TAAAATTGAT	AGTGT-TTTG
msa47199.2{394_090}	AGAGATGACA	TCTGGTAAAC	CTGAATATT	TAAAATTGAT	AGTGT-TTTG
msa47199.2{394_18RS21}	AGAGATGACA	TCTGGTAAAC	CTGAATATT	TAAAATTGAT	AGTGT-TTTG
msa47199.2{394_2603}	AGAGATGACA	TCTGGTAAAC	CTGAATATT	TAAAATTGAT	AGTGT-TTTG
msa47199.2{394_CJB110}	AGAGATGACA	TCTGGTAAAC	CTGAATATT	TAAAATTGAT	AGTGT-TTTG
msa47199.2{394_COH1}	AGAGATGACA	TCTGGTAAAC	CTGAATATT	TAAAATTGAT	AGTGT-TTTG
msa47199.2{394_M732}	AGAGATGACA	TCTGGTAAAC	CTGAATATT	TAAAATTGAT	AGTGT-TTTG
msa47199.2{394_M781}	AGAGATGACA	TCTGGTAAAC	CTGAATATT	TAAAATTGAT	AGTGT-TTTG
msa47199.2{394_1169NT}	AGAGATGACA	TCTGGTAAAC	CTGAATATT	TAAAATTGAT	AGTGT-TTTG
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	AACAAATGGA	AATTTTACGT	GCTAGTTCAAG	CATTACCAAG	AGTCTCAAAG
msa47199.2{394_H36B}	AACAAATGGA	AATTTTACGT	GCTAGTTCAAG	CATTACCAAG	AGTCTCAAAG
msa47199.2{394_JM9130013}	AACAAATGGA	AATTTTACGT	GCTAGTTCAAG	CATTACCAAG	AGTCTCAAAG
msa47199.2{394_090}	AACAAATGGA	AATTTTACGT	GCTAGTTCAAG	CATTACCAAG	AGTCTCAAAG
msa47199.2{394_18RS21}	AACAAATGGA	AATTTTACGT	GCTAGTTCAAG	CATTACCAAG	AGTCTCAAAG
msa47199.2{394_2603}	AACAAATGGA	AATTTTACGT	GCTAGTTCAAG	CATTACCAAG	AGTCTCAAAG
msa47199.2{394_CJB110}	AACAAATGGA	AATTTTACGT	GCTAGTTCAAG	CATTACCAAG	AGTCTCAAAG
msa47199.2{394_COH1}	AACAAATGGA	AATTTTACGT	GCTAGTTCAAG	CATTACCAAG	AGTCTCAAAG
msa47199.2{394_M732}	AACAAATGGA	AATTTTACGT	GCTAGTTCAAG	CATTACCAAG	AGTCTCAAAG
msa47199.2{394_M781}	AACAAATGGA	AATTTTACGT	GCTAGTTCAAG	CATTACCAAG	AGTCTCAAAG
msa47199.2{394_1169NT}	AACAAATGGA	AATTTTACGT	GCTAGTTCAAG	CATTACCAAG	AGTCTCAAAG
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	ATGGTTGTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_H36B}	ATGGTTGTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_JM9130013}	ATGGTTGTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_090}	ATGGTTGATT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_18RS21}	ATGGTTGATT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_2603}	ATGGTTGATT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_CJB110}	ATGGTTGATT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_COH1}	ATGGTTGATT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_M732}	ATGGTTGATT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_M781}	ATGGTTGATT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_1169NT}	ATGGTTGATT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	TATCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_H36B}	TATCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_JM9130013}	TATCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_090}	TATCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_18RS21}	TATCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_2603}	TATCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_CJB110}	TATCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_COH1}	TATCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_M732}	TATCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_M781}	TATCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_1169NT}	TATCCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	501	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG
msa47199.2{394_H36B}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_JM9130013}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_090}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_18RS21}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_2603}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_CJB110}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_COH1}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_M732}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_M781}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_1169NT}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	551	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG
msa47199.2{394_H36B}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_JM9130013}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_090}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_18RS21}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_2603}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_CJB110}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_COH1}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_M732}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_M781}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
msa47199.2{394_1169NT}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAG	TGGACGATTG
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	601	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAAGA
msa47199.2{394_H36B}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAAGA	CAGCCTCGAA
msa47199.2{394_JM9130013}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAAGA	CAGCCTCGAA
msa47199.2{394_090}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAAGA	CAGCCTCGAA
msa47199.2{394_18RS21}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAAGA	CAGCCTCGAA
msa47199.2{394_2603}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAAGA	CAGCCTCGAA
msa47199.2{394_CJB110}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAAGA	CAGCCTCGAA
msa47199.2{394_COH1}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAAGA	CAGCCTCGAA
msa47199.2{394_M732}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAAGA	CAGCCTCGAA
msa47199.2{394_M781}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAAGA	CAGCCTCGAA
msa47199.2{394_1169NT}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAAGA	CAGCCTCGAA
Consensus	*****	*****	*****	*****	*****
msa47199.2{394_A909}	651	cCGGTACCAA	CAGTATAATA	ATAGCCTTGA	AAAGGTATG AGCCTTGAAA

Table 77: Comparative Sequences relating to SAG2059

msa47199.2{394_H36B}	cCGGTACCAA CAGTATAATA ATAGcCTTGA AAAGGTATG AGCCTTGAAA		
msa47199.2{394_JM9130013}	cCGGTACCAA CAGTATAATA ATAGcCTTGA AAAGGTATG AGCCTTGAAA		
msa47199.2{394_090}	tCGGTACCAA CAGTATAATA ATAGtCTTGA AAAGGTATG AGCCTTGAAA		
msa47199.2{394_18RS21}	tCGGTACCAA CAGTATAATA ATAGtCTTGA AAAGGTATG AGCCTTGAAA		
msa47199.2{394_2603}	tCGGTACCAA CAGTATAATA ATAGtCTTGA AAAGGTATG AGCCTTGAAA		
msa47199.2{394_CJB110}	tCGGTACCAA CAGTATAATA ATAGtCTTGA AAAGGTATG AGCCTTGAAA		
msa47199.2{394_COH1}	tCGGTACCAA CAGTATAATA ATAGtCTTGA AAAGGTATG AGCCTTGAAA		
msa47199.2{394_M732}	tCGGTACCAA CAGTATAATA ATAGtCTTGA AAAGGTATG AGCCTTGAAA		
msa47199.2{394_M781}	tCGGTACCAA CAGTATAATA ATAGtCTTGA AAAGGTATG AGCCTTGAAA		
msa47199.2{394_1169NT}	tCGGTACCAA CAGTATAATA ATAGcCTTGA AAAGGTATG AGCCTTGAAA		
Consensus	-*****	-*****	-*****
msa47199.2{394_A909}	701	750	
msa47199.2{394_H36B}	AAACAGGGCA TCTATTGCA ATTAGaCCaA GTAAgAGCTT GGTTATTGgC		
msa47199.2{394_JM9130013}	AAACAGGGCA TCTATTGCA ATTAGaCCaA GTAAgAGCTT GGTTATTGgC		
msa47199.2{394_090}	AAACAGGGCA TCTATTGCA ATTAGaCCaA GTAAgAGCTT GGTTATTGgC		
msa47199.2{394_18RS21}	AAACAGGGCA TCTATTGCA ATTAGaCCaA GTAAgAGCTT GGTTATTGgC		
msa47199.2{394_2603}	AAACAGGGCA TCTATTGCA ATTAGaCCaA GTAAgAGCTT GGTTATTGgC		
msa47199.2{394_CJB110}	AAACAGGGCA TCTATTGCA ATTAGaCCaA GTAAgAGCTT GGTTATTGgC		
msa47199.2{394_COH1}	AAACAGGGCA TCTATTGCA ATTAGaCCaA GTAAgAGCTT GGTTATTGgC		
msa47199.2{394_M732}	AAACAGGGCA TCTATTGCA ATTAGaCCaA GTAAgAGCTT GGTTATTGgC		
msa47199.2{394_M781}	AAACAGGGCA TCTATTGCA ATTAGaCCaA GTAAgAGCTT GGTTATTGgC		
msa47199.2{394_1169NT}	AAACAGGGCA TCTATTGCA ATTAGgCCaA GTAAaAGCTT GGTTATTGTC		
Consensus	*****	*****	*****
msa47199.2{394_A909}	751	800	
msa47199.2{394_H36B}	CGCTTAGAGA AGAAATCCGGA TAAACTTGT AGTATTATC AGCTTGGTAT		
msa47199.2{394_JM9130013}	CGCTTAGAGA AGAAATCCGGA TAAACTTGT AGTATTATC AGCTTGGTAT		
msa47199.2{394_090}	CGCTTAGAGA AGAAATCCGGA TAAACTTGT AGTATTATC AGCTTGGTAT		
msa47199.2{394_18RS21}	CGCTTAGAGA AGAAATCCGGA TAAACTTGT AGTATTATC AGCTTGGTAT		
msa47199.2{394_2603}	CGCTTAGAGA AGAAATCCGGA TAAACTTGT AGTATTATC AGCTTGGTAT		
msa47199.2{394_CJB110}	CGCTTAGAGA AGAAATCCGGA TAAACTTGT AGTATTATC AGCTTGGTAT		
msa47199.2{394_COH1}	CGCTTAGAGA AGAAATCCGGA TAAACTTGT AGTATTATC AGCTTGGTAT		
msa47199.2{394_M732}	CGCTTAGAGA AGAAATCCGGA TAAACTTGT AGTATTATC AGCTTGGTAT		
msa47199.2{394_M781}	CGCTTAGAGA AGAAATCCGGA TAAACTTGT AGTATTATC AGCTTGGTAT		
msa47199.2{394_1169NT}	CGCTTAGAGA AGAAATCCGGA TAAACTTGT AGTATTATC AGCTTGGTAT		
Consensus	*****	*****	*****
msa47199.2{394_A909}	801	849	
msa47199.2{394_H36B}	GAAAGATGCT AAAAGTggGA TGCCCTGAGCT GAATAGTTAT CTAATGAAA		
msa47199.2{394_JM9130013}	GAAAGATGCT AAAAGTggGA TGCCCTGAGCT GAATAGTTAT CTAATGAAA		
msa47199.2{394_090}	GAAAGATGCT AAAAGTggGA TGCCCTGAGCT GAATAGTTAT CTAATGAAA		
msa47199.2{394_18RS21}	GAAAGATGCT AAAAGTggGA TGCCCTGAGCT GAATAGTTAT CTAATGAAA		
msa47199.2{394_2603}	GAAAGATGCT AAAAGTggGA TGCCCTGAGCT GAATAGTTAT CTAATGAAA		
msa47199.2{394_CJB110}	GAAAGATGCT AAAAGTggGA TGCCCTGAGCT GAATAGTTAT CTAATGAAA		
msa47199.2{394_COH1}	GAAAGATGCT AAAAGTggGA TGCCCTGAGCT GAATAGTTAT CTAATGAAA		
msa47199.2{394_M732}	GAAAGATGCT AAAAGTggGA TGCCCTGAGCT GAATAGTTAT CTAATGAAA		
msa47199.2{394_M781}	GAAAGATGCT AAAAGTggGA TGCCCTGAGCT GAATAGTTAT CTAATGAAA		
msa47199.2{394_1169NT}	GAAAGATGCT AAAAGTggGA TGCCCTGAGCT GAATAGTTAT CTAATGAAA		
Consensus	*****	*****	*****

SEQ ID NO. 7712

STRAIN 2603 frame: 1

PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFSRQRERALRY
NKYLSPHPKYMMSLRSWFRGPNFKVNDFTYYEVPMKLDVFDDAEFKKSSIDFYVVATEMTS
GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSTYQLGMKDASGMPELNSYLMK

SEQ ID NO. 7713

STRAIN 090 frame: 1

PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKIDGIVSVSAGALFGVNFSRQRERALRY
NKYLSPHPKYMMSLRSWLRGNFKVNDFTYYEVPMKLDVFDDAEFKKSSIDFYVVATEMTS
GKPEYFKIDSVFQMEILRASSALPVVSKMVVWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSTYQLGMKDASGMPELNSYLMK

SEQ ID NO. 7714

STRAIN A909 frame: 1

PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKVDGIISVSAGALFGVNFSRQRERALRY
NKYLSPHPKYMMSLRSWLRGNFKVNDFTYYEVPMKLDVFDDAEFKKSSIDFYAVATEMTS
GKPEYFKIDSVFQMEILRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKL
IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNSLEKVMMSLEKTGDLFAI
RPSKSLVIGRLEKNPDKLDSTYQLGMKDASGMPELNSYLMK

SEQ ID NO. 7715

STRAIN H36B frame: 1

PMLSVGLVLEGGGMRGLYTAGVLDAFLDAGIKVDGIISVSAGALFGVNFSRQRERALRY
NKYLSPHPKYMMSLRSWLRGNFKVNDFTYYEVPMKLDVFDDAEFKKSSIDFYAVATEMTS

Table 77: Comparative Sequences relating to SAG2059

GKPEYFKIDSVFEQMEILRASSALPVVSKMWWQGKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNNSLEKVMMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSTYQLGMKDAKSGMPPELNSYLMK

SEQ ID NO. 7716

STRAIN 18RS21 frame: 1

PMLSVGLVLEGGGMRLYTAGVLDAGIKIDGIVSVSAGALFGVNFSRQRERALRY
 NKKYLSPHKYMSLRSWLRGNFVNKDFTYYEVPMKLDVFDEAFKSSIDFYVVATEMTS
 GKPEYFKIDSVFEQMEILRASSALPVVSKMWDWQGKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNNSLEKVMMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSTYQLGMKDAKSGMPPELNSYLMK

SEQ ID NO. 7717

STRAIN M732 frame: 1

PMLSVGLVLEGGGMRLYTAGVLDAGIKIDGIVSVSAGALFGVNFSRQRERALRY
 NKKYLSPHKYMSLRSWLRGNFVNKDFTYYEVPMKLDVFDEAFKSSIDFYVVATEMTS
 GKPEYFKIDSVFEQMEILRASSALPVVSKMWDWQGKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNNSLEKVMMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSTYQLGMKDAKSGMPPELNSYLMK

SEQ ID NO. 7718

STRAIN COH1 frame: 1

PMLSVGLVLEGGGMRLYTAGVLDAGIKIDGIVSVSAGALFGVNFSRQRERALRY
 NKKYLSPHKYMSLRSWLRGNFVNKDFTYYEVPMKLDVFDEAFKSSIDFYVVATEMTS
 GKPEYFKIDSVFEQMEILRASSALPVVSKMWDWQGKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNNSLEKVMMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSTYQLGMKDAKSGMPPELNSYLMK

SEQ ID NO. 7719

STRAIN M781 frame: 1

PMLSVGLVLEGGGMRLYTAGVLDAGIKIDGIVSVSAGALFGVNFSRQRERALRY
 NKKYLSPHKYMSLRSWLRGNFVNKDFTYYEVPMKLDVFDEAFKSSIDFYVVATEMTS
 GKPEYFKIDSVFEQMEILRASSALPVVSKMWDWQGKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNNSLEKVMMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSTYQLGMKDAKSGMPPELNSYLMK

SEQ ID NO. 7720

STRAIN CJB110 frame: 1

PMLSVGLVLEGGGMRLYTAGVLDAGIKIDGIVSVSAGALFGVNFSRQRERALRY
 NKKYLSPHKYMSLRSWLRGNFVNKDFTYYEVPMKLDVFDEAFKSSIDFYVVATEMTS
 GKPEYFKIDSVFEQMEILRASSALPVVSKMWDWQGKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNNSLEKVMMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSTYQLGMKDAKSGMPPELNSYLMK

SEQ ID NO. 7721

STRAIN JM9130013 frame: 1

PMLSVGLVLEGGGMRLYTAGVLDAGIKVDGIIISVSAGALFGVNFSRQRERALRY
 NKKYLSPHKYMSLRSWLRGNFVNKDFTYYEVPMKLDVFDEAFKSSIDFYAVATEMTS
 GKPEYFKIDSVFEQMEILRASSALPVVSKMWWQGKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNNSLEKVMMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSTYQLGMKDAKSGMPPELNSYLMK

SEQ ID NO. 7722

STRAIN 1169NT frame: 1

PMLSVGLVLEGGGMRLYTAGVLDAGIKIDGIVSVSAGALFGVNFSRQRERALRY
 NKKYLSPHKYMSLRSWLRGNFVNKDFTYYEVPMKLDVFDEAFKSSIDFYAVATEMTS
 GKPEYFKIDSVFEQMEILRASSALPVVSKMWDWQGKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNNSLEKVMMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSTYQLGMKDAKSGMPPELNSYLMK

SEQ ID NO. 7723

STRAIN 1169NT frame: 1

PMLSVGLVLEGGGMRLYTAGVLDAGIKIDGIVSVSAGALFGVNFSRQRERALRY
 NKKYLSPHKYMSLRSWLRGNFVNKDFTYYEVPMKLDVFDEAFKSSIDFYAVATEMTS
 GKPEYFKIDSVFEQMEILRASSALPVVSKMWDWQGKKYLDGGLSDSIPVDFARGLGFDKL
 IVVMTRPLNYQKKPSSGRLYKTLYRKYPNFVKTASNRYQQYNNNSLEKVMMSLEKTGDLFAI
 RPSKSLVIGRLEKNPDKLDSTYQLGMKDAKSGMPPELNSYLMK

	1		50
msa47322.2{394_A909}	PMLSVGLVLE GGGMRLYTA GVLDALFDAG IKvDGIIISVS AGALFGVNFB		
msa47322.2{394_H36B}	PMLSVGLVLE GGGMRLYTA GVLDALFDAG IKvDGIIISVS AGALFGVNFB		
msa47322.2{394_JM9130013}	PMLSVGLVLE GGGMRLYTA GVLDALFDAG IKvDGIIISVS AGALFGVNFB		
msa47322.2{394_090}	PMLSVGLVLE GGGMRLYTA GVLDALFDAG IKiDGIVSVS AGALFGVNFB		
msa47322.2{394_1169NT}	PMLSVGLVLE GGGMRLYTA GVLDALFDAG IKiDGIVSVS AGALFGVNFB		
msa47322.2{394_18RS21}	PMLSVGLVLE GGGMRLYTA GVLDALFDAG IKiDGIVSVS AGALFGVNFB		
msa47322.2{394_2603}	PMLSVGLVLE GGGMRLYTA GVLDALFDAG IKiDGIVSVS AGALFGVNFB		
msa47322.2{394_CJB110}	PMLSVGLVLE GGGMRLYTA GVLDALFDAG IKiDGIVSVS AGALFGVNFB		
msa47322.2{394_COH1}	PMLSVGLVLE GGGMRLYTA GVLDALFDAG IKiDGIVSVS AGALFGVNFB		
msa47322.2{394_M732}	PMLSVGLVLE GGGMRLYTA GVLDALFDAG IKiDGIVSVS AGALFGVNFB		
msa47322.2{394_M781}	PMLSVGLVLE GGGMRLYTA GVLDALFDAG IKiDGIVSVS AGALFGVNFB		
Consensus	*****	*****	*****

	51		100
msa47322.2{394_A909}	SRQRERALRY NKKYLSPHKY MSLRSWLRGT NFVNKDFTYY EVPMKLDVFD		
msa47322.2{394_H36B}	SRQRERALRY NKKYLSPHKY MSLRSWLRGT NFVNKDFTYY EVPMKLDVFD		
msa47322.2{394_JM9130013}	SRQRERALRY NKKYLSPHKY MSLRSWLRGT NFVNKDFTYY EVPMKLDVFD		
msa47322.2{394_090}	SRQRERALRY NKKYLSPHKY MSLRSWLRGT NFVNKDFTYY EVPMKLDVFD		
msa47322.2{394_1169NT}	SRQRERALRY NKKYLSPHKY MSLRSWLRGT NFVNKDFTYY EVPMKLDVFD		
msa47322.2{394_18RS21}	SRQRERALRY NKKYLSPHKY MSLRSWLRGT NFVNKDFTYY EVPMKLDVFD		

Table 77: Comparative Sequences relating to SAG2059

msa47322.2{394_2603}	SRQRERALRY NKKYLSHPkY MSLRSWIRTG NFVNKDFTYY EVPMKLDVFD	
msa47322.2{394_CJB110}	SRQRERALRY NKKYLSHPkY MSLRSWIRTG NFVNKDFTYY EVPMKLDVFD	
msa47322.2{394_COH1}	SRQRERALRY NKKYLSHPeY MSLRSWIRTG NFVNKDFTYY EVPMKLDVFD	
msa47322.2{394_M732}	SRQRERALRY NKKYLSHPeY MSLRSWIRTG NFVNKDFTYY EVPMKLDVFD	
msa47322.2{394_M781}	SRORERALRY NKKYLSHPeY MSLRSWIRTG NFVNKDFTYY EVPMKLDVFD	
Consensus	*****	*****
		150
msa47322.2{394_A909}	DEAFKKSSID FYaVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM	
msa47322.2{394_H36B}	DEAFKKSSID FYaVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM	
msa47322.2{394_JM9130013}	DEAFKKSSID FYaVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM	
msa47322.2{394_090}	DEAFKKSSID FYvVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM	
msa47322.2{394_1169NT}	DEAFKKSSID FYvVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM	
msa47322.2{394_18RS21}	DEAFKKSSID FYvVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM	
msa47322.2{394_2603}	DEAFKKSSID FYvVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM	
msa47322.2{394_CJB110}	DEAFKKSSID FYvVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM	
msa47322.2{394_COH1}	DEAFKKSSID FYvVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM	
msa47322.2{394_M732}	DEAFKKSSID FYvVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM	
msa47322.2{394_M781}	DEAFKKSSID FYvVATEMTS GKPEYFKIDS VFEQMEILRA SSALPVVSKM	
Consensus	*****	*****
		200
msa47322.2{394_A909}	VvWQGKKYLD GGLSDSIPVD FARGLGFDFKL IVVVTRPLNY QKKPSSGRLY	
msa47322.2{394_H36B}	VvWQGKKYLD GGLSDSIPVD FARGLGFDFKL IVVVTRPLNY QKKPSSGRLY	
msa47322.2{394_JM9130013}	VvWQGKKYLD GGLSDSIPVD FARGLGFDFKL IVVVTRPLNY QKKPSSGRLY	
msa47322.2{394_090}	VdWQGKKYLD GGLSDSIPVD FARGLGFDFKL IVVVTRPLNY QKKPSSGRLY	
msa47322.2{394_1169NT}	VdWQGKKYLD GGLSDSIPVD FARGLGFDFKL IVVVTRPLNY QKKPSSGRLY	
msa47322.2{394_18RS21}	VdWQGKKYLD GGLSDSIPVD FARGLGFDFKL IVVVTRPLNY QKKPSSGRLY	
msa47322.2{394_2603}	VdWQGKKYLD GGLSDSIPVD FARGLGFDFKL IVVVTRPLNY QKKPSSGRLY	
msa47322.2{394_CJB110}	VdWQGKKYLD GGLSDSIPVD FARGLGFDFKL IVVVTRPLNY QKKPSSGRLY	
msa47322.2{394_COH1}	VdWQGKKYLD GGLSDSIPVD FARGLGFDFKL IVVVTRPLNY QKKPSSGRLY	
msa47322.2{394_M732}	VdWQGKKYLD GGLSDSIPVD FARGLGFDFKL IVVVTRPLNY QKKPSSGRLY	
msa47322.2{394_M781}	VdWQGKKYLD GGLSDSIPVD FARGLGFDFKL IVVVTRPLNY QKKPSSGRLY	
Consensus	*****	*****
		250
msa47322.2{394_A909}	KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIGR	
msa47322.2{394_H36B}	KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIGR	
msa47322.2{394_JM9130013}	KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIGR	
msa47322.2{394_090}	KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIGR	
msa47322.2{394_1169NT}	KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIGR	
msa47322.2{394_18RS21}	KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIGR	
msa47322.2{394_2603}	KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIGR	
msa47322.2{394_CJB110}	KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIGR	
msa47322.2{394_COH1}	KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIGR	
msa47322.2{394_M732}	KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIGR	
msa47322.2{394_M781}	KTLYRKYPNF VKTASNRYQQ YNNSLEKVMS LEKTGDLFAI RPSKSLVIGR	
Consensus	*****	*****
		282
msa47322.2{394_A909}	LEKNPDKLDS IYQLGMKDak SgMPELNSYL MK	
msa47322.2{394_H36B}	LEKNPDKLDS IYQLGMKDak SgMPELNSYL MK	
msa47322.2{394_JM9130013}	LEKNPDKLDS IYQLGMKDak SgMPELNSYL MK	
msa47322.2{394_090}	LEKNPDKLDS IYQLGMKDak SgMPELNSYL MK	
msa47322.2{394_1169NT}	LEKNPDKLDS IYQLGMKDak SgMPELNSYL MK	
msa47322.2{394_18RS21}	LEKNPDKLDS IYQLGMKDak SgMPELNSYL MK	
msa47322.2{394_2603}	LEKNPDKLDS IYQLGMKDak SgMPELNSYL MK	
msa47322.2{394_CJB110}	LEKNPDKLDS IYQLGMKDak SgMPELNSYL MK	
msa47322.2{394_COH1}	LEKNPDKLDS IYQLGMKDak SgMPELNSYL MK	
msa47322.2{394_M732}	LEKNPDKLDS IYQLGMKDak SgMPELNSYL MK	
msa47322.2{394_M781}	LEKNPDKLDS IYQLGMKDak SgMPELNSYL MK	
Consensus	*****	**

Table 78: Comparative Sequences relating to SAG1016**SEQ ID NO. 7801****STRAIN 2603**

ATGAAAGTTAGTAGTTGATGATGAACCAAGTTGCACGTAAACGAAATTAAACCTTCTT
 AATAAGTATGATCTAACCTCGTTATAGCAGAGGGCATGATATGGCTACTGCATTAGCT
 ATTTTACTTAGAGAAACTTTGATGATGACTGTTAGATATCCATCTCAGAGATGATTCT
 GGTTGCAATTAGCAGCTATCAATAAATGCCAAACCACCATTTGATATTGCG
 ACTGCTTATGATCAATATGCTATTCAAGCTTTGAGCATGATGCGCGTGATTGTTA
 AAACCCATTGATTTGATAGGCTAAAGCAAGCTATGGATAGAGTAAAGGAGCGCTAAAGT
 ACATCTCAAACTATAGAGGCTAACTCCGGTCTCTCAAGCAACAGTATCCATTG
 ACAGTAAAGATGCAATTCTATGGTCTGGCGGATGATATCCTTTGATTGAAGCTATG
 CAAGAAAACCTGATTATACAAACACCTGATAAAATTATGAAATTGATGGCTCTCACAA
 CAATGGCAAGATAAAACTACCCATCTCAATTGTAACGGTACATCGCTCTACATTGTG
 AACATTAATGCTATTAAACGATTGAAACCTGGTTAACCAAACACTTCAGTTACACCTT
 TGTAATAAAATAACAGTTCTGTTAGCAGAGCAATGTAACACCCCTAAACAAATGTTA
 GGCATATCTACC

SEQ ID NO. 7802**STRAIN 090**

CGAATTAAATTACCTCTTAATAAAGTATGATTCTAACCTCGTTATAGCAG
 AGGCCATGATATGGCTACTGCATTAGCTATTACTTAGAGAAACTTT
 GATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTGCAATT
 AGCAGAGTATATCAATAAATGCCAAACCACCATTTGATATTGCG
 CTGCTTATGATCAATATGCTATTCAAGCTTTGAGCATGATGCGCGTGAT
 TATTGTTAAACCCATTGATTTGATAGGCTAAAGCAAGCTATGGATAG
 AGTAAAAGGAGGCTAAAGTACATCTACAATTATAGAGAGCGTAACCTCCG
 GTCTCTCTCAAGCAACACTATCCATTGACAGTAGAAAGATCGAATCTAT
 CTGGTGTGGCGGATGATATCCTTTGATTGAAGCTATGCAAGGAAAACCT
 GATTATACAAACACCTGATAAAATTATGAAATTGATGGCTCTACAAAC
 AATGGCAAGATAAAACTACCCATCTCAATTGTAACGGTACATCGCTCT
 TACATTGTGAACATTATGCTATTAAACGATTGAAACCTGGTTAACCA
 AACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCTGTTAGCAGAG
 CAAATGTAACACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7803**STRAIN A909**

AAAGTTTAGTAGTTGATGATGAACCAAGTTGCACGTAAAC
 GAATTAAATTACCTCTTAATAAAGTATGATTCTAACCTCGTTATAGCAGA
 GGCATGATATGGCTACTGCATTAGCTATTACTTAGAGAAACTTTG
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTGCAATT
 GCAGAGTATATCAATAAATGCCAAACCACCATTTGATATTGCG
 TGCTTATGATCAATATGCTATTCAAGCTTTGAGCATGATGCGCGTGATT
 ATTGTTAAACCCATTGAGTTGATAGGCTAAAGCAAGCTATGGATAGA
 GTAAAAGGAGGCTAAAGTACATCTACAATTATAGAGAGCGTAACCTC
 CCCTCTCTCAAGCAACACTATCCATTGACAGTAGAAAGATCGAATCTATC
 TGGTGTGGCGGATGATATCCTTTGATTGAAGCTATGCAAGGAAAACCT
 ATTATACAAACACCTGATAAAATTATGAAATTGATGGCTCTACAAACA
 ATGGCAAGATAAAACTACCCATCTCAATTGTAACGGTGCACCGCTCT
 ACATTGTGAATTAATGCTATTAAACGATTGAAACCTGGTTAACCA
 AACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCTGTTAGCAGAGC
 AAATGTAACACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7804**STRAIN H36B**

AAAGTTTAGTAGTTGATGATGAACCAAGTTGCACGT
 AACGAATTAAATTACCTCTTAATAAAGTATGATTCTAACCTCGTTATAGC
 AGAGGCATGATATGGCTACTGCATTAGCTATTACTTAGAGAAACCTT
 TTGATGTCAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTGCAAA
 TTAGCAGAGTATATCAATAAATGCCAAACCACCATTTGATATTGCG
 GACTGCTTATGATCAATATGCTATTCAAGCTTTGAGCATGATGCGCGTG
 ATTATTGTTAAACCCATTGAGTTGATAGGCTAAAGCAAGCTATGGAT
 AGAGTAAAAGGAGGCTAAAGTACATCTACAATTATAGAGAGCGTAACCTC
 CGGCCCTCTCTCAAGCAACAGTATCCATTGACAGTAGAAAGATCGAATCT
 ATCTGGTGTGGCGGATGATATCCTTTGATTGAAGCTATGCAAGGAAA
 CTGATTATACAAACACCTGATAAAATTATGAAATTGATGGCTCTACAA
 ACAATGGCAAGATAAAACTACCCATCTCAATTGTAACGGTGCACCGCT
 CTACATTGTGAATTAATGCTATTAAACGATTGAAACCTGGTTAAC
 CAAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCTGTTAGCAG
 AGCAAATGTAACACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7805**STRAIN 18RS21**

AAAGTTTAGTAGTTGATGATGAACCAAGTTGCACGTAAAC
 GAATTAAATTACCTCTTAATAAAGTATGATTCTAACCTCGTTATAGCAGA
 GGCATGATATGGCTACTGCATTAGCTATTACTTAGAGAAACCTT
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTGCAATT
 GCAGAGTATATCAATAAATGCCAAACCACCATTTGATATTGCG
 TGCTTATGATCAATATGCTATTCAAGCTTTGAGCATGATGCGCGTGAT
 ATTGTTAAACCCATTGATTGATAGGCTAAAGCAAGCTATGGATAGA
 GTAAAAGGAGGCTAAAGTACATCTACAATTATAGAGAGCGTAACCTCCG
 TCCTCTCTCAAGCAACAGTATCCATTGACAGTAGAAAGATCGAATCTATC
 TGGTGTGGCGGATGATATCCTTTGATTGAAGCTATGCAAGGAAAACCT

Table 78: Comparative Sequences relating to SAG1016

ATTATAACAAACACCTGATAAAAATTATGAAATTGATGGCTCTACAACA
 ATGCCAAGATAAAACTACCCTCATCTCAATTGTACGGGACATCGCTCTT
 ACATGTGAAACATTAATGCTATTAAACGATTGAACCTGGTTAACCAA
 ACACCTCAGTTACACCTTGTAAATAAAAATAACAGTTCCCTAGCAGAGC
 AAATGTAAAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7806

STRAIN M732

AAAGTTTTAGTAGTTGATGATGAACCGAGTT
 GCACGTAAAGGAGCTAACTTACCTCTTAATAAGTATGATTCTAACCTCGT
 TATAGCAGAGCGCATGATATGGCTACTGCATTAGCTATTACTAGAG
 AAACTTTGTGATGCTAGCACTGTAGATATCCATCTCAGAGATGAIITCTGG
 TTGCAATTAGCAGAGTATATCAATAAAATGCCAAACCAACCTTATTGAT
 ATTGCGACTCTCTATGATCAATATGCTATTAGGCTTTGAGCTAGGAGATG
 CGCGTATTATTGTTAAAACCCCTATGAGTTGATAGGTTAAAGCAGCT
 ATGGATAGATAAAAGGAGCGCTAAAGTACATCTACAATTATAGAGAGCCT
 AGCTTCGGTCTCTTCAGCAACAGTATCCATTGACAGTAGAAAGATC
 GAATCTATCTGGTGTGGGGATGATATCCTTTGATTGAAGCTATGCA
 GGAAAACGATTATAACAAACACCTGATAAAAATTATGAAATTGATGGCTC
 TCTACAACATGGCAAGATAAAACTACCATCATCTCAATTGTTACGGGTAC
 ATGCGCTTACATTGTAATTATGCTATTAAACGATTGAAACCTTGG
 TTTAACCAACACTTCAGTTACACCTTGTAATAAAAATAACAGTTCCGT
 TAGCAGAGCAAATGTAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7807

STRAIN COH1

AAAGTTTTAGTAGTTGATGATGAACCGAGTTGCACGTA
 ACGAATTAAATTACCTCTTAATAAGTATGATTCTAACCTCGTTATAGC
 GAGGGCATGATATGGCTACTGCATTAGCTATTACTAGAGAAACCTT
 TGATGTGACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAAT
 TAGCAGAGTATATCAATAAAATGCCAAACCCATTATTGATATTGCG
 ACTGCTATGATCAATATGCTATTAGGCTTTGAGCAGGATGCGCTGA
 TTATTGTTAAAACCCCTATGAGTTGATAGGTTAAAGCAAGCTATGGATA
 GAGTAAAAGGAGCGCTAAAGTACATCTACAATTATAGAGAGCGTAGCT
 GGTCTCTCTCAAGCAACAGTATCCATTGACAGTAGAAAGATGAACT
 TCTGGTGTGGGGATGATATCCTTTGATTGAAGCTATGCAAGGAAAAC
 TGATTATAACAAACACCTGATAAAAATTATGAAATTGATGGCTCTACAA
 CAATGGCAAGATAAAACTACCATCATCTCAATTGCTACGGGTACATCGCTC
 TTACATTGTAATTATGCTATTAAACGATTGAAACCTTGGTTAAC
 AACACTTCAGTTACACCTTGTAATAAAAATAACAGTTCCGTAGCAGA
 GCAAATGTAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7808

STRAIN M781

AAAGTTTTAGTAGTTGATGATGAACCGAGTTGCACGTAAC
 GAATAATTACCTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
 GGGCGCATGATATGGCTACTGCATTAGCTATTACTAGAGAAACCTT
 ATGATGACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATT
 GCAGAGTATATCAATAAAATGCCAAACCCATTATTGATATTGCGCAC
 TGCTTATGATCAATATGCTATTAGGCTTTGAGCAGGATGCGCTGATT
 ATTGTTAAAACCCCTATGAGTTGATAGGTTAAAGCAAGCTATGGATAGA
 GTAAAGGAGCGCTAAAGTACATCTACAATTATAGAGAGCGTAGCT
 TCTCTCTCAAGCAACAGTATCCATTGACAGTAGAAAGATGAACT
 TGTTGTGGGGATGATATCCTTTGATTGAAGCTATGCAAGGAAAAC
 ATTATACAAACACCTGATAAAAATTATGAAATTGATGGCTCTACAA
 ATGGCAAGATAAAACTACCATCATCTCAATTGTCAGGGTACATCGCTCT
 ACATGTAATTAAATGCTATTAAACGATTGAAACCTTGGTTAAC
 ACACTTCAGTTACACCTTGTAATAAAAATAACAGTTCCGTAGCAGAGC
 AAATGTAACCCCTAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7809

STRAIN CJB110

CTTAATAAGTATGATTCTAACCTCGTTAGCAGAGGCGCATGATATGGC
 TACTGCATTAGCTATTACTAGAGAAACCTTGTAGTACACTGTTAG
 ATATCCATCTCAGAGATGATTCTGGGTTGCAATTAGCAGAGTATATCAAT
 AAAATGCCAAACCCATTATTGATATTGCGACTGCTATGATCAATA
 TGCTTCAAGCTTTGAGCATGATGCGCTGATTATTGTTAAAACCCCT
 ATGAGTTGATAGGCTAAAGCAAGGATGATAGAGTAAAGGAGCGCTA
 AGTACATCTCAATTATAGAGAGCGTAACCTCCGGCCCTCTTCAGGCA
 ACAGTATCCATTGACAGTAGAAAGATGAACTATGCTATTGGTGTGGGGATG
 ATATCCTTTGATTGAAGCTATGCAAGGAAAACGATTATACAAACACCT
 GATAAAAATTATGAAATTGATGGCTCTACAAACAAATGGCAAGATAAACT
 ACCATCATCTCAATTGTCAGGGTGCACCGCTTACATTGTAATT
 ATGCTATTAAACGATTGAAACCTTGGTTAACCAAACACTTCAGTTACAC
 CTGTAATAAAATAACAGTTCCGTAGCAGAGCAAATGTTAAACCCCT
 AAACAAATGTTAGG

SEQ ID NO. 7810

STRAIN 1169NT

AAAGTTTTAGTAGTTGATGATGAACCGAG
 TTGCACGTAACGAAATTAAATTATCCTCTTAATAAGTATGATTCTAACCTC
 GTATAGCAGAGGCGCATGATAGCTACTGCATTAGCTATTACTAG

Table 78: Comparative Sequences relating to SAG1016

AGAAAACTTTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTG
 GGTGCAATTAGCAGAGTATATCAATAAAATGCCAACCAACCAATTATTG
 ATATTCCGCACIGCTTATGATCAATATGCTATTGAGCTTTGAGCATGA
 TGCGCGTGAATTGGTAAACCCCTATGAGTTGATAGGCTAAAGCAAG
 CTATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGC
 GTAACTTCCGGCCCTCTTCAGCAACAGTATCCATTGACAGTAGAAAGA
 TCGAATCTATCTGGTGTGGGAGATATCTTGTAGCTTGTAGGCTATG
 AAGGAAAACCTGATTATAACAAACACCTGATAAAATTATGAAATTGATGG
 TCTCTACAACAATGGCAAGATAAAACTACCATCATCTCAATTGTAACGG
 GCACCGCTCTTACATTGTAATTAATGCTATTAAACGATGAAACCTT
 GTTTAACCAAACACTTCAGTACACCTTGTAAATAAAATAACAGTTCTG
 GTTAGCAGAGCAAATGTAACCCCTAAACAAATGTTAGGCATATCTAC
 C

SEQ ID NO. 7811

STRAIN JM9130013

AAAGTTTGTAGTTGATGTGAACCGT
 TGACGTAACGATTAAATTACCTCTTAATAAGTATGATTCTAACCTCG
 TTATAGCAGAGCGCATGATATGGCTACTGCAATTGCTATTACTTAGA
 GAAACTTTGATGTAGCACTGTTAGATATCTCATCTCAGAGATGATTCTG
 GTGCAATTAGCAGAGTATATCAATAAAATGCCAACCAACCAATTATG
 TATTCGCGACTGCTTATGATCAATATGCTATTCAAGCTTTGAGCATGAT
 GCCCGTGATTATTGTTAAACCCCTATGAGTTGATAGGCTAAAGCAAGC
 TATGGATAGATAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCG
 TAACCTCCGGCCCTCTTCAGCAACAGTATCATTGACAGTAGAAAGAT
 CGAATCTATCTGGTGTGGCGGATGATATCTTGTAGGAAAGCTATGCA
 AGGAAAACCTGATATAACAAACACCTGATAAAATTATGAAATTGATGGCT
 CTCTACAACAATGGCAAGATAAAACTACCATCATCTCAATTGTAACGGG
 CACCGCTTACATTGTAATTAATGCTATTAAACGATGAAACCTT
 GTTTAACCAAACACTTCAGTACACCTTGTAAATAAAATAACAGTTCTG
 TTAGCAGAGCAAATGTAACCCCTAAACAAATGTTAGGCATATCTACC

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa141507.2(*) April 10, 2003 06:36 ..

	1						50
msa141507.2{399_A909}	~~aaagttt	tagtagttga	tgatgaacca	gttgcacgta	acgaattaat		
msa141507.2{399_CJB110}	-----	-----	-----	-----	-----		
msa141507.2{399_H36B}	~~aaagttt	tagtagttga	tgatgaacca	gttgcacgta	acgaattaat		
msa141507.2{399_JM9130013}	~~aaagttt	tagtagttga	tgatgaacca	gttgcacgta	acgaattaat		
msa141507.2{399_1169NT}	~~aaagttt	tagtagttga	tgatgaacca	gttgcacgta	acgaattaat		
msa141507.2{399_090}	~~aaagttt	tagtagttga	tgatgaacca	gttgcacgta	acgaattaat		
msa141507.2{399_18RS21}	~~aaagttt	tagtagttga	tgatgaacca	gttgcacgta	acgaattaat		
msa141507.2{399_2603}	atgaaaggttt	tagtagttga	tgatgaacca	gttgcacgta	acgaattaat		
msa141507.2{399_COH1}	~~aaagttt	tagtagttga	tgatgaacca	gttgcacgta	acgaattaat		
msa141507.2{399_M732}	~~aaagttt	tagtagttga	tgatgaacca	gttgcacgta	acgaattaat		
msa141507.2{399_M781}	~~aaagttt	tagtagttga	tgatgaacca	gttgcacgta	acgaattaat		
Consensus	*****	-----	-----	-----	-----		
	51						100
msa141507.2{399_A909}	ttacacctT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGGCATG		
msa141507.2{399_CJB110}	-----	CTT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGGCATG	
msa141507.2{399_H36B}	ttacacctT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGGCATG		
msa141507.2{399_JM9130013}	ttacacctT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGGCATG		
msa141507.2{399_1169NT}	ttatcttT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGGCATG		
msa141507.2{399_090}	ttacacctT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGGCATG		
msa141507.2{399_18RS21}	ttacacctT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGGCATG		
msa141507.2{399_2603}	ttacacctT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGGCATG		
msa141507.2{399_COH1}	ttacacctT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGGCATG		
msa141507.2{399_M732}	ttacacctT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGGCATG		
msa141507.2{399_M781}	ttacacctT	AATAAGTATG	ATTCTAACCT	CGTTATAGCA	GAGGGCATG		
Consensus	-----*	*****	*****	*****	*****		
	101						150
msa141507.2{399_A909}	ATATggCTAC	TGCATTAGCT	ATTTTACTTA	GAGAAACTTT	TGATGTAGCA		
msa141507.2{399_CJB110}	ATATggCTAC	TGCATTAGCT	ATTTTACTTA	GAGAAACTTT	TGATGTAGCA		
msa141507.2{399_H36B}	ATATggCTAC	TGCATTAGCT	ATTTTACTTA	GAGAAACTTT	TGATGTAGCA		
msa141507.2{399_JM9130013}	ATATggCTAC	TGCATTAGCT	ATTTTACTTA	GAGAAACTTT	TGATGTAGCA		
msa141507.2{399_1169NT}	ATATAgCTAC	TGCATTAGCT	ATTTTACTTA	GAGAAACTTT	TGATGTAGCA		
msa141507.2{399_090}	ATATggCTAC	TGCATTAGCT	ATTTTACTTA	GAGAAACTTT	TGATGTAGCA		
msa141507.2{399_18RS21}	ATATggCTAC	TGCATTAGCT	ATTTTACTTA	GAGAAACTTT	TGATGTAGCA		
msa141507.2{399_2603}	ATATggCTAC	TGCATTAGCT	ATTTTACTTA	GAGAAACTTT	TGATGTAGCA		
msa141507.2{399_COH1}	ATATggCTAC	TGCATTAGCT	ATTTTACTTA	GAGAAACTTT	TGATGTAGCA		
msa141507.2{399_M732}	ATATggCTAC	TGCATTAGCT	ATTTTACTTA	GAGAAACTTT	TGATGTAGCA		
msa141507.2{399_M781}	ATATggCTAC	TGCATTAGCT	ATTTTACTTA	GAGAAACTTT	TGATGTAGCA		
Consensus	*****	*****	*****	*****	*****		
	151						200
msa141507.2{399_A909}	CTGTTAGATA	TCCATCTCA	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA		
msa141507.2{399_CJB110}	CTGTTAGATA	TCCATCTCA	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA		
msa141507.2{399_H36B}	CTGTTAGATA	TCCATCTCA	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA		
msa141507.2{399_JM9130013}	CTGTTAGATA	TCCATCTCA	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA		
msa141507.2{399_1169NT}	CTGTTAGATA	TCCATCTCA	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA		

Table 78: Comparative Sequences relating to SAG1016

msa141507.2{399_090}	CTGTTAGATA	TCCATCTCA	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_18RS21}	CTGTTAGATA	TCCATCTCA	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_2603}	CTGTTAGATA	TCCATCTCA	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_COH1}	CTGTTAGATA	TCCATCTCA	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_M732}	CTGTTAGATA	TCCATCTCA	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_M781}	CTGTTAGATA	TCCATCTCA	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
Consensus	*****	*****	*****	*****	*****
	201			250	
msa141507.2{399_A909}	TATCAATAAA	ATGCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_CJB110}	TATCAATAAA	ATGCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_H36B}	TATCAATAAA	ATGCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_JM9130013}	TATCAATAAA	ATGCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_1169NT}	TATCAATAAA	ATGCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_090}	TATCAATAAA	ATGCCAAAC	CACCATTATT	GATATTtGCG	ACTGCTTATG
msa141507.2{399_18RS21}	TATCAATAAA	ATGCCAAAC	CACCATTATT	GATATTtGCG	ACTGCTTATG
msa141507.2{399_2603}	TATCAATAAA	ATGCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_COH1}	TATCAATAAA	ATGCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_M732}	TATCAATAAA	ATGCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_M781}	TATCAATAAA	ATGCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
Consensus	*****	*****	*****	*****-***	*****
	251			300	
msa141507.2{399_A909}	ATCAATATGC	TATTCAAgGCT	TTTGAGGATG	ATGCCGTGA	TTATTGTTA
msa141507.2{399_CJB110}	ATCAATATGC	TATTCAAgGCT	TTTGAGGATG	ATGCCGTGA	TTATTGTTA
msa141507.2{399_H36B}	ATCAATATGC	TATTCAAgGCT	TTTGAGGATG	ATGCCGTGA	TTATTGTTA
msa141507.2{399_JM9130013}	ATCAATATGC	TATTCAAgGCT	TTTGAGGATG	ATGCCGTGA	TTATTGTTA
msa141507.2{399_1169NT}	ATCAATATGC	TATTCAGGCT	TTTGAGGATG	ATGCCGTGA	TTATTGTTA
msa141507.2{399_090}	ATCAATATGC	TATTCAGGCT	TTTGAGGATG	ATGCCGTGA	TTATTGTTA
msa141507.2{399_18RS21}	ATCAATATGC	TATTCAGGCT	TTTGAGGATG	ATGCCGTGA	TTATTGTTA
msa141507.2{399_2603}	ATCAATATGC	TATTCAGGCT	TTTGAGGATG	ATGCCGTGA	TTATTGTTA
msa141507.2{399_COH1}	ATCAATATGC	TATTCAGGCT	TTTGAGGATG	ATGCCGTGA	TTATTGTTA
msa141507.2{399_M732}	ATCAATATGC	TATTCAGGCT	TTTGAGGATG	ATGCCGTGA	TTATTGTTA
msa141507.2{399_M781}	ATCAATATGC	TATTCAGGCT	TTTGAGGATG	ATGCCGTGA	TTATTGTTA
Consensus	*****	*****	*****	*****	*****
	301			350	
msa141507.2{399_A909}	AAACCTATG	AgtTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_CJB110}	AAACCTATG	AgtTTGATAG	GcTAAAGCAA	GtTATGGATA	GAGTAAAAGG
msa141507.2{399_H36B}	AAACCTATG	AgtTTGATAG	GcTAAAGCAA	GtTATGGATA	GAGTAAAAGG
msa141507.2{399_JM9130013}	AAACCTATG	AgtTTGATAG	GcTAAAGCAA	GtTATGGATA	GAGTAAAAGG
msa141507.2{399_1169NT}	AAACCTATG	AgtTTGATAG	GcTAAAGCAA	GtTATGGATA	GAGTAAAAGG
msa141507.2{399_090}	AAACCTATG	AgtTTGATAG	GcTAAAGCAA	GtTATGGATA	GAGTAAAAGG
msa141507.2{399_18RS21}	AAACCTATG	AgtTTGATAG	GcTAAAGCAA	GtTATGGATA	GAGTAAAAGG
msa141507.2{399_2603}	AAACCTATG	AgtTTGATAG	GcTAAAGCAA	GtTATGGATA	GAGTAAAAGG
msa141507.2{399_COH1}	AAACCTATG	AgtTTGATAG	GcTAAAGCAA	GtTATGGATA	GAGTAAAAGG
msa141507.2{399_M732}	AAACCTATG	AgtTTGATAG	GcTAAAGCAA	GtTATGGATA	GAGTAAAAGG
msa141507.2{399_M781}	AAACCTATG	AgtTTGATAG	GcTAAAGCAA	GtTATGGATA	GAGTAAAAGG
Consensus	*****	-*****	*****	*****	*****
	351			400	
msa141507.2{399_A909}	ACCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_CJB110}	ACCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_H36B}	ACCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_JM9130013}	ACCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_1169NT}	ACCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_090}	ACCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_18RS21}	ACCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_2603}	ACCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_COH1}	ACCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_M732}	ACCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_M781}	ACCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
Consensus	*****	*****	*****	*****	*****
	401			450	
msa141507.2{399_A909}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAC	ATcGAATCTA	TCTGGTGTGCG
msa141507.2{399_CJB110}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAC	ATnGAATCTA	TCTGGTGTGCG
msa141507.2{399_H36B}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAC	ATcGAATCTA	TCTGGTGTGCG
msa141507.2{399_JM9130013}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAC	ATcGAATCTA	TCTGGTGTGCG
msa141507.2{399_1169NT}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAC	ATcGAATCTA	TCTGGTGTGCG
msa141507.2{399_090}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAC	ATcGAATCTA	TCTGGTGTGCG
msa141507.2{399_18RS21}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAC	ATcGAATCTA	TCTGGTGTGCG
msa141507.2{399_2603}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAC	ATcGAATCTA	TCTGGTGTGCG
msa141507.2{399_COH1}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAC	ATcGAATCTA	TCTGGTGTGCG
msa141507.2{399_M732}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAC	ATcGAATCTA	TCTGGTGTGCG
msa141507.2{399_M781}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAC	ATcGAATCTA	TCTGGTGTGCG
Consensus	*****	*****	*****	*****	*****
	451			500	
msa141507.2{399_A909}	GCGGATGATA	TCCCTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_CJB110}	GCGGATGATA	TCCCTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_H36B}	GCGGATGATA	TCCCTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_JM9130013}	GCGGATGATA	TCCCTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA

Table 78: Comparative Sequences relating to SAG1016

msa141507.2{399_1169NT}	GCGGATGATA	TCCTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_090}	GCGGATGATA	TCCTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_18RS21}	GCGGATGATA	TCCTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_2603}	GCGGATGATA	TCCTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_COH1}	GCGGATGATA	TCCTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_M732}	GCGGATGATA	TCCTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_M781}	GCGGATGATA	TCCTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
Consensus	*****	*****	*****	*****	*****
	501			550	
msa141507.2{399_A909}	AAACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_CJB110}	AAACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_H36B}	AAACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_JM9130013}	AAACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_1169NT}	AAACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_090}	AAACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_18RS21}	AAACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_2603}	AAACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_COH1}	AAACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_M732}	AAACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_M781}	AAACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
Consensus	*****	*****	*****	*****	*****
	551			600	
msa141507.2{399_A909}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCacCGCTC	TTACATTGTG
msa141507.2{399_CJB110}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCacCGCTC	TTACATTGTG
msa141507.2{399_H36B}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCacCGCTC	TTACATTGTG
msa141507.2{399_JM9130013}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCacCGCTC	TTACATTGTG
msa141507.2{399_1169NT}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCacCGCTC	TTACATTGTG
msa141507.2{399_090}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCacCGCTC	TTACATTGTG
msa141507.2{399_18RS21}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_2603}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_COH1}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_M732}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_M781}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
Consensus	*****	*****	*****	*****	*****
	601			650	
msa141507.2{399_A909}	AATATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_CJB110}	AATATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_H36B}	AATATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_JM9130013}	AATATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_1169NT}	AATATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_090}	AACATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_18RS21}	AACATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_2603}	AACATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_COH1}	AATATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_M732}	AATATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
msa141507.2{399_M781}	AATATTAATG	CTATTAAAAC	GATTGAACCT	TGGTTTAACC	AAACACTTCA
Consensus	*****	*****	*****	*****	*****
	651			700	
msa141507.2{399_A909}	GTTACACCTT	TGTAATAAAA	TAACAGTTC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_CJB110}	GTTACACCTT	TGTAATAAAA	TAACAGTTC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_H36B}	GTTACACCTT	TGTAATAAAA	TAACAGTTC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_JM9130013}	GTTACACCTT	TGTAATAAAA	TAACAGTTC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_1169NT}	GTTACACCTT	TGTAATAAAA	TAACAGTTC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_090}	GTTACACCTT	TGTAATAAAA	TAACAGTTC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_18RS21}	GTTACACCTT	TGTAATAAAA	TAACAGTTC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_2603}	GTTACACCTT	TGTAATAAAA	TAACAGTTC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_COH1}	GTTACACCTT	TGTAATAAAA	TAACAGTTC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_M732}	GTTACACCTT	TGTAATAAAA	TAACAGTTC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_M781}	GTTACACCTT	TGTAATAAAA	TAACAGTTC	TGTTAGCAGA	GCAAATGTAA
Consensus	*****	*****	*****	*****	*****
	701			732	
msa141507.2{399_A909}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_CJB110}	AACCCCTAAA	ACAAATGTTA	GG-----	--	
msa141507.2{399_H36B}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_JM9130013}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_1169NT}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_090}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_18RS21}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_2603}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_COH1}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_M732}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_M781}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 7812

STRAIN 2603 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEHDMATALIILRLETFDVALLDIHLRDDSG
LQAEYINKMPKPLLIFATAYDQYAIQAFEHARDYLLKPYDFDRLKQAMDRVKGALST

Table 78: Comparative Sequences relating to SAG1016

STIIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAICTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7813

STRAIN 090 frame: 1

KVLVVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETDFVALLDIHLRDDSG
LQLAEYINKMPKPPLIIFATAYDQYAIQAFEHHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAICTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7814

STRAIN A909 frame: 1

KVLVVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETDFVALLDIHLRDDSG
LQLAEYINKMPKPPLIIFATAYDQYAIQAFEHHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAICTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7815

STRAIN H36B frame: 1

KVLVVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETDFVALLDIHLRDDSG
LQLAEYINKMPKPPLIIFATAYDQYAIQAFEHHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAICTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7816

STRAIN 18RS21 frame: 1

KVLVVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETDFVALLDIHLRDDSG
LQLAEYINKMPKPPLIIFATAYDQYAIQAFEHHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAICTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7817

STRAIN M732 frame: 1

KVLVVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETDFVALLDIHLRDDSG
LQLAEYINKMPKPPLIIFATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIIESVASGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAICTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7818

STRAIN COH1 frame: 1

KVLVVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETDFVALLDIHLRDDSG
LQLAEYINKMPKPPLIIFATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIIESVASGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAICTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7819

STRAIN M781 frame: 1

KVLVVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETDFVALLDIHLRDDSG
LQLAEYINKMPKPPLIIFATAYDQYAIQAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
STIIIESVASGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAICTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7820

STRAIN CJB110 frame: 1

LNNKYDSNLVIAEAHDATALAILLRETDFVALLDIHLRDDSGLQLAEYINKMPKPPLIIF
ATAYDQYAIQAFEHHDARDYLLKPYEFDRLKQXMDRVKGALSTSTIIIESVTSGPLFKQQY
LTVEDXIYLVSADDILLIEAMQGKLI IQTPDKNYEIDGSLQQWQDKLPSSQFVRVHRSYI
VNINAICTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG

SEQ ID NO. 7821

STRAIN 1169NT frame: 1

KVLVVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETDFVALLDIHLRDDSG
LQLAEYINKMPKPPLIIFATAYDQYAIQAFEHHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAICTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

SEQ ID NO. 7822

STRAIN JM9130013 frame: 1

KVLVVVDEPVARNELIYLLNKYDSNLVIAEAHDATALAILLRETDFVALLDIHLRDDSG
LQLAEYINKMPKPPLIIFATAYDQYAIQAFEHHDARDYLLKPYEFDRLKQAMDRVKGALST
STIIIESVTSGPLFKQQYPLTVEDRIYLVSADDILLIEAMQGKLI IQTPDKNYEIDGSLQQ
WQDKLPSSQFVRVHRSYIVNINAICTIEPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
IST

Table 78: Comparative Sequences relating to SAG1016

PRETTY of: /biotmp/msa141801.2{*} April 10, 2003 06:38 ..

		1		50
msa141801.2{399_COH1}	kvlvvvdddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI
msa141801.2{399_M732}	kvlvvvdddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI
msa141801.2{399_M781}	kvlvvvdddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI
msa141801.2{399_090}	kvlvvvdddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI
msa141801.2{399_18RS21}	kvlvvvdddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI
msa141801.2{399_2603}	kvlvvvdddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI
msa141801.2{399_A909}	kvlvvvdddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI
msa141801.2{399_H36B}	kvlvvvdddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI
msa141801.2{399_JM9130013}	kvlvvvdddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI
msa141801.2{399_1169NT}	kvlvvvdddepv	arneliyLLN	KYDSNLVIAE	AHDmATALAI
msa141801.2{399_CJB110}	-----	LN	KYDSNLVIAE	AHDmATALAI
Consensus	-----	-----	*****	*****
		51		100
msa141801.2{399_COH1}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	AYDQYAIQAF
msa141801.2{399_M732}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	EqDARDYLLK
msa141801.2{399_M781}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	EqDARDYLLK
msa141801.2{399_090}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	EqDARDYLLK
msa141801.2{399_18RS21}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	EqDARDYLLK
msa141801.2{399_2603}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	EqDARDYLLK
msa141801.2{399_A909}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	EqDARDYLLK
msa141801.2{399_H36B}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	EqDARDYLLK
msa141801.2{399_JM9130013}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	EqDARDYLLK
msa141801.2{399_1169NT}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	EqDARDYLLK
msa141801.2{399_CJB110}	LDIHLRDDSG	LQLAEYINKM	PKPPLLIFAT	EqDARDYLLK
Consensus	*****	*****	*****	*****
		101		150
msa141801.2{399_COH1}	PYeFDRLKQa	MDRVKGALST	STIIIESVAsG	PLFKQQYPLT
msa141801.2{399_M732}	PYeFDRLKQa	MDRVKGALST	STIIIESVAsG	VEDriIYLVSA
msa141801.2{399_M781}	PYeFDRLKQa	MDRVKGALST	STIIIESVAsG	PLFKQQYPLT
msa141801.2{399_090}	PydFDRLKQa	MDRVKGALST	STIIIESVtSG	PLFKQQYPLT
msa141801.2{399_18RS21}	PydFDRLKQa	MDRVKGALST	STIIIESVtSG	VEDriIYLVSA
msa141801.2{399_2603}	PydFDRLKQa	MDRVKGALST	STIIIESVtSG	PLFKQQYPLT
msa141801.2{399_A909}	PyeFDRLKQa	MDRVKGALST	STIIIESVtSG	PLFKQQYPLT
msa141801.2{399_H36B}	PyeFDRLKQa	MDRVKGALST	STIIIESVtSG	PLFKQQYPLT
msa141801.2{399_JM9130013}	PyeFDRLKQa	MDRVKGALST	STIIIESVtSG	PLFKQQYPLT
msa141801.2{399_1169NT}	PyeFDRLKQa	MDRVKGALST	STIIIESVtSG	PLFKQQYPLT
msa141801.2{399_CJB110}	PyeFDRLKQx	MDRVKGALST	STIIIESVtSG	PLFKQQYPLT
Consensus	*****	*****	*****	*****
		151		200
msa141801.2{399_COH1}	DDILLIEAMQ	GKLIIQTPDK	NYEIDGSLQQ	WQDKLPSSQF
msa141801.2{399_M732}	DDILLIEAMQ	GKLIIQTPDK	NYEIDGSLQQ	VRVHRSYIVN
msa141801.2{399_M781}	DDILLIEAMQ	GKLIIQTPDK	NYEIDGSLQQ	WQDKLPSSQF
msa141801.2{399_090}	DDILLIEAMQ	GKLIIQTPDK	NYEIDGSLQQ	VRVHRSYIVN
msa141801.2{399_18RS21}	DDILLIEAMQ	GKLIIQTPDK	NYEIDGSLQQ	WQDKLPSSQF
msa141801.2{399_2603}	DDILLIEAMQ	GKLIIQTPDK	NYEIDGSLQQ	VRVHRSYIVN
msa141801.2{399_A909}	DDILLIEAMQ	GKLIIQTPDK	NYEIDGSLQQ	WQDKLPSSQF
msa141801.2{399_H36B}	DDILLIEAMQ	GKLIIQTPDK	NYEIDGSLQQ	VRVHRSYIVN
msa141801.2{399_JM9130013}	DDILLIEAMQ	GKLIIQTPDK	NYEIDGSLQQ	WQDKLPSSQF
msa141801.2{399_1169NT}	DDILLIEAMQ	GKLIIQTPDK	NYEIDGSLQQ	VRVHRSYIVN
msa141801.2{399_CJB110}	DDILLIEAMQ	GKLIIQTPDK	NYEIDGSLQQ	WQDKLPSSQF
Consensus	*****	*****	*****	*****
		201		243
msa141801.2{399_COH1}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg
msa141801.2{399_M732}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg
msa141801.2{399_M781}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg
msa141801.2{399_090}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg
msa141801.2{399_18RS21}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg
msa141801.2{399_2603}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg
msa141801.2{399_A909}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg
msa141801.2{399_H36B}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg
msa141801.2{399_JM9130013}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg
msa141801.2{399_1169NT}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg
msa141801.2{399_CJB110}	INAIKTIEPW	FNQTLQLHLC	NKITVPVSRA	NVKPLKQMLg
Consensus	*****	*****	*****	---

Table 79: Comparative Sequences relating to SAG2150**SEQ ID NO. 7901****STRAIN 2603**

ATGGGAATTGAATTAAAAATGTAAGTTACCTATCAAGCCGGCACTCCTTGAGGG
 CGTGCCTTGTGACGTCATCGAAAATGAAAGATGCTTCTATACCGCGTCATTGGG
 CACACAGGTTCTGAAAATCAACTATTATGCAACTTTTGATGGTTACATATCCCTACA
 AAAGGTGAGGAAATTGCGATGTTTCTATTAAGCAGGGGACAAGAACAAAGGAAATC
 AAATTATAAGGCAAAGTTGTTTAGTTCAATTTCAGAAAGTCAGTTTGAA
 GAGACAGTTAAAGGATGTTCTTGGACCACAAAATTGGTATTCAGATTGAA
 GCTGAAAGGCTGGTCAAGGAAATTAAAGGTTAGTTGCTATCAGTGAGGATTATTGAT
 AAAAATCCATTGCACTTCTGGGGCAGATGAGGCCGGTCTGCTATACCTGTTATT
 GCGATGAAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGATCTAAGGGA
 AGAAAAGAATTAAATGACTCTTTAAAAATCTTCATAAAAAGGAATGACTATCGTCITA
 GTGACTCTTAATGAGCAGTGGGATTATGCTGACTATGTTATGAGGAA
 GGGAAAGTAACTTATCAGGACACCAAAACGATTTCAAGAAGTAGAACATTAGA
 AGTAACACAATTAGGAGTTCCAAAATCACAAGTTGCTCAAAGACTATCTCATAAAGG
 TAAATTACCTAGTTACCAATTACTATTAACGAAATTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7902**STRAIN 090**

GGAATTGAATTAAAAATGTAAGTTACCTATCAAGCC
 GGCACCTCTTGTGAGGGCGTGCCTTGTGACGTCATCGAAAATTGA
 AGATGCTTCTATACCGCGTCATTGGGACACAGGTTCTGAAAATCAA
 CTATTATGCAACTTTGAATGTTTACATATCCCTACAAAAGGTGAGGTA
 ATTTGCGATGATTCTTCTATTAAGCAGGGGACAAGAACAAAGGAAATCAA
 ATTATAAGGCAAAGTTGTTTAGTTCAATTCCAGAAAGTCAGC
 TTGAGAGAGCAGTTAAAGGATGTTCTTGGACCCACAAAATT
 GGTATTCTCAGATTGAGCTGAAGGCTGGCTGAAGGAAATTAAAGGT
 ACTTGGTATCAGTGAGCATTATCGATAAAATCCATTGAACTTCTG
 GAGGGCAGATGAGGCCGGTTGCTATAGCTGTTTTAGCGATGGAACCC
 AAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCTAAGGGAAG
 AAAAGAATTAAATGACTCTTTAAAAATCTTCATAAAAAGGAATGACTA
 TCGCTTGTGACTCATTAAAGCAGATGTAGCGGATTATGCTGACTAT
 GTGATGTTGAAGCAGGGAAAGTAACTTATCAGGACACCAAAACA
 GATTTTCAAGAAGTAGAACTTTAGAAAGTAAACAATTAGGAGTTCCA
 AAATCACAAGTTGCTCAAAGACTATCTCATAAAGGGATTAAATTACCT
 ACTTACCAATTACTATTAACGAAATTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7903**STRAIN A909**

GGAATTGAATTAAAAATGTAAGTTACCTATCAA
 GCGGGCACTCTTGTGAGGGCGTGCCTTGTGACGTCATCGAAAAT
 TGAAGATGCTTCTATACCGCGTCATTGGGACACAGGTTCTGAAAAT
 CAACATTATGCAACTTTGAATGTTTACATATTCCCTACAAAAGGTGAG
 GTATTGCGATGATTCTTCTATTAAGCAGGGACAAGAACAAAGGAAAT
 CAAATTATAAGGCAAAGTTGTTTAGTTCAATTCCAGAAAGTC
 AGCTTGTGAGGAGCAGTTAAAGGATGTTGCTTGGACCCACAAAAT
 TTGGTATTCTCAGATTGAGCTGAAAGGCTGGCTGAAGGAAAATTAAAG
 GTTGTGTTGATCAGTGAGGATTATCGATAAAATCCATTGAACTTT
 CTGGAGGGCAGATGAGGCCGGTTGCTATAGCTGTTTTAGCGATGGA
 CCCAAAGTACTAGTACTAGTACGACGCAACAGCTGGACTTGATCTAAGGG
 AAGAAAAGAATTAAATGACTCTTTAAAAATCTTCATAAAAAGGAATGA
 CTATCGCTTGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGAC
 TAGTGTGATGTTAGAAGCAGGGAAAGTAACTTATCAGGACACCAAA
 GCAGATTCTCAAGAAGTAGAACCTTTAGAAAGTAAACAATTAGGAGTT
 CCAAAATCACAAGTTGCTCAAAGGCTATCTCATAAAGGGATTAAATT
 CCTAGTTACCAATTACTATTAACGAAATTGTGGAGGCTATTAAGCATGGA
 A

SEQ ID NO. 7904**STRAIN H36B**

GGAATTGAATTAAAAATGTAAGTTAC
 CTATCAAGCCGGCACTCTTGTGAGGGCGTGCCTTGTGACGTCATC
 TGAATTGAAAGATGCTTCTATACCGCGTCATTGGGACACAGGTTCT
 GAAAATCAACTAATGCAACTTTGAATGTTTACATATTCCCTACAAA
 AGCTGAGGAAATTGCGATGATTCTTCTATTAAGCAGGGACAAGAAC
 AAGAAATCAAATTATAAGCAGGTTAGTTGATTTCTAATTCC
 GAAGTCAGCTTGAAGGAGCAGTTAAAGGATGTTGCTTGGAC
 ACAAAATTGCTTCTCAGATTGAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAAGGTTAGTGGTATCAGTGAGGATTATCGATAAAATCATT
 GACTTTCTGGGGAGATGAGGCCGGTTGCTATAGCTGGTTTTAGC
 GATGGAACCCAAAGTACTAGTACTAGATGAGCCAACAGCTGGACTTGATC
 CTAAGGGAAGAAAAGAATTATGACTCTTTAAAAATCTCATAAAAAA
 GGATGACTATGCTTGTGACTCACTTAATGGACGATGTAGCGGATT
 TGCTGACTATGTTAGAAGCAGGGAAAGTAACTTATCAGGAC
 AACCAAAGCAGATTCTCAAGAAGTAGAACCTTTAGAAAGTAAACATT
 GGAGTTCCAAAATCACAAGTTGCTCAAAGGCTATCTCATAAAGGGATT
 AAATTACCTAGTTACCAATTACTATTAACGAAATTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7905**STRAIN 18RS21**

GGAATTGAATTAAAAATGTAAGTTAC
 CTATCAAGCCGGCACTCTTGTGAGGGCGTGCCTTGTGACGTCATC

Table 79: Comparative Sequences relating to SAG2150

TGAAAATTGAAGATGCTTCCTATACCGCGTCAATTGGGCACACAGGTTCT
 CGAAAATTCAACTATTGCAACTTTTGAAATGGTTTACATATTCCCTACAAA
 AGGTGAGGTAATTGTCGATGATTTCCTATAAAGCAGGGGACAAGAAC
 AAGAAATCAAATTATAAGGCAAAAGTTGGTTAGTTTCATATTCCA
 GAAAGTCAGCTTTGAAGGACAGTTAAAGGATGTTGCTTTGGACC
 ACAAAATTGGTATTTCAGATTGAAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAGGTTAGGGTATCGAGGATTTCGATAAAATCTCATT
 GAACTTCTGGAGGGCAGATGAGGGGGTGTATAGCTGGTATTAGC
 GATGGAACTATGGATGACCCAAACAGCTGGACTTGATC
 CTAAGGAAAGAAAGATAATGACTCTTTAAAAATCTCATAAAAAAA
 GGAATGACTATCGCTTAGTCACTTAATGGACATGTTAGCGGATTA
 TGTGACTATGTGTTAGGAAAGCTTACAGGAC
 AACCAAAACAGATTTCAGAAGTAGAAACTTTAGAAAGTAAACAAATT
 GGAGTTCCAAAATCACAAGTTGCTCAAAGACTATCTCATAAGGGATT
 AAATTACCTAGTTACCAATTACTATTAAACGAATTGTGGAGGCTTAA
 AGCATGGA

SEQ ID NO. 7906

STRAIN M732

GGAATTGAATTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTGAAGGGCGTGCCTTTGACGTCAATC
 TGAAAATTGAAGATGTTCTATACCGCGTCAATTGGGCACACAGGTTCT
 CGAAAATTCAACTATTGCAACTTTTGAAATGGTTTACATATTCCCTACAAA
 AGGTGAGGTAATTGTCGATGATTTCCTATAAAGCAGGGGACAAGAAC
 AAGAAATCAAATTATAAGGCAAAAGTTGGTTAGTTTCATATTCCA
 GAAAGTCAGCTTTGAAGGACAGTTAAAGGATGTTGCTTTGGACC
 ACAAAATTGGTATTTCAGATTGAAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAGGTTAGGGTATCGAGGATTTCGATAAAATCTCATT
 GAACTTCTGGAGGGCAGATGAGGGGGTGTATAGCTGGTATTAGC
 GATGGAAACCCAAAGTACTGACTGGATGACCCAAACAGCTGGACTTGATC
 CTAAGGAAAGAAAGATAATGACTCTTTAAAAATCTCATAAAAAAA
 GGAATGACTATCGCTTAGTCACTTAATGGACATGTTAGCGGATTA
 TGTGACTATGTGTTAGGAAAGCTTACAGGAC
 AACCAAAACAGATTTCAGAAGTAGAAACTTTAGAAAGTAAACAAATT
 GGAGTTCCAAAATCACAAGTTGCTCAAAGACTATCTCATAAGGGATT
 AAATTACCTAGTTACCAATTACTATTAAACGAATTGTGGAGGCTTAA
 AGCATGGA

SEQ ID NO. 7907

STRAIN COH1

GGAATTGAATTAAAAATGTAAGTTATACCTATCAAGC
 GGCACCTCTTGAAGGGCGTGCCTTTGACGTCAATCTGAAAATTGA
 AGATGTTCTPATACCCGGTCATTGGGCACACAGGTTCTGGAAAATCAA
 CTATTATGCACCTTGAATGGTTACATATTCTCATAAAAGGTGAGGTA
 ATTGTCGATGATTTCCTATAAAGCAGGGACAAGAACAAAGAAC
 ATTATAAGGCAAAAGTTGGTTAGTTCAATTGGACCAAAGGTT
 GGTATTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAATTAAAGGTT
 AGTGGTATCAGTGAGGATTTCGATAAAATCCATTGAACTTTCTG
 GAGGGCAGATGAGGGGGTGTCTAGTGGTATTAGCGATGGAAACCC
 AAAGTACTGACTGGATGAGCCAAACAGCTGGACTTGATCTAAGGGAAAG
 AAAAGAATTAATGACTCTTTAAAAATCTCATAAAAAAGGAATGACTA
 TCGCTCTAGTCACTTAATGGACGATGAGGGATTATGCTGACTAT
 GTGATGTTAGAAGCAGGAAAGTAACCTTATCAGGACAACCAAAACA
 GATTTCAGAAGTAGAAACTTTAGAAAGTAAACAAATTAGGAGTCCC
 AAATCACAAGTTGCTCAAAGACTATCTCATAAGGGATTAAATTACCT
 AGTTACCAATTACTATTAAACGAATTGTGGAGGCTTAAAGCATGGA

SEQ ID NO. 7908

STRAIN M781

GGAATTGAATTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTGAAGGGCGTGCCTTTGACGTCAATC
 TGAAAATTGAAGATGTTCTATACCGCGTCAATTGGGCACACAGGTTCT
 CGAAAATTCAACTATTGCAACTTTGAATGGTTTACATATTCCCTACAAA
 AGGTGAGGTAATTGTCGATGATTTCCTATAAAGCAGGGGACAAGAAC
 AAGAAATCAAATTATAAGGCAAAAGTTGGTTAGTTTCATATTCCA
 GAAAGTCAGCTTTGAAGGACAGTTAAAGGATGTTGCTTTGGACC
 ACAAAATTGGTATTTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
 AATTAAGGTTAGGGTATCGAGGAGTTTCGATAAAATCTCATT
 GAACTTCTGGAGGGCAGATGAGGGGGTGTCTAGTGGTATTAGC
 GATGGAAACCCAAAGTACTGACTGGATGACCCAAACAGCTGGACTTGATC
 CTAAGGAAAGAAAGATAATGACTCTTTAAAAATCTCATAAAAAAA
 GGAATGACTATCGCTTAGTCACTTAATGGACATGTTAGCGGATTA
 TGTGACTATGTGTTAGGAAAGCAGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTCAGAAGTAGAACTTTAGAAAGTAAACAAATT
 GGAGTTCCAAAATCACAAGTTGCTCAAAGACTATCTCATAAGGGATT
 AAATTACCTAGTTACCAATTACTATTAAACGAATTGTGGAGGCTTAA
 AGCATGGA

SEQ ID NO. 7909

STRAIN CJB110

GGAATTGAATTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCACTCCTTGAAGGGCGTGCCTTTGACGTCAATC

Table 79: Comparative Sequences relating to SAG2150

TGAAAATTGAAGATGCTCCTATACCGCGTTCATGGGCACACAGGGTCT
 GAAATCAACTATTATGCAACTTTGAATGGTTACATATTCCCTACAAA
 AGGTGAGGTAAATTCGATGATTTCATATAAGCAGGGACAAGAAC
 AAGAATCAAATTATAAGGCAAAAGTGGTTAGTTTCAATTCCA
 GAAAGTCAGTTTGAGAGACAGTTAAAGGATGTTGCTTTGGACC
 ACAAAATTGCTATTCTCAGATTGAAAGCTGGCTGAAGAAA
 AATTAAAGGTTAGCTGGTATCAGTGAGGATTATTCGATAAAAATCCATT
 GAACTTCTGGAGGGCAGATGAGGCCGGTGTATAGCTGTATTAGC
 GATGGAACCCAAGTACTAGTACTGGATGAGCCAACAGCTGACTGATC
 CTAAGGAAAGAAAATTAAGTACTCTTTAAAAATCTCATAAAAA
 GGAATGACTATCGTCTTAGTGAECTACTAATGACGATGAGCGATT
 TGCTGACTATGTTAGTGAAGCAGGGAAAGTAACCTTATCAGGAC
 AACCAAAACAGATTTCAGGAAAGTAAACCTTAAAGGAAACTTAA
 GGAGTTCCAAAATCAGGTTGCTCAAAGACTATCTCATAAAGGATT
 AAATTACCTAGTTACCAATTACTATTAACGAATTGTGGAGGCTATT
 AGCATGGA

SEQ ID NO. 7910

STRAIN 1169NT

GGAAATTGAATTAAAAATGTA
 GTTATACCTATCAAGCCGGCACTCCTTTGAAGGGCGTGCCTTGTGAC
 GTCAATCTGAAAATTGAAGATGCTCCTATACCGCGTTCATGGGCACAC
 AGGTCTGAAATCAACTATTGCAACTTTGAATGGTTACATATTCTC
 CTACAAAAGGTGAGGTAAATTGCTGATGATTTCATATAAGCAGGGAC
 AAGAACAAAGAACATCAAATTATAAGGCAAAAGTGGTTAGTTTCA
 ATTTCAGGAAAGTCAGCTTTTGAGAGACAGTTAAAGGATGTTGCTT
 TTGACCTTGGTATTCTCAGATTGAGGCTGGCTATAGCTGTT
 GAAGAAAAATTAAAGGTTAGCTGGTATCAGTGAGGATTATTCGATAAAA
 TCCATTGGAATTCTGGAGGGCAGATGAGGCCGGTGTATAGCTGTT
 TTAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGA
 CTGATCCTAAAGGAAAGAACATTAAGTACTCTTTAAAAATCTICA
 TAAAAAGGAATGACTATCGTCTTAGTGAECTACTAATGGACGATGAG
 CGATGACTATGACTATGTTAGAAGCAGGGAAAGTAACCTTA
 TCAGGACAACCAAACAGATTTCAGGAAAGTAGAACTTTAGAAAGTAA
 ACAATTAGGAGTTCCAAAATCAGGTTGCTCAAAGACTATCTCATAA
 AGGAGTTAAATTACCTAGTTACCAATTACTATTAACGAATTGTGGAG
 GCTATTAAAGCATGGA

SEQ ID NO. 7911

STRAIN JM9130013

GGAAATTGAATTAAAAATGTAAGTT
 ATACCTATCAAGCCGGCACTCCTTTGAAGGGCGTGCCTTGTGAC
 ATCTGAAAATTGAAGATGCTCCTATACCGCATTCAATTGGCACACAGG
 TTCTGGAAAATCAACTATTGCAACTTTGAATGGTTACATATTCTCIA
 CAAAGGTGAGGTAAATTGCTGATGATTTCATATAAGCAGGGAC
 AACAAAGAACATCAAATTATAAGGCAAAAGTGGTTAGTTTCAATT
 TCCAGGAAAGTCAGCTTTTGAGAGACAGTTAAAGGATGTTGCTT
 GACCCAAAATTGGTATTCTCAGATTGAAGCTGAAAGCTGGCTGAA
 GAAAATTAAAGGTTAGCTGGTATTAGTGAGGATTATTCGATAAAAATCC
 ATTGGAACCTTGGAGGGCAGATGAGGCCGGTGTATAGCTGTT
 TAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGAGCT
 GATCTAAGGGAAGAACATTAATGACTCTTTAAAAATCTCATAA
 AAAAGGAATGACTATGCTCTAGTACTTAATGGACGATGTTAGCGG
 ATTATGCTGACTATGTTAGTGTATAGCAGGGAAAGTAACCTTATCA
 GGACAACCAAACAGATTTCAGGAAAGTAGAACTTTAGAAAGTAA
 ATTAGGAGTTCCAAAATCAGGTTGCTCAAAGACTATCTCATAAAG
 GATTAATTACCTAGTTACCAATTACTATTAACGAATTGTGGAGGCT
 ATTAAGCATGGA

PRETTY of: /biotmp/msa238454.2{*} May 14, 2003 06:55 ..

msa238454.2{401_A909}	1	50
msa238454.2{401_H36B}	---	GGAATTG AATTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_090}	---	GGAATTG AATTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_1169NT}	---	GGAATTG AATTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_18RS21}	---	GGAATTG AATTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_2603}	atg	GGAATTG AATTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_CJB110}	---	GGAATTG AATTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_COH1}	---	GGAATTG AATTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_M732}	---	GGAATTG AATTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_M781}	---	GGAATTG AATTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
msa238454.2{401_JM9130013}	---	GGAATTG AATTAAAAA TGTAAGTTAT ACCTATCAAG CCGGCACTCC
Consensus	*****	*****

msa238454.2{401_A909}	51	100
msa238454.2{401_H36B}	TTTGAAAGGG CGTGCCTT TTGACGTCAA TCTGAAATT GAAGATGCTT	
msa238454.2{401_090}	TTTGAAAGGG CGTGCCTT TTGACGTCAA TCTGAAATT GAAGATGCTT	
msa238454.2{401_1169NT}	TTTGAAAGGG CGTGCCTT TTGACGTCAA TCTGAAATT GAAGATGCTT	
msa238454.2{401_18RS21}	TTTGAAAGGG CGTGCCTT TTGACGTCAA TCTGAAATT GAAGATGCTT	
msa238454.2{401_2603}	TTTGAAAGGG CGTGCCTT TTGACGTCAA TCTGAAATT GAAGATGCTT	
msa238454.2{401_CJB110}	TTTGAAAGGG CGTGCCTT TTGACGTCAA TCTGAAATT GAAGATGCTT	

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_COH1}	TTTTGAAGGG	CGTGCCTT	TTGACGTcAA	TCTGAAAATT	GAAGATGtTT
msa238454.2{401_M732}	TTTTGAAGGG	CGTGCCTT	TTGACGTcAA	TCTGAAAATT	GAAGATGtTT
msa238454.2{401_M781}	TTTTGAAGGG	CGTGCCTT	TTGACGTcAA	TCTGAAAATT	GAAGATGtTT
msa238454.2{401_JM9130013}	TTTTGAAGGG	CGTGCCTT	TTGACGTcAA	TCTGAAAATT	GAAGATGcTT
Consensus	*****	*****	*****	*****	*****
	101				150
msa238454.2{401_A909}	CCTATACCGC	gTTCATGGG	CACACAGGT	CTGGAAAATC	AACTATTATG
msa238454.2{401_H36B}	CCTATACCGC	gTTCATGGG	CACACAGGT	CTGGAAAATC	AACTATTATG
msa238454.2{401_090}	CCTATACCGC	gTTCATGGG	CACACAGGT	CTGGAAAATC	AACTATTATG
msa238454.2{401_1169NT}	CCTATACCGC	gTTCATGGG	CACACAGGT	CTGGAAAATC	AACTATTATG
msa238454.2{401_18RS21}	CCTATACCGC	gTTCATGGG	CACACAGGT	CTGGAAAATC	AACTATTATG
msa238454.2{401_2603}	CCTATACCGC	gTTCATGGG	CACACAGGT	CTGGAAAATC	AACTATTATG
msa238454.2{401_CJB110}	CCTATACCGC	gTTCATGGG	CACACAGGT	CTGGAAAATC	AACTATTATG
msa238454.2{401_COH1}	CCTATACCGC	gTTCATGGG	CACACAGGT	CTGGAAAATC	AACTATTATG
msa238454.2{401_M732}	CCTATACCGC	gTTCATGGG	CACACAGGT	CTGGAAAATC	AACTATTATG
msa238454.2{401_M781}	CCTATACCGC	attCATGGG	CACACAGGT	CTGGAAAATC	AACTATTATG
msa238454.2{401_JM9130013}	CCTATACCGC	*****	*****	*****	*****
Consensus	*****	*****	*****	*****	*****
	151				200
msa238454.2{401_A909}	CAACTTTG	ATGGTTTACA	TATTCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_H36B}	CAACTTTG	ATGGTTTACA	TATTCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_090}	CAACTTTG	ATGGTTTACA	TATTCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_1169NT}	CAACTTTG	ATGGTTTACA	TATTCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_18RS21}	CAACTTTG	ATGGTTTACA	TATTCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_2603}	CAACTTTG	ATGGTTTACA	TATTCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_CJB110}	CAACTTTG	ATGGTTTACA	TATTCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_COH1}	CAACTTTG	ATGGTTTACA	TATTCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_M732}	CAACTTTG	ATGGTTTACA	TATTCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_M781}	CAACTTTG	ATGGTTTACA	TATTCTACA	AAAGGTGAGG	TAATTGTCGA
msa238454.2{401_JM9130013}	CAACTTTG	ATGGTTTACA	TATTCTACA	AAAGGTGAGG	TAATTGTCGA
Consensus	*****	*****	*****	*****	*****
	201				250
msa238454.2{401_A909}	TGATTTTCT	ATTAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTATAA
msa238454.2{401_H36B}	TGATTTTCT	ATTAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTATAA
msa238454.2{401_090}	TGATTTTCT	ATTAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTATAA
msa238454.2{401_1169NT}	TGATTTTCT	ATTAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTATAA
msa238454.2{401_18RS21}	TGATTTTCT	ATTAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTATAA
msa238454.2{401_2603}	TGATTTTCT	ATTAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTATAA
msa238454.2{401_CJB110}	TGATTTTCT	ATTAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTATAA
msa238454.2{401_COH1}	TGATTTTCT	ATTAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTATAA
msa238454.2{401_M732}	TGATTTTCT	ATTAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTATAA
msa238454.2{401_M781}	TGATTTTCT	ATTAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTATAA
msa238454.2{401_JM9130013}	TGATTTTCT	ATTAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTATAA
Consensus	*****	*****	*****	*****	*****
	251				300
msa238454.2{401_A909}	GCCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTC	GCTTTTGAA
msa238454.2{401_H36B}	GCCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTC	GCTTTTGAA
msa238454.2{401_090}	GCCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTC	GCTTTTGAA
msa238454.2{401_1169NT}	GCCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTC	GCTTTTGAA
msa238454.2{401_18RS21}	GCCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTC	GCTTTTGAA
msa238454.2{401_2603}	GCCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTC	GCTTTTGAA
msa238454.2{401_CJB110}	GCCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTC	GCTTTTGAA
msa238454.2{401_COH1}	GCCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTC	GCTTTTGAA
msa238454.2{401_M732}	GCCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTC	GCTTTTGAA
msa238454.2{401_M781}	GCCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTC	GCTTTTGAA
msa238454.2{401_JM9130013}	GCCAAAAAGT	TGGTTTAGTT	TTTCAATTTC	CAGAAAGTC	GCTTTTGAA
Consensus	*****	*****	*****	*****	*****
	301				350
msa238454.2{401_A909}	GAGACAGTT	TAAAaGATGT	TGCTTTGGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_H36B}	GAGACAGTT	TAAAaGATGT	TGCTTTGGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_090}	GAGACAGTT	TAAAaGATGT	TGCTTTGGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_1169NT}	GAGACAGTT	TAAAaGATGT	TGCTTTGGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_18RS21}	GAGACAGTT	TAAAaGATGT	TGCTTTGGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_2603}	GAGACAGTT	TAAAaGATGT	TGCTTTGGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_CJB110}	GAGACAGTT	TAAAaGATGT	TGCTTTGGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_COH1}	GAGACAGTT	TAAAaGATGT	TGCTTTGGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_M732}	GAGACAGTT	TAAAaGATGT	TGCTTTGGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_M781}	GAGACAGTT	TAAAaGATGT	TGCTTTGGA	CCACAAAATT	TTGGTATTTC
msa238454.2{401_JM9130013}	GAGACAGTT	TAAAaGATGT	TGCTTTGGA	CCACAAAATT	TTGGTATTTC
Consensus	*****	*****	*****	*****	*****
	351				400
msa238454.2{401_A909}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_H36B}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_090}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_1169NT}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_18RS21}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_2603}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_CJB110}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTGGTA
msa238454.2{401_COH1}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTGGTA
msa238454.2{401_M732}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTGGTA
msa238454.2{401_M781}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTGGTA
msa238454.2{401_JM9130013}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTGGTA
Consensus	*****	*****	*****	*****	*****
	401				450
msa238454.2{401_A909}	TcAGTGAGGA	TTTATTGCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_H36B}	TcAGTGAGGA	TTTATTGCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_090}	TcAGTGAGGA	TTTATTGCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_1169NT}	TcAGTGAGGA	TTTATTGCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_18RS21}	TcAGTGAGGA	TTTATTGCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_2603}	TcAGTGAGGA	TTTATTGCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_CJB110}	TcAGTGAGGA	TTTATTGCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_COH1}	TcAGTGAGGA	TTTATTGCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_M732}	TcAGTGAGGA	TTTATTGCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_M781}	TcAGTGAGGA	TTTATTGCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
msa238454.2{401_JM9130013}	TtAGTGAGGA	TTTATTGCGAT	AAAAATCCAT	TTGAACCTTC	TGGAGGGCAG
Consensus	*****	*****	*****	*****	*****
	451				500
msa238454.2{401_A909}	ATGAGGCCGGG	TTGCTATAGC	TGGTATTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_H36B}	ATGAGGCCGGG	TTGCTATAGC	TGGTATTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_090}	ATGAGGCCGGG	TTGCTATAGC	TGGTATTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_1169NT}	ATGAGGCCGGG	TTGCTATAGC	TGGTATTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_18RS21}	ATGAGGCCGGG	TTGCTATAGC	TGGTATTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_2603}	ATGAGGCCGGG	TTGCTATAGC	TGGTATTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_CJB110}	ATGAGGCCGGG	TTGCTATAGC	TGGTATTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_COH1}	ATGAGGCCGGG	TTGCTATAGC	TGGTATTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_M732}	ATGAGGCCGGG	TTGCTATAGC	TGGTATTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_M781}	ATGAGGCCGGG	TTGCTATAGC	TGGTATTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_JM9130013}	ATGAGGCCGGG	TTGCTATAGC	TGGTATTTA	GCGATGGAAC	CCAAAGTACT
Consensus	*****	*****	*****	*****	*****
	501				550
msa238454.2{401_A909}	AGTACTaGAT	GAGCCAACAG	CTGGACTTGA	TCCTAACGGGA	AGAAAAGAAT
msa238454.2{401_H36B}	AGTACTaGAT	GAGCCAACAG	CTGGACTTGA	TCCTAACGGGA	AGAAAAGAAT
msa238454.2{401_090}	AGTACTaGAT	GAGCCAACAG	CTGGACTTGA	TCCTAACGGGA	AGAAAAGAAT
msa238454.2{401_1169NT}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAACGGGA	AGAAAAGAAT
msa238454.2{401_18RS21}	AGTACtgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAACGGGA	AGAAAAGAAT
msa238454.2{401_2603}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAACGGGA	AGAAAAGAAT
msa238454.2{401_CJB110}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAACGGGA	AGAAAAGAAT
msa238454.2{401_COH1}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAACGGGA	AGAAAAGAAT
msa238454.2{401_M732}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAACGGGA	AGAAAAGAAT
msa238454.2{401_M781}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAACGGGA	AGAAAAGAAT
msa238454.2{401_JM9130013}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAACGGGA	AGAAAAGAAT
Consensus	*****	*****	*****	*****	*****
	551				600
msa238454.2{401_A909}	TAATGACTCT	TTTTAAAAAT	CITCATAAAA	AAGGAATGAC	TATCGCTTTA
msa238454.2{401_H36B}	TAATGACTCT	TTTTAAAAAT	CITCATAAAA	AAGGAATGAC	TATCGCTTTA
msa238454.2{401_090}	TAATGACTCT	TTTTAAAAAT	CITCATAAAA	AAGGAATGAC	TATCGCTTTA
msa238454.2{401_1169NT}	TAATGACTCT	TTTTAAAAAT	CITCATAAAA	AAGGAATGAC	TATCGCTTTA
msa238454.2{401_18RS21}	TAATGACTCT	TTTTAAAAAT	CITCATAAAA	AAGGAATGAC	TATCGCTTTA
msa238454.2{401_2603}	TAATGACTCT	TTTTAAAAAT	CITCATAAAA	AAGGAATGAC	TATCGCTTTA
msa238454.2{401_CJB110}	TAATGACTCT	TTTTAAAAAT	CITCATAAAA	AAGGAATGAC	TATCGCTTTA
msa238454.2{401_COH1}	TAATGACTCT	TTTTAAAAAT	CITCATAAAA	AAGGAATGAC	TATCGCTTTA
msa238454.2{401_M732}	TAATGACTCT	TTTTAAAAAT	CITCATAAAA	AAGGAATGAC	TATCGCTTTA
msa238454.2{401_M781}	TAATGACTCT	TTTTAAAAAT	CITCATAAAA	AAGGAATGAC	TATCGCTTTA
msa238454.2{401_JM9130013}	TAATGACTCT	TTTTAAAAAT	CITCATAAAA	AAGGAATGAC	TATCGCTTTA
Consensus	*****	*****	*****	*****	*****
	601				650
msa238454.2{401_A909}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_H36B}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_090}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_1169NT}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_18RS21}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_2603}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_CJB110}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_COH1}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_M732}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_M781}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_JM9130013}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
Consensus	*****	*****	*****	*****	*****
	651				700
msa238454.2{401_A909}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAG	CAGATTTTC
msa238454.2{401_H36B}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAG	CAGATTTTC
msa238454.2{401_090}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAG	CAGATTTTC
msa238454.2{401_1169NT}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAG	CAGATTTTC
msa238454.2{401_18RS21}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAG	CAGATTTTC

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_2603}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTC
msa238454.2{401_CJB110}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTC
msa238454.2{401_COH1}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTC
msa238454.2{401_M732}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTC
msa238454.2{401_M781}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTC
msa238454.2{401_JM9130013}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTC
Consensus	*****	*****	*****	*****	*****
	701				750
msa238454.2{401_A909}	AAGAAGTACA	ACTTTTAGAA	AGTAACAAAT	TAGGAGTTCC	AAAAATCACC
msa238454.2{401_H36B}	AAGAAGTACA	ACTTTTAGAA	AGTAACAAAT	TAGGAGTTCC	AAAAATCACC
msa238454.2{401_090}	AAGAAGTACA	ACTTTTAGAA	AGTAACAAAT	TAGGAGTTCC	AAAAATCACC
msa238454.2{401_1169NT}	AAGAAGTACA	ACTTTTAGAA	AGTAACAAAT	TAGGAGTTCC	AAAAATCACC
msa238454.2{401_18RS21}	AAGAAGTACA	ACTTTTAGAA	AGTAACAAAT	TAGGAGTTCC	AAAAATCACC
msa238454.2{401_2603}	AAGAAGTACA	ACTTTTAGAA	AGTAACAAAT	TAGGAGTTCC	AAAAATCACC
msa238454.2{401_CJB110}	AAGAAGTACA	ACTTTTAGAA	AGTAACAAAT	TAGGAGTTCC	AAAAATCACC
msa238454.2{401_COH1}	AAGAAGTACA	ACTTTTAGAA	AGTAACAAAT	TAGGAGTTCC	AAAAATCACC
msa238454.2{401_M732}	AAGAAGTACA	ACTTTTAGAA	AGTAACAAAT	TAGGAGTTCC	AAAAATCACC
msa238454.2{401_M781}	AAGAAGTACA	ACTTTTAGAA	AGTAACAAAT	TAGGAGTTCC	AAAAATCACC
msa238454.2{401_JM9130013}	AAGAAGTACA	ACTTTTAGAA	AGTAACAAAT	TAGGAGTTCC	AAAAATCACC
Consensus	*****	*****	*****	*****	*****
	751				800
msa238454.2{401_A909}	AAAGCTATC	TCATAAGGGA	TTAAATTTC	CTAGTTTACC	
msa238454.2{401_H36B}	AAAGCTATC	TCATAAGGGA	TTAAATTTC	CTAGTTTACC	
msa238454.2{401_090}	AAAGCTATC	TCATAAGGGA	TTAAATTTC	CTAGTTTACC	
msa238454.2{401_1169NT}	AAAGCTATC	TCATAAGGGA	TTAAATTTC	CTAGTTTACC	
msa238454.2{401_18RS21}	AAAGCTATC	TCATAAGGGA	TTAAATTTC	CTAGTTTACC	
msa238454.2{401_2603}	AAAGCTATC	TCATAAGGGA	TTAAATTTC	CTAGTTTACC	
msa238454.2{401_CJB110}	AAAGCTATC	TCATAAGGGA	TTAAATTTC	CTAGTTTACC	
msa238454.2{401_COH1}	AAAGCTATC	TCATAAGGGA	TTAAATTTC	CTAGTTTACC	
msa238454.2{401_M732}	AAAGCTATC	TCATAAGGGA	TTAAATTTC	CTAGTTTACC	
msa238454.2{401_M781}	AAAGCTATC	TCATAAGGGA	TTAAATTTC	CTAGTTTACC	
msa238454.2{401_JM9130013}	AAAGCTATC	TCATAAGGGA	TTAAATTTC	CTAGTTTACC	
Consensus	*****	*****	*****	*****	*****
	801				840
msa238454.2{401_A909}	AATTACTATT	AACGAATTTC	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_H36B}	AATTACTATT	AACGAATTTC	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_090}	AATTACTATT	AACGAATTTC	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_1169NT}	AATTACTATT	AACGAATTTC	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_18RS21}	AATTACTATT	AACGAATTTC	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_2603}	AATTACTATT	AACGAATTTC	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_CJB110}	AATTACTATT	AACGAATTTC	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_COH1}	AATTACTATT	AACGAATTTC	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_M732}	AATTACTATT	AACGAATTTC	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_M781}	AATTACTATT	AACGAATTTC	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_JM9130013}	AATTACTATT	AACGAATTTC	TGGAGGCTAT	TAAGCATGGA	
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 7912

STRAIN 2603 frame: 1

MGIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
 ERLAEEKLRLLVGISEDLFDKNPFELSGGQMRRAIAIGILAMEPKVVLVLDPTAGLDPKGR
 KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVVLEAGKVTLSGQPQKQIFQEVELLES
 KQLGVVKITKFAQRSLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7913

STRAIN 090 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
 ERLAEEKLRLLVGISEDLFDKNPFELSGGQMRRAIAIGILAMEPKVVLVLDPTAGLDPKGR
 KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVVLEAGKVTLSGQPQKQIFQEVELLES
 KQLGVVKITKFAQRSLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7914

STRAIN 090 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
 ERLAEEKLRLLVGISEDLFDKNPFELSGGQMRRAIAIGILAMEPKVVLVLDPTAGLDPKGR
 KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVVLEAGKVTLSGQPQKQIFQEVELLES
 KQLGVVKITKFAQRSLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7915

STRAIN H36B frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVIVDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFGISQIEA
 ERLAEEKLRLLVGISEDLFDKNPFELSGGQMRRAIAIGILAMEPKVVLVLDPTAGLDPKGR
 KELMTLFKNLHKKGMTIVLVTHLMDDVADYADYVVLEAGKVTLSGQPQKQIFQEVELLES
 KQLGVVKITKFAQRSLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7916

Table 79: Comparative Sequences relating to SAG2150

STRAIN 18RS21 frame: 1
 GIEFKNVSYTYQAGTPFEGRALFDVNLKI EDASYTA FIGHTGSGKSTIMQLLNLH I PTK
 GEVI VDDFSI KAGDKNKEI KFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFG I SQIEA
 ERLAEEKLR LVG I SEDLF DKNPFELSGGQMRRAIA GILAMEPKVVLVDEPTAGLDPKGR
 KELMTLFKNLHKKGMTI VLVTI HLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
 KQLGVPKITKFAQRSLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7917

STRAIN M732 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKI EDVSYT A FIGHTGSGKSTIMQLLNLH I PTK
 GEVI VDDFSI KAGDKNKEI KFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFG I SQIEA
 ERLAEEKLR LVG I SEDLF DKNPFELSGGQMRRAIA GILAMEPKVVLVDEPTAGLDPKGR
 KELMTLFKNLHKKGMTI VLVTI HLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
 KQLGVPKITKFAQRSLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7918

STRAIN COH1 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKI EDVSYT A FIGHTGSGKSTIMQLLNLH I PTK
 GEVI VDDFSI KAGDKNKEI KFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFG I SQIEA
 ERLAEEKLR LVG I SEDLF DKNPFELSGGQMRRAIA GILAMEPKVVLVDEPTAGLDPKGR
 KELMTLFKNLHKKGMTI VLVTI HLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
 KQLGVPKITKFAQRSLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7919

STRAIN M781 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKI EDVSYT A FIGHTGSGKSTIMQLLNLH I PTK
 GEVI VDDFSI KAGDKNKEI KFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFG I SQIEA
 ERLAEEKLR LVG I SEDLF DKNPFELSGGQMRRAIA GILAMEPKVVLVDEPTAGLDPKGR
 KELMTLFKNLHKKGMTI VLVTI HLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
 KQLGVPKITKFAQRSLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7920

STRAIN CJB110 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKI EDASYTA FIGHTGSGKSTIMQLLNLH I PTK
 GEVI VDDFSI KAGDKNKEI KFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFG I SQIEA
 ERLAEEKLR LVG I SEDLF DKNPFELSGGQMRRAIA GILAMEPKVVLVDEPTAGLDPKGR
 KELMTLFKNLHKKGMTI VLVTI HLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
 KQLGVPKITKFAQRSLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7921

STRAIN 1169NT frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKI EDASYTA FIGHTGSGKSTIMQLLNLH I PTK
 GEVI VDDFSI KAGDKNKEI KFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFG I SQIEA
 ERLAEEKLR LVG I SEDLF DKNPFELSGGQMRRAIA GILAMEPKVVLVDEPTAGLDPKGR
 KELMTLFKNLHKKGMTI VLVTI HLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
 KQLGVPKITKFAQRSLSHKGGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7922

STRAIN JM9130013 frame: 1

GIEFKNVSYTYQAGTPFEGRALFDVNLKI EDASYTA FIGHTGSGKSTIMQLLNLH I PTK
 GEVI VDDFSI KAGDKNKEI KFIRQKVGLVFQFPESQLFEETVLKDVAFGPQNFG I SQIEA
 ERLAEEKLR LVG I SEDLF DKNPFELSGGQMRRAIA GILAMEPKVVLVDEPTAGLDPKGR
 KELMTLFKNLHKKGMTI VLVTI HLMDDVADYADYVYVLEAGKVTLSGQPKQIFQEVELLES
 KQLGVPKITKFAQRSLSHKGGLNLPSPITINEFVEAIKHG

PRETTY of: /biotmp/msa238553.2{ *} May 14, 2003 06:55 ..

msa238553.2{401_090}	1	-GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
msa238553.2{401_1169NT}		-GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
msa238553.2{401_18RS21}		-GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
msa238553.2{401_2603}		-GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
msa238553.2{401_CJB110}		-GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
msa238553.2{401_H36B}		-GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
msa238553.2{401_JM9130013}		-GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
msa238553.2{401_COH1}		-GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDvSYTAFIG HTGSGKSTIM
msa238553.2{401_M732}		-GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDvSYTAFIG HTGSGKSTIM
msa238553.2{401_M781}		-GIEFKNVSY TYQAGTPFEG RALFDVNLKI EDvSYTAFIG HTGSGKSTIM
Consensus		***** * ***** * ***** * ***** * *****
	51	
msa238553.2{401_090}	51	QLNLGLH I PT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_1169NT}		QLNLGLH I PT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_18RS21}		QLNLGLH I PT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_2603}		QLNLGLH I PT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_CJB110}		QLNLGLH I PT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_H36B}		QLNLGLH I PT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_JM9130013}		QLNLGLH I PT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_COH1}		QLNLGLH I PT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_M732}		QLNLGLH I PT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_M781}		QLNLGLH I PT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
	100	

Table 79: Comparative Sequences relating to SAG2150

Consensus	*****	*****	*****	*****	*****	*****	*****
msa238553.2{401_090}	101						150
msa238553.2{401_1169NT}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ		
msa238553.2{401_18RS21}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ		
msa238553.2{401_2603}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ		
msa238553.2{401_CJB110}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ		
msa238553.2{401_H36B}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ		
msa238553.2{401_JM9130013}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ		
msa238553.2{401_COH1}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ		
msa238553.2{401_M732}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ		
msa238553.2{401_M781}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa238553.2{401_090}	151						200
msa238553.2{401_1169NT}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKEMLTLPKN	LHKKGMTIVL		
msa238553.2{401_18RS21}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKEMLTLPKN	LHKKGMTIVL		
msa238553.2{401_2603}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKEMLTLPKN	LHKKGMTIVL		
msa238553.2{401_CJB110}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKEMLTLPKN	LHKKGMTIVL		
msa238553.2{401_H36B}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKEMLTLPKN	LHKKGMTIVL		
msa238553.2{401_JM9130013}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKEMLTLPKN	LHKKGMTIVL		
msa238553.2{401_COH1}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKEMLTLPKN	LHKKGMTIVL		
msa238553.2{401_M732}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKEMLTLPKN	LHKKGMTIVL		
msa238553.2{401_M781}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKEMLTLPKN	LHKKGMTIVL		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa238553.2{401_090}	201						250
msa238553.2{401_1169NT}	VTHLMDDVAD	YADYYVYLEA	GKVTLSGQPK	QIFQEVELLE	SKQLGVPKIT		
msa238553.2{401_18RS21}	VTHLMDDVAD	YADYYVYLEA	GKVTLSGQPK	QIFQEVELLE	SKQLGVPKIT		
msa238553.2{401_2603}	VTHLMDDVAD	YADYYVYLEA	GKVTLSGQPK	QIFQEVELLE	SKQLGVPKIT		
msa238553.2{401_CJB110}	VTHLMDDVAD	YADYYVYLEA	GKVTLSGQPK	QIFQEVELLE	SKQLGVPKIT		
msa238553.2{401_H36B}	VTHLMDDVAD	YADYYVYLEA	GKVTLSGQPK	QIFQEVELLE	SKQLGVPKIT		
msa238553.2{401_JM9130013}	VTHLMDDVAD	YADYYVYLEA	GKVTLSGQPK	QIFQEVELLE	SKQLGVPKIT		
msa238553.2{401_COH1}	VTHLMDDVAD	YADYYVYLEA	GKVTLSGQPK	QIFQEVELLE	SKQLGVPKIT		
msa238553.2{401_M732}	VTHLMDDVAD	YADYYVYLEA	GKVTLSGQPK	QIFQEVELLE	SKQLGVPKIT		
msa238553.2{401_M781}	VTHLMDDVAD	YADYYVYLEA	GKVTLSGQPK	QIFQEVELLE	SKQLGVPKIT		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa238553.2{401_090}	251						280
msa238553.2{401_1169NT}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG				
msa238553.2{401_18RS21}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG				
msa238553.2{401_2603}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG				
msa238553.2{401_CJB110}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG				
msa238553.2{401_H36B}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG				
msa238553.2{401_JM9130013}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG				
msa238553.2{401_COH1}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG				
msa238553.2{401_M732}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG				
msa238553.2{401_M781}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG				
Consensus	*****	*****	*****	*****	*****	*****	*****

Table 80: Comparative Sequences relating to SAG1266**SEQ ID NO. 8001****STRAIN 2603**

GTGAACCACTTAACTTAACCTCAGTAAAGAAAATATAGCTAAAATAGATTGACTTTCTT
 ATGGGGCACTTAAATGCAAATTAITCGTTGAAAGAATTAGTAGATGAACATAAAATTC
 AAAGAACGGACAGTAAAGGTGGTCCAAAAAAAGACTCTCGAACGATAAAATCTTGAC
 GATGGCCTTATCAATAAACATATAGTTCCCTAGATCGTCAGATTATAACATTATCCA
 GTCATTCATITGCTAATGTACATGACTACTGTTTATAACCCAGAAAAGGGAGAATTCT
 AAAAATATAGAATATACAACACTACAGTGATTATGAAATGGAGTTAACATGAGGATAGG
 CAACAATTTCAAAATATGAAACAGTTGATTAGACCAATIGATACTTGTGATATT
 AATATTGACTACATTCATCATATTAAACAATA

SEQ ID NO. 8002**STRAIN H36B**

AACCACTTAACTTCAGTAAAGAAAATATAGCT
 AAAATAGATTGACTTTCTTAAATGAGGCACCTTAATGCAAATATTGCTT
 GAAAGAATTAGTAGATGAACATAAAATTCAAAAGAACCTGGACAGTAAAG
 GTGGTCCAAAAAAAGACTCTCGAACGATAAAATCTTGACGATGGCCTT
 ATCAATTAAACATATAGTTCCCTAGATCGTCAGATTATAACATTATCCA
 AGTCATTCCATTGCTAATGTACATGACTACTGTTTATAACCCAGAAA
 GGGAGAATTCTAAAATATAGAATATACAACACTACAGTGATTATGAAATG
 GAGTTAAATCAATGAGGATAGGCAACAAATTCTAAAATATGAAACAGTTG
 TTAGACCAATTGAGTACTTGTGATATTAAATATTGATGACTACATT
 CATCATATTAAACAATA

SEQ ID NO. 8003**STRAIN 18RS21**

AACCACTTAACTTCAGTAAAGAAAATATAG
 CTTAAATGATTGACTTTCTTAAATGAGGCACCTTAATGCAAATATTGCTT
 TTGAAAGAATTAGTAGATGAACATAAAATTCAAAAGAACCTGGACAGTAA
 AGGTGGTCCAAAAAAAGACTCTCGAACGATAAAATCTTGACGATGGC
 TTATCAATAAACATATAGTTCCCTAGATCGTCAGATTATAACATTATC
 CAAGTCATTCCATTGCTAATGTACATGACTACTGTTTATAACCCAGAAA
 AAGGGAGAATTCTAAAATATAGAATATACAACACTACAGTGATTATGAA
 TGAGGTTAAATCAATGAGGATAGGCAACAAATTCTAAAATATGAAACAGTT
 GATTAGACCAATTGAGTACTTGTGATATTAAATATTGATGACTACAT
 TTCATCATATTAAACAATA

PRETTY of: /biotmp/msa49308.2{*} February 19, 2003 07:45 ..

msa49308.2{408_18RS21}	1	50
msa49308.2{408_2603}	---AACCACT TACTTAACCT CAGTAAAGAA AATATAGCTA AAATAGATT	
msa49308.2{408_H36B}	gtgAACCACT TACTTAACCT CAGTAAAGAA AATATAGCTA AAATAGATT	
Consensus	~~~AACCACT TACTTAACCT CAGTAAAGAA AATATAGCTA AAATAGATT	*****
msa49308.2{408_18RS21}	51	100
msa49308.2{408_2603}	TGACTTTCTT AATGAGGCAC TTAATGCAA TATTGTTTG AAAGAATTAG	
msa49308.2{408_H36B}	TGACTTTCTT AATGAGGCAC TTAATGCAA TATTGTTTG AAAGAATTAG	
Consensus	*****	*****
msa49308.2{408_18RS21}	101	150
msa49308.2{408_2603}	TAGATGAAC TAAAATTC AAAAAGACTGG ACAGTAAAGG TTGGTCCAAA	
msa49308.2{408_H36B}	TAGATGAAC TAAAATTC AAAAAGACTGG ACAGTAAAGG TTGGTCCAAA	
Consensus	*****	*****
msa49308.2{408_18RS21}	151	200
msa49308.2{408_2603}	AAAGACTCTC GAACGATAAA AATCTTGTAC GATGCCCTTA TCAATAAACAA	
msa49308.2{408_H36B}	AAAGACTCTC GAACGATAAA AATCTTGTAC GATGCCCTTA TCAATAAACAA	
Consensus	*****	*****
msa49308.2{408_18RS21}	201	250
msa49308.2{408_2603}	TATAGTTCC CTAGATCGTG CAGATTATAA CATTATCCAA GTCATTCCAT	
msa49308.2{408_H36B}	TATAGTTCC CTAGATCGTG CAGATTATAA CATTATCCAA GTCATTCCAT	
Consensus	*****	*****
msa49308.2{408_18RS21}	251	300
msa49308.2{408_2603}	TTGCTAATGT ACATGACTA CTGTTTTAA TACCAAGAAAG GGAGAATTCT	
msa49308.2{408_H36B}	TTGCTAATGT ACATGACTA CTGTTTTAA TACCAAGAAAG GGAGAATTCT	
Consensus	*****	*****
msa49308.2{408_18RS21}	301	350
msa49308.2{408_2603}	AAAAATTATA GAATATACAA CTACAGTGTAT TATGAAATGG AGTTAACAA	
msa49308.2{408_H36B}	AAAAATTATA GAATATACAA CTACAGTGTAT TATGAAATGG AGTTAACAA	
Consensus	*****	*****

Table 80: Comparative Sequences relating to SAG1266

msa49308.2{408_18RS21}	351	TGAGGATAGG CAACAATTT CAAAATATGA AACAGTTGAT TTAGACCAAT	400
msa49308.2{408_2603}		TGAGGATAGG CAACAATTT CAAAATATGA AACAGTTGAT TTAGACCAAT	
msa49308.2{408_H36B}		TGAGGATAGG CAACAATTT CAAAATATGA AACAGTTGAT TTAGACCAAT	
Consensus		*****	*****
msa49308.2{408_18RS21}	401	TGATACTTGT TGATATTTTG AATATTGATG ACTACATTTC ATCATATTAA	450
msa49308.2{408_2603}		TGATACTTGT TGATATTTTG AATATTGATG ACTACATTTC ATCATATTAA	
msa49308.2{408_H36B}		TGATACTTGT TGATATTTTG AATATTGATG ACTACATTTC ATCATATTAA	
Consensus		*****	*****
msa49308.2{408_18RS21}	451	ACAATA	
msa49308.2{408_2603}		ACAATA	
msa49308.2{408_H36B}		ACAATA	
Consensus		*****	
SEQ ID NO. 8004			
STRAIN 2603 frame: 1			
VNHLLNLSKENIAKIDFDLNEALNANIRLKEVLDELKISKELDSKGWSKKDSRTIKILYD			
DGLINKHIVSLDRADYNIIQVIPFANVHVLLFLIPERENSKNYRIYNYSDYEMELINEDRQ			
QQFSKYETVLDLQLILVDIFNIDDYISSYLTI			
SEQ ID NO. 8005			
STRAIN H36B frame: 1			
NHLLNLSKENIAKIDFDLNEALNANIRLKEVLDELKISKELDSKGWSKKDSRTIKILYD			
GLINKHIVSLDRADYNIIQVIPFANVHVLLFLIPERENSKNYRIYNYSDYEMELINEDRQ			
QQFSKYETVLDLQLILVDIFNIDDYISSYLTI			
SEQ ID NO. 8006			
STRAIN 18RS21 frame: 1			
NHLLNLSKENIAKIDFDLNEALNANIRLKEVLDELKISKELDSKGWSKKDSRTIKILYD			
GLINKHIVSLDRADYNIIQVIPFANVHVLLFLIPERENSKNYRIYNYSDYEMELINEDRQ			
QQFSKYETVLDLQLILVDIFNIDDYISSYLTI			
PRETTY of: /biotmp/msa49418.2{*} February 19, 2003 07:47 ..			
msa49418.2{408_18RS21}	1	-NHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK	50
msa49418.2{408_2603}		-NHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK	
msa49418.2{408_H36B}		-NHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK	
Consensus		*****	*****
msa49418.2{408_18RS21}	51	KDSRTIKILY DGLINKHIVS LDRADYNIIQ VIPFANVHVL LFLIPERENS	100
msa49418.2{408_2603}		KDSRTIKILY DGLINKHIVS LDRADYNIIQ VIPFANVHVL LFLIPERENS	
msa49418.2{408_H36B}		KDSRTIKILY DGLINKHIVS LDRADYNIIQ VIPFANVHVL LFLIPERENS	
Consensus		*****	*****
msa49418.2{408_18RS21}	101	KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDYISSYL	150
msa49418.2{408_2603}		KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDYISSYL	
msa49418.2{408_H36B}		KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDYISSYL	
Consensus		*****	*****
msa49418.2{408_18RS21}	151	TI	
msa49418.2{408_2603}		TI	
msa49418.2{408_H36B}		TI	
Consensus		**	

Table 81: Comparative Sequences relating to SAG0011**SEQ ID NO. 8101****STRAIN 090**

```

AGCAAGCCTAATGTTGTTCAAGTTAAA
TAATCAATATAATTAAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAAATCGTTAATGGGTTGGGTTCTTATTTGTCACTG
CTTTTATTTATTTACCCACTTATAATTAGTTAAGAGTTACAGAACCTT
ACAAGAACGTCGTCAGAAGTTAACTTAAACGAAAGACTATCAGACAT
TAACTAATAGAACGTTAGAGACCAGAAGTTACTAGCAAACAACTAAAAAA
CCAGATTACGTTAAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
CGCGAAATGATTIACCCATTACAGACCTTTACCAAAA

```

SEQ ID NO. 8102**STRAIN A909**

```

AGCAAGCCTAATGTTGTTCAAGTTAAAATAATCAATA
TAATCAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGGAGTTACGCCGAAAAAAATCG
TTTATGGGTTGGGTTCTTATTTGTCACTGTTATTATTTACCCACTTATAATT
AGTTAAGAGTTACAGAACCTTACAAGAACGTCGTCAGAAGTTAGTAAACGAAAGA
CTATCAGACATTAACTAATAGAACGTTAGAGACCAGAAGTTACTAGCAAACAACTAAAAAA
TCCAGATTACGTTAAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGACCGGGCGAAAT
GATTIACCCATTACAGACCT

```

SEQ ID NO. 8103**STRAIN H36B**

```

AGCAAGCCTAATGTTGTTCAAGTTAAA
TAATCAATATAATTAAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAAATCGTTAATGGGTTGGGTTCTTATTTGTCACTG
CTTTTATTTATTTACCCACTTATAATTAGTTAAGAGTTACAGAACCTT
ACAAGAACGTCGTCAGAAGTTAGTAAACGAAAGACTATCAGACAT
TAACTAATAGAACGTTAGAGACCAGAAGTTACTAGCAAACAACTAAAAAA
CCAGATTACGTTAAAAAATATGCTCGAGCTAAGTATTATTTCTCTAAGAC
CGCGAAATGATTIACCCATTACAGACCTTTACCAAAA

```

SEQ ID NO. 8104**STRAIN 18RS21**

```

AGCAAGCCTAATGTTGTTCAAGTTAAAATAATCAATATAACGATGAGAATCTAAAAAA
CGTTACGAAGCTGAGGAGTTACGCCGAAAAAAATCGTTAATGGGTTGGGTTCTTATTTT
GTCACTGTTATTTATTTACCCACTTATAATTAGTTAAGAGTTACAGAACCTTACAA
GAACGTCGTCAGAAGTTGTAACGAAAGACTATCAGACATTAACTAATAGAAC
GAGAACGAGTTGCTAGCAAACAACTAAAAATCCAGATTACGTTCAAATATGCT
CGAGCTAAGTATTATTTCTCTAAGACCGGGCGAAATGATTIACCCATTACAGACCTTTA
CCA

```

SEQ ID NO. 8105**STRAIN M732**

```

AGCAAGCCTAATGTTGTTCAAGTTAAA
TAATCAATATAATTAAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAAATCGTTAATGGGTTGGGTTCTTATTTGTCACTG
CTTTTATTTATTTACCCACTTATAATTAGTTAAGAGTTACAGAACCTT
ACAAGAACGTCGTCAGAAGTTGTAACGAAAGACTATCAGACAT
TAACTAATAGAACGTTAGAGACCAGAAGTTACTAGCAAACAACTAAAAAA
CCAGATTACGTTAAAAAATATGCTCGAGCGAAGTATTATTTCTCTAAGAC
CGCGAAATGATTIACCCATTACAGACCTTTACCAAAA

```

SEQ ID NO. 8106**STRAIN COH1**

```

AGCAAGCCTAATGTTGTTCAAGTTAAAATAATC
AATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGGAGTTA
CGCGAAAAAAATCGTTAATGGGTTGGGTTCTTATTTGTCACTGTT
ATTATTTACCCACTTATAATTAGTTAAGAGTTACAGAACCTTACAA
AACGTCGTCAGAAGTTGTAACGAAAGACTATCAGACATTAACT
AATAGAACGTTAGAGACCAGAAGTTACTAGCAAACAACTAAAAATCCAGA
TTACGTTCAAATATGCTCGAGCGAAGTATTATTTCTCTAAGACCGGGCG
AAATGATTIACCCATTACAGACCTTTACCAAAA

```

SEQ ID NO. 8107**STRAIN M781**

```

AGCaAGCCTAATGTTGTTCAAGTTAAAATAATC
AATAATCAATATAATTAAACGATGAGAATCTAAAAAAACGTTACGAAGCTG
AGGAGTTACGCCGAAAAAAATCGTTAATGGGTTGGGTTCTTATTTGT
ATGCTTTATTTATTTACCCACTTATAATTAGTTAAGAGTTACAGAAC
TTACAAGAACGTCGTCAGAAGTTGTAACGAAAGACTATCAGA
CATTAACAACTAATAGAACGTTAGAGACCAGAAGTTACTAGCAAACAACTAAA
AAATCCAGATTACGTTAAAAAATATGCTCGAGCGAAGTATTATTTCTCTAA
GACCGGGCGAAATGATTIACCCATTACAGACCTTTACCAAAA

```

SEQ ID NO. 8108**STRAIN CJB110**

```

AGCAAGCCTAATGTTGTTCAAGTTAAAATAATC
AATATTAACGATGAGAATCTAAAAAAACGTTACGAAGCTGAGGAGTTA
CGCGAAAAAAATCGTTAATGGGTTGGGTTCTTATTTGTCACTGTT
ATTATTTACCCACTTATAATTAGTTAAGAGTTACAGAACCTTACAAG

```

Table 81: Comparative Sequences relating to SAG0011

AACTCGTCAGAAGTTGAAAAATAACGAAAGACTATCAGACATTAAC
AATAGAACCTGAGAACCCAGAAGTTGCTAGCAAAACAATTAAAATCCAGA
TTACGTTCAAAAATATGCTCGAGCTAAGTATTATTCCTCTAAGACC GGCG
AAATGATTCTTACCCATTACCGAGCTTTACCAAAA

SEQ ID NO. 8109

STRAIN 1169NT

AGCAAGCCTAATGTTGTTCAAGTTAAA

SEQ ID NO. 8110

STRAIN JM9130013

AGCaAGCCTAATGTTGTTCAAGTTAAA

ACCGAACCCTTAACTGTTTATCTTAA
TAATCAATATAATTCAGATGAGAACCTAAAAAAACGGTTACGAAGCTGAGG
AGTTACGCCAATTTATCGTTAATGGGTTTATTATTTTGTCATG
CTTTATTTATTTATCCCACTTAAATAATTAGTAAAGAGTTACACAAGATT
ACAGAACGCTCTCAAGAGTTGTAAAATTAAACGAAAGACTATCACGACAT
TAATCTTAAGAACCTGAGAACCCAGAAAGTTACTACCAAAACATAAAAT
CCAGATTACGTCAAAAATATGCTCGGACGGAAGTATTATTTCTTAAGAC
CCCCAAAATGATTACCCATTACCGACCTTACACAAAA

SEQ ID NO. 8111

STRAIN 2603

PRETTY of: /biotmp/msa25643.2{*} . April 29, 2002 05:59 ...

	1	50
msa25643.2{418_COH1}	AGCAAGCTA	ATGTTGTTCA
msa25643.2{418_M732}	AGCAAGCTA	ATGTTGTTCA
msa25643.2{418_M781}	AGCAAGCTA	ATGTTGTTCA
msa25643.2{418_JM9130013}	AGCAAGCTA	ATGTTGTTCA
msa25643.2{418_090}	AGCAAGCTA	ATGTTGTTCA
msa25643.2{418_18RS21}	AGCAAGCTA	ATGTTGTTCA
msa25643.2{418_2603}	AGCAAGCTA	ATGTTGTTCA
msa25643.2{418_CJB2110}	AGCAAGCTA	ATGTTGTTCA
msa25643.2{418_1169NT}	AGCAAGCTA	ATGTTGTTCA
msa25643.2{418_A909}	AGCAAGCTA	ATGTTGTTCA
msa25643.2{418_H36B}	AGCAAGCTA	ATGTTGTTCA
Consensus	*****	*****

	51	100			
msa25643.2{418_COH1}	TCTAAAAAAA	CGTTACGAAG	CTGAGGGAGTT	ACGCCGAAAA	AATCGTTTAA
msa25643.2{418_M732}	TCTAAAAAAA	CGTTACGAAG	CTGAGGGAGTT	ACGCCGAAAA	AATCGTTTAA
msa25643.2{418_M781}	TCTAAAAAAA	CGTTACGAAG	CTGAGGGAGTT	ACGCCGAAAA	AATCGTTTAA
msa25643.2{418_JM9130013}	TCTAAAAAAA	CGTTACGAAG	CTGAGGGAGTT	ACGCCGAAAA	AATCGTTTAA
msa25643.2{418_O90}	TCTAAAAAAA	CGTTACGAAG	CTGAGGGAGTT	ACGCCGAAAA	AATCGTTTAA
msa25643.2{418_18RS21}	TCTAAAAAAA	CGTTACGAAG	CTGAGGGAGTT	ACGCCGAAAA	AATCGTTTAA
msa25643.2{418_2603}	TCTAAAAAAA	CGTTACGAAG	CTGAGGGAGTT	ACGCCGAAAA	AATCGTTTAA
msa25643.2{418_CJB110}	TCTAAAAAAA	CGTTACGAAG	CTGAGGGAGTT	ACGCCGAAAA	AATCGTTTAA
msa25643.2{418_1169NT}	TCTAAAAAAA	CGTTACGAAG	CTGAGGGAGTT	ACGCCGAAAA	AATCGTTTAA
msa25643.2{418_A909}	TCTAAAAAAA	CGTTACGAAG	CTGAGGGAGTT	ACGCCGAAAA	AATCGTTTAA
msa25643.2{418_H36B}	TCTAAAAAAA	CGTTACGAAG	CTGAGGGAGTT	ACGCCGAAAA	AATCGTTTAA
	*****	*****	*****	*****	*****

	101	150			
msa25643.2{418_COH1}	TGGGTTGGGT	TCTTATTTTT	GTCATGCTTT	TATTATTTTT	ACCCACTTAT
msa25643.2{418_M732}	TGGGTTGGGT	TCTTATTTTT	GTCATGCTTT	TATTATTTTT	ACCCACTTAT
msa25643.2{418_M781}	TGGGTTGGGT	TCTTATTTTT	GTCATGCTTT	TATTATTTTT	ACCCACTTAT
msa25643.2{418_JM9130013}	TGGGTTGGGT	TCITATTTTT	GTCATGCTTT	TATTATTTTT	ACCCACTTAT
msa25643.2{418_090}	TGGGTTGGGT	TCTTATTTTT	GTCATGCTTT	TATTATTTTT	ACCCACTTAT
msa25643.2{418_18RS21}	TGGGTTGGGT	TCTTATTTTT	GTCATGCTTT	TATTATTTTT	ACCCACTTAT
msa25643.2{418_2603}	TGGGTTGGGT	TCTTATTTTT	GTCATGCTTT	TATTATTTTT	ACCCACTTAT
msa25643.2{418_CJB110}	TGGGTTGGGT	TCTTATTTTT	GTCATGCTTT	TATTATTTTT	ACCCACTTAT
msa25643.2{418_1169NT}	TGGGTTGGGT	TCTTATTTTT	GTCATGCTTT	TATTATTTTT	ACCCACTTAT
msa25643.2{418_A909}	TGGGTTGGGT	TCTTATTTTT	GTCATGCTTT	TATTATTTTT	ACCCACTTAT
msa25643.2{418_H368}	TGGGTTGGGT	TCTTATTTTT	GTCATGCTTT	TATTATTTTT	ACCCACTTAT

Table 81: Comparative Sequences relating to SAG0011

msa25643.2{418_COH1}	151	AATTTAGTTA AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_M732}		AATTTAGTTA AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_M781}		AATTTAGTTA AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_JM9130013}		AATTTAGTTA AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_090}		AATTTAGTTA AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_18RS21}		AATTTAGTTA AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_2603}		AATTTAGTTA AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_CJB110}		AATTTAGTTA AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_1169NT}		AATTTAGTTA AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_A909}		AATTTAGTTA AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_H36B}		AATTTAGTTA AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
Consensus		*****	*****	*****	*****
msa25643.2{418_COH1}	201	AAAATTAACG AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCGAGA
msa25643.2{418_M732}		AAAATTAACG AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCGAGA
msa25643.2{418_M781}		AAAATTAACG AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCGAGA
msa25643.2{418_JM9130013}		AAAATTAACG AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCGAGA
msa25643.2{418_090}		AAAATTAACG AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCGAGA
msa25643.2{418_18RS21}		AAAATTAACG AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCGAGA
msa25643.2{418_2603}		AAAATTAACG AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCGAGA
msa25643.2{418_CJB110}		AAAATTAACG AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCGAGA
msa25643.2{418_1169NT}		AAAATTAACG AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCGAGA
msa25643.2{418_A909}		AAAATTAACG AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCGAGA
msa25643.2{418_H36B}		AAAATTAACG AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCGAGA
Consensus		*****	*****	*****	*****
msa25643.2{418_COH1}	251	AGTTaCTAGC AAAACAACCA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_M732}		AGTTaCTAGC AAAACAACCA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_M781}		AGTTaCTAGC AAAACAACCA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_JM9130013}		AGTTaCTAGC AAAACAACCA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_090}		AGTTgCTAGC AAAACAACCA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_18RS21}		AGTTgCTAGC AAAACAACCA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_2603}		AGTTgCTAGC AAAACAACCA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_CJB110}		AGTTgCTAGC AAAACAACCA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_1169NT}		AGTTgCTAGC AAAACAACCA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_A909}		AGTTaCTAGC AAAACAACCA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_H36B}		AGTTaCTAGC AAAACAACCA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
Consensus		*****	*****	*****	*****
msa25643.2{418_COH1}	301	CGAGCgAACT ATTATTTCTC	TAAGACGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_M732}		CGAGCgAACT ATTATTTCTC	TAAGACGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_M781}		CGAGCgAACT ATTATTTCTC	TAAGACGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_JM9130013}		CGAGCgAACT ATTATTTCTC	TAAGACGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_090}		CGAGCtAACT ATTATTTCTC	TAAGACGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_18RS21}		CGAGCtAACT ATTATTTCTC	TAAGACGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_2603}		CGAGCtAACT ATTATTTCTC	TAAGACGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_CJB110}		CGAGCtAACT ATTATTTCTC	TAAGACGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_1169NT}		CGAGCtAACT ATTATTTCTC	TAAGACGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_A909}		CGAGCtAACT ATTATTTCTC	TAAGACGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_H36B}		CGAGCtAACT ATTATTTCTC	TAAGACGGC	GAAATGATTT	ACCCATTACC
Consensus		*****	*****	*****	*****
msa25643.2{418_COH1}	351	AGACCTttta caaaaa			
msa25643.2{418_M732}		AGACCTttta caaaaa			
msa25643.2{418_M781}		AGACCTttta caaaaa			
msa25643.2{418_JM9130013}		AGACCTttta caaaaa			
msa25643.2{418_090}		AGACCTttta caaaaa			
msa25643.2{418_18RS21}		AGACCTttta caaaaa			
msa25643.2{418_2603}		AGACCTttta caaaaa			
msa25643.2{418_CJB110}		AGACCTttta caaaaa			
msa25643.2{418_1169NT}		AGACCTttta caaaaa			
msa25643.2{418_A909}		AGACCT----			
msa25643.2{418_H36B}		AGACCTttta caaaaa			
Consensus		*****	-----	-----	
SEQ ID NO. 8112	366				
STRAIN 090					
SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL					
VKSRTLQERRQEVVKLTQDYLQTLNRTEQNLKLLAKQLKNPDYVQKYARAKYYFSKTGEM					
IYPLPDLLPK					
SEQ ID NO. 8113					
STRAIN A909					
SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL					
VKSRTLQERRQEVVKLTQDYLQTLNRTEQNLKLLAKQLKNPDYVQKYARAKYYFSKTGEM					

Table 81: Comparative Sequences relating to SAG0011

IYPLPD
SEQ ID NO. 8114
STRAIN H36B
 SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
 VKSYRTLQERRRQEVVKLTQDYZQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8115
STRAIN 18RS21
 SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNLVKSYRTLQ
 ERROEVVKLTQDYZQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEMIYPLPDLL
 PK

SEQ ID NO. 8116
STRAIN M732
 SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
 VKSYRTLQERRRQEVVKLTQDYZQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8117
STRAIN COH1
 SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNLVK
 SYRTLQERRRQEVVKLTQDYZQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEMIY
 PLPDLLPK

SEQ ID NO. 8118
STRAIN M781
 SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYN
 LVKSYRTLQERRRQEVVKLTQDYZQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGE
 MIYPLPDLLPK

SEQ ID NO. 8119
STRAIN CJB110
 SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNLVK
 SYRTLQERRRQEVVKLTQDYZQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEMIY
 PLPDLLPK

SEQ ID NO. 8120
STRAIN 1169NT
 SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
 VKSYRTLQERRRQEVVKLTQDYZQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8121
STRAIN JM9130013
 SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNL
 VKSYRTLQERRRQEVVKLTQDYZQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEM
 IYPLPDLLPK

SEQ ID NO. 8122
STRAIN 2603
 SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLIFVMLLFILPTYNLVKSYRTLQ
 ERROEVVKLTQDYZQTLTNRTENQKLLAKQLKNPDYVQKYARAKYYFSKTGEMIYPLPDLL
 PK

MSA Alignment Results: Pretty output
 PRETTY of: /biotmp/msa20122.2{*} April 29, 2002 06:08 ..

	1		50
msa20122.2{418_090}	SKPNVVQLNN QYINDENLKK RYEAEELRRK NRRLMGWVLIF VMMLFILPTY		
msa20122.2{418_A909}	SKPNVVQLNN QYINDENLKK RYEAEELRRK NRRLMGWVLIF VMMLFILPTY		
msa20122.2{418_1169NT}	SKPNVVQLNN QYINDENLKK RYEAEELRRK NRRLMGWVLIF VMMLFILPTY		
msa20122.2{418_18RS21}	SKPNVVQLNN QYINDENLKK RYEAEELRRK NRRLMGWVLIF VMMLFILPTY		
msa20122.2{418_2603}	SKPNVVQLNN QYINDENLKK RYEAEELRRK NRRLMGWVLIF VMMLFILPTY		
msa20122.2{418_CJB110}	SKPNVVQLNN QYINDENLKK RYEAEELRRK NRRLMGWVLIF VMMLFILPTY		
msa20122.2{418_COH1}	SKPNVVQLNN QYINDENLKK RYEAEELRRK NRRLMGWVLIF VMMLFILPTY		
msa20122.2{418_H36B}	SKPNVVQLNN QYINDENLKK RYEAEELRRK NRRLMGWVLIF VMMLFILPTY		
msa20122.2{418_JM9130013}	SKPNVVQLNN QYINDENLKK RYEAEELRRK NRRLMGWVLIF VMMLFILPTY		
msa20122.2{418_M732}	SKPNVVQLNN QYINDENLKK RYEAEELRRK NRRLMGWVLIF VMMLFILPTY		
msa20122.2{418_M781}	SKPNVVQLNN QYINDENLKK RYEAEELRRK NRRLMGWVLIF VMMLFILPTY		
Consensus	*****		
			100
msa20122.2{418_090}	NLVKSYRTLQ ERRQEVVKLT KDYQTLTNRT ENQKLLAKQL KNPDYVQKYA		
msa20122.2{418_A909}	NLVKSYRTLQ ERRQEVVKLT KDYQTLTNRT ENQKLLAKQL KNPDYVQKYA		

Table 81: Comparative Sequences relating to SAG0011

msa20122.2{418_1169NT}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_18RS21}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_2603}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_CJB110}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_COH1}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_H36B}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_JM9130013}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_M732}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_M781}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
Consensus	*****	*****	*****	*****	*****
	101	122			
msa20122.2{418_090}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_A909}	RAKYYFSKTG	EMIYPLPD-	--		
msa20122.2{418_1169NT}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_18RS21}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_2603}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_CJB110}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_COH1}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_H36B}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_JM9130013}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_M732}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_M781}	RAKYYFSKTG	EMIYPLPD11	pk		
Consensus	*****	*****	--		

Table 82: Comparative Sequences relating to SAG0165**SEQ ID NO. 8201****STRAIN 2603**

ATGAAAAAATTGGTAAATGTAGGATAAGAAGGTTAACGATTTACCTTTAGAA
 TGTGGTAGCATGGTACAAATCACAGGAGCTTACTAGTTATCAAGGACTGACAAA
 TTGTTGGCTAACAGATAGTAGTGATGTCCTCTCCAGTCAGTCTGAATGGGTATTAA
 ACTCAGCAACTAAATGAGCAGAAATTGAAGGCCTCATCTGAAATTTAAAGACAGAACAAA
 CTTATTTACGTAAGCAGATAAGGTTACCTTGGCAAATCTAATAAAGATGATTTC
 CGTAAGACAGGTATGATGGTCAGGTTATCAACCAATGGTTATGGTTAGACAATTG
 CAAATGAGTCAGACCAAAAGTATGGTAAACTTGTTTTATTTAAGGACGGGTTAAA
 AGGACATTTACTATGATTTAAAGAAGAACTTAA

SEQ ID NO. 8202**STRAIN 090**

AATCGAAGGCCTCACTTGGAAATATTTAACGACAGAACAAACTTTATTAA
 CGTAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATT
 CGTAAGACAGGTATGATGGTCAGGTTATCAACCAATGGTTATGGGT
 TAGACAATTGTCAAATGAGTCACACCCAAAGTATGGTAAACTTGT
 TATTTAAGGACGGGTTAAAAGGACATTTACTATGATTTAAAGAAGA
 AACT

SEQ ID NO. 8203**STRAIN A909**

CAGAATTGAAAGGCCTCATCTGAAATATTTAACGACAGAACAAACTTTAT
 TTACGTAAGAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAA
 TTCCGTAAGACAGGTATGATGGTCAGGTTATCAACCAATGGTTATGG
 GTTAGACAATTGTCACATGAGTCAGACCCAAAGTATGGTAAACTTGT
 TTATTTAAGGACGGGTTAAAAGGACATTTACTATGATTTAAAGA
 AGAAACT

SEQ ID NO. 8204**STRAIN H36B**

ATGCGAATTGAAAGGCCTCATCTGAAATATTTAACGACAGAACAAACTT
 TATTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGA
 TGATTCCGTAAGACAGGTATGATGGTCAGGTTATCAACCAATGGTTATGG
 ATGGGTTAGACAATTGTCACATGAGTCAGACCCAAAGTATGGTAAACTT
 GTTTTTATTTAAGGACGGGTTAAAAGGACATTTACTATGATTTAA
 AGAAGAAACT

SEQ ID NO. 8205**STRAIN 18RS21**

AGAATTGAAAGGCCTCATCTGAAATATTTAACGACAGAACAAACTTTAT
 TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TTCCGTAAGACAGGTATGATGGTCAGGTTATCAACCAATGGTTATGG
 GTTAGACAATTGTCACATGAGTCAGACCCAAAGTATGGTAAACTTGT
 TTATTTAAGGACGGGTTAAAAGGACATTTACTATGATTTAAAGA
 GAAACT

SEQ ID NO. 8206**STRAIN M732**

CAGAATTGAAAGGCCTCATCTGAAATATTTAACGACAGAACAAACTTTAT
 TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAA
 TTCCGTAAGACAGGTATGATGGTCAGGTTATCAACCAATGGTTATGG
 GTTAGACAATTGTCACATGAGTCAGACCCAAAGTATGGTAAACTTGT
 TTATTTAAGGACGGGTTAAAAGGACATTTACTATGATTTAAAGA
 AGAAACT

SEQ ID NO. 8207**STRAIN COH1**

GAATTGAAAGGCCTCACTTGGAAATATTTAACGACAGAACAAACTTTATT
 ACGTAAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATT
 TCCGTAAGACAGGTATGATGGTCAGGTTATCAACCAATGGTTATGG
 GTTAGACAATTGTCACATGAGTCAGACCCAAAGTATGGTAAACTTGT
 TTATTTAAGGACGGGTTAAAAGGACATTTACTATGATTTAAAGAAG
 AACT

SEQ ID NO. 8208**STRAIN M781**

AGAATTGAAAGGCCTCACTTGGAAATATTTAACGACAGAACAAACTTTAT
 TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TTCCGTAAGACAGGTATGATGGTCAGGTTATCAACCAATGGTTATGG
 GTTAGACAATTGTCACATGAGTCAGACCCAAAGTATGGTAAACTTGT
 TTATTTAAGGACGGGTTAAAAGGACATTTACTATGATTTAAAGA
 GAAACT

SEQ ID NO. 8209**STRAIN CJB110**

GAATTGAAAGGCCTCACTTGGAAATATTTAACGACAGAACAAACTTTATT
 ACGTAAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATT
 TCCGTAAGACAGGTATGATGGTCAGGTTATCAACCAATGGTTATGG
 GTTAGACAATTGTCACATGAGTCAGACCCAAAGTATGGTAAACTTGT
 TTATTTAAGGACGGGTTAAAAGGACATTTACTATGATTTAAAGAAG
 AACT

Table 82: Comparative Sequences relating to SAG0165

SEQ ID NO. 8210

STRAIN 1169NT

```
TCGAAGGCGCTCACTTGGAAATTTAAGACAGAACAAACTTTATTTACGT
AAGCAAGATAAGATTGTAACCTTTGCAAATCTAATAAAAGATGATTTACG
TAAGACAGGTTATGATGTCGAGGTTATCAACCAATGGTTATGGGTTAG
ACAATTGTCAAATGAGTCACCAACAAAGATGGTAAAACCTTTTAT
TTAAGGACGGTTAAAAGGACATTTACTATGATTAAAGAAGAAC
```

T

SEQ ID NO. 8211

STRAIN JM9130013

```
TGAGAAATTGAAAGGCGCTCATCTGGAAATTTAAGACAGAACAAACTT
ATTACGTAAGCAAGATAAGATTGTAACCTTTGCAAATCTAATAAAAGAT
GATTTCGTAAGACAGGTTATGATGTCGAGGTTATCAACCAATGGTTA
TGGGTAGACAATTGTCAAATGAGTCAGACACAAAGATGGTAAAACCTG
TTTTTATTTAAGGACGGTTAAAAGGACATTTACTATGATTTTAA
GAAGAAACT
```

PRETTY of: /biotmp/msa128189.2{*} February 7, 2003 08:19 ..

<pre>msa128189.2{6_18RS21} msa128189.2{6_2603} msa128189.2{6_A909} msa128189.2{6_H36B} msa128189.2{6_JM9130013} msa128189.2{6_COH1} msa128189.2{6_M732} msa128189.2{6_M781} msa128189.2{6_090} msa128189.2{6_CJB110} msa128189.2{6_1169NT} Consensus</pre>	1	<pre>atgaaaaatt tattgttaaa atgttaaggat aagaaggta aagcattac</pre>	50
	51		100
	101		150
	151		200
	201		250

```
acttttagaa tgggtttag cattggttac aatcacagga gctttactag
```

```
tttatcaagg actgacaaa ttgttggtc aacagatgt agtgatgttc
```

```
tctccagtc agtctgaatg ggtgttatta actcagcaac taaATGCaga
```

```
atTtGAAGGC GCTCAtcTGG AATATTTAAG ACAGAACAAA CTTTATTTCAC
```

Table 82: Comparative Sequences relating to SAG0165

msa128189.2{6_JM9130013}	atTtGAAGGC GCTCAtcTGG AATATTTAAG ACAGAACAAA CTTTATTTCAC	
msa128189.2{6_COH1}	atTcGAAGGC GCTCActTGG AATATTTAAG ACAGAACAAA CTTTATTTCAC	
msa128189.2{6_M732}	atTcGAAGGC GCTCActTGG AATATTTAAG ACAGAACAAA CTTTATTTCAC	
msa128189.2{6_M781}	atTcGAAGGC GCTCActTGG AATATTTAAG ACAGAACAAA CTTTATTTCAC	
msa128189.2{6_090}	atTcGAAGGC GCTCActTGG AATATTTAAG ACAGAACAAA CTTTATTTCAC	
msa128189.2{6_CJB110}	atTcGAAGGC GCTCActTGG AATATTTAAG ACAGAACAAA CTTTATTTCAC	
msa128189.2{6_1169NT}	--TcGAAGGC GCTCActTGG AATATTTAAG ACAGAACAAA CTTTATTTCAC	
Consensus	----- *----- *----- *----- *----- *----- *-----	
	251	300
msa128189.2{6_18RS21}	GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc	
msa128189.2{6_2603}	GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc	
msa128189.2{6_A909}	GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc	
msa128189.2{6_H36B}	GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc	
msa128189.2{6_JM9130013}	GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc	
msa128189.2{6_COH1}	GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc	
msa128189.2{6_M732}	GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc	
msa128189.2{6_M781}	GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc	
msa128189.2{6_090}	GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc	
msa128189.2{6_CJB110}	GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc	
msa128189.2{6_1169NT}	GTAAGCAAGA TAAGATTGTA ACCTTTGGCA AATCTAATAA AGATGATTTc	
Consensus	***** *----- *----- *----- *----- *-----	
	301	350
msa128189.2{6_18RS21}	CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGTT	
msa128189.2{6_2603}	CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGTT	
msa128189.2{6_A909}	CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGTT	
msa128189.2{6_H36B}	CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGTT	
msa128189.2{6_JM9130013}	CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGTT	
msa128189.2{6_COH1}	CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGTT	
msa128189.2{6_M732}	CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGTT	
msa128189.2{6_M781}	CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGTT	
msa128189.2{6_090}	CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGTT	
msa128189.2{6_CJB110}	CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGTT	
msa128189.2{6_1169NT}	CGTAAGACAG GTTATgATGG TCGAGGTTAT CAACCAATGG TTTATGGTT	
Consensus	***** *----- *----- *----- *----- *-----	
	351	400
msa128189.2{6_18RS21}	AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT	
msa128189.2{6_2603}	AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT	
msa128189.2{6_A909}	AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT	
msa128189.2{6_H36B}	AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT	
msa128189.2{6_JM9130013}	AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT	
msa128189.2{6_COH1}	AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT	
msa128189.2{6_M732}	AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT	
msa128189.2{6_M781}	AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT	
msa128189.2{6_090}	AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT	
msa128189.2{6_CJB110}	AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT	
msa128189.2{6_1169NT}	AGACAATTGT CAAATGAGTC AgACCAAAAG TATGGTAAAA CTTGTTTTTT	
Consensus	***** *----- *----- *----- *----- *-----	
	401	450
msa128189.2{6_18RS21}	ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATT TAAAGAACAA	
msa128189.2{6_2603}	ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATT TAAAGAACAA	
msa128189.2{6_A909}	ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATT TAAAGAACAA	
msa128189.2{6_H36B}	ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATT TAAAGAACAA	
msa128189.2{6_JM9130013}	ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATT TAAAGAACAA	
msa128189.2{6_COH1}	ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATT TAAAGAACAA	
msa128189.2{6_M732}	ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATT TAAAGAACAA	
msa128189.2{6_M781}	ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATT TAAAGAACAA	
msa128189.2{6_090}	ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATT TAAAGAACAA	
msa128189.2{6_CJB110}	ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATT TAAAGAACAA	
msa128189.2{6_1169NT}	ATTTTAAGGA CGGGTTAAAA AGGACATTTT ACTATGATT TAAAGAACAA	
Consensus	***** *----- *----- *----- *----- *-----	
	451	
msa128189.2{6_18RS21}	ACT~~~	
msa128189.2{6_2603}	ACTtaa	
msa128189.2{6_A909}	ACT~~~	
msa128189.2{6_H36B}	ACT~~~	
msa128189.2{6_JM9130013}	ACT~~~	
msa128189.2{6_COH1}	ACT~~~	
msa128189.2{6_M732}	ACT~~~	
msa128189.2{6_M781}	ACT~~~	
msa128189.2{6_090}	ACT~~~	
msa128189.2{6_CJB110}	ACT~~~	
msa128189.2{6_1169NT}	ACT~~~	
Consensus	*****	

SEQ ID NO. 8212

STRAIN 2603 frame: 1

MKNLLLKCKDKVKAFTLLECLVALVTITGALLVYQGLTKLLAQQIVVMSSSSQSEWVLL
TQQLNAEFGAHLEYLRQNKLRLRKQDKIVTFGKSNSKDDFRKTGYDGRGYQPMVYGLDNC

Table 82: Comparative Sequences relating to SAG0165

QMSQT KSMV KLV FKY FKD GLK RTF YY DFKEET.

SEQ ID NO. 8213

STRAIN 090 frame: 3
EFGAHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMV KLV FKY FKD GLK RTF YY DFKEET

SEQ ID NO. 8214

STRAIN A909 frame: 3
EFGAHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMV KLV FKY FKD GLK RTF YY DFKEET

SEQ ID NO. 8215

STRAIN H36B frame: 3
AEFGAHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMV KLV FKY FKD GLK RTF YY DFKEET

SEQ ID NO. 8216

STRAIN 18RS21 frame: 2
EFGAHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMV KLV FKY FKD GLK RTF YY DFKEET

SEQ ID NO. 8217

STRAIN M732 frame: 3
EFGAHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMV KLV FKY FKD GLK RTF YY DFKEET

SEQ ID NO. 8218

STRAIN COH1 frame: 1
EFGAHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMV KLV FKY FKD GLK RTF YY DFKEET

SEQ ID NO. 8219

STRAIN M781 frame: 2
EFGAHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMV KLV FKY FKD GLK RTF YY DFKEET

SEQ ID NO. 8220

STRAIN CJB110 frame: 1
EFGAHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMV KLV FKY FKD GLK RTF YY DFKEET

SEQ ID NO. 8221

STRAIN 1169NT frame: 3
EFGAHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
VKLV FKY FKD GLK RTF YY DFKEET

SEQ ID NO. 8222

STRAIN JM9130013 frame: 2
AEFGAHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
KSMV KLV FKY FKD GLK RTF YY DFKEET

PRETTY of: /biotmp/msa128319.2{*} February 7, 2003 08:27 ..

	1	50
msa128319.2{6_090}	-----	
msa128319.2{6_1169NT}	-----	
msa128319.2{6_18RS21}	-----	
msa128319.2{6_2603}	mkn111kckd kkvkaftlle clvalvtitg allvyqgltk llaqqivvms	
msa128319.2{6_H36B}	-----	
msa128319.2{6_JM9130013}	-----	
msa128319.2{6_A909}	-----	
msa128319.2{6_CJB110}	-----	
msa128319.2{6_COH1}	-----	
msa128319.2{6_M732}	-----	
msa128319.2{6_M781}	-----	
Consensus	*****	
	51	100
msa128319.2{6_090}	-----fEG AHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK	
msa128319.2{6_1169NT}	-----EG AHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK	
msa128319.2{6_18RS21}	-----EfEG AHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK	
msa128319.2{6_2603}	sssqsewvll tqqlnAEfEG AHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK	
msa128319.2{6_H36B}	-----AEfEG AHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK	
msa128319.2{6_JM9130013}	-----AEfEG AHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK	
msa128319.2{6_A909}	-----EfEG AHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK	
msa128319.2{6_CJB110}	-----EfEG AHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK	
msa128319.2{6_COH1}	-----EfEG AHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK	
msa128319.2{6_M732}	-----EfEG AHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK	
msa128319.2{6_M781}	-----EfEG AHLEYLRQNKLRLRKQDKIVTFGKSNNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK	
Consensus	*****	

Table 82: Comparative Sequences relating to SAG0165

	101	150
msa128319.2{6_090}	RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE	
msa128319.2{6_1169NT}	RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE	
msa128319.2{6_18RS21}	RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE	
msa128319.2{6_2603}	RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE	
msa128319.2{6_H36B}	RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE	
msa128319.2{6_JM9130013}	RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE	
msa128319.2{6_A909}	RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE	
msa128319.2{6_CJB110}	RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE	
msa128319.2{6_COH1}	RKTGYNGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE	
msa128319.2{6_M732}	RKTGYNGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE	
msa128319.2{6_M781}	RKTGYNGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKEE	
Consensus	*****-*****	*****-*****
	151	
msa128319.2{6_090}	T-	
msa128319.2{6_1169NT}	T-	
msa128319.2{6_18RS21}	T-	
msa128319.2{6_2603}	T-	
msa128319.2{6_H36B}	T-	
msa128319.2{6_JM9130013}	T-	
msa128319.2{6_A909}	T-	
msa128319.2{6_CJB110}	T-	
msa128319.2{6_COH1}	T-	
msa128319.2{6_M732}	T-	
msa128319.2{6_M781}	T-	
Consensus	**	

Table 83: Comparative Sequences relating to SAG0108**SEQ ID NO. 8301****STRAIN 2603**

atgaaaaagattcgttatcaagtttataaaatgattgttattttgttttaatt
 atgttagcagctgttttattttccacgttgcccaagttcgagatgataaatcctt
 attcaaatggtaacgttaacgctggaaactcttatatgcttgcataaaatccttgc
 aagcttataaaggaaaaatagaatgacaacaaaataaaagcaagttgtttggat
 gttcctgttgcataagacagttgttcatgtttgcataatgc
 aaagagaatatacgatgttgcataatgttgcataatgttgcataatgttgcata
 cctgacaatattgcacatgttgcataatgttgcataatgttgcataatgttgcata
 cgccgagaacatattcaatggcagatgttgcataatgttgcataatgttgcata
 actttatgttgcataatgttgcataatgttgcataatgttgcataatgttgcata
 ccttagtcgggtttatcatgttgcataatgttgcataatgttgcataatgttgcata
 aaatccggctaaagatgttgcataatgttgcataatgttgcataatgttgcata
 acaatcttcaatcagatgttgcataatgttgcataatgttgcataatgttgcata
 aaaaagaataatttaccgccttttattcatgttgcataatgttgcataatgttgcata
 agtatgtttatgacaactataaagctacacgcggtaagaaagagcttattgtaaaa
 gggcaaaacatcgcaaatcttgcataatgttgcataatgttgcataatgttgcata
 atgttttgcataatgttgcataatgttgcataatgttgcataatgttgcataatgttgcata

SEQ ID NO. 8302**STRAIN 090**

GCTAGTTTATTTCCACGTTGCCAAGTTCG
 AGATGATAATCCTTATTCGAATGGTAACGTAAGCCTGGAAACTCTT
 TATATGCCTATGATAATCCTTGTGATAAGCTATTAAAGCAAAAATAGAA
 ATGACAACCAAATAATAAGCAAGTTGCTTGGTATGTTCTGCTGCTAA
 GAAACTCATAAAGCAGCTGTTGCTGTTCATGGTTTGCAATGAAAG
 AGAATATGAAGGCAATGGTGTGTTGCTTGTGTTGCTGTTGAAATGAAAG
 CTTATGCCATGACAATATTGCAATGGTGTGTTGCTGTTGAAATGAAAG
 CTATGGCTGGAACGACCGCGAGAACATTATCAATGGCAGAAATGAAAG
 TTGATAAGGATAATTTGTTCAACAAAGTATGTTTATGACAACATATAA
 GGAGCAACAGTCATGATGGCTAGTGGTGAAGAAATTACCTAGTCAGTTGT
 TAATATCATGAGATTGGCTTATTCTAGTGTGTTGGATGAAATTAAAAT
 TTCAGGCTAAAGGATGTATGGTTACCGCCTTCCACTTTATATGAA
 GTTCAACAAATTCTAAAGATCAGAGCAGGTTTTCGTTGACAAGCAAG
 TAGTGTGAAACAATTGAAAAAGATAATTACCGCCCTTTTATCATG
 GTGATAAGGATAATTGTTCAACAAAGTATGTTTATGACAACATATAA
 GCTACAGCAGGTAAGAAAGAGCTTATTGTAAAAGGGCAAAACATGC
 GAAATCTTTGAAACAGAGCAGAAAATATGAGAAACGTATCTTAGTT
 TTTGAAAAAATATGAAAAAA

SEQ ID NO. 8303**STRAIN A909**

AATCCCTTATTCAAATGGTCAACGTAAGCCTGGAAACTCTTATATGCT
 TATGATAATCCTTGTATAAGCTATTAAAGCAAAAATAGAAATGACAAA
 CCAAAATATAAGCAAGTTGCTTGTATGTTCTGCTGCTAAGAAAATCTC
 ATAAGACACTGTTGCTTGTATGTTTGTGAAATAGCAAAGAGAAATATG
 AAGGCAATGGTGTGCTTGTATGTTGTGAAACTGATGAAATGAAAG
 TGACAACATTGCAATGGTGAAGTCATGGCAGTTGATAGGCTATGGCT
 GGAACGACCGCGAGAACATTATCAAAATGGACAGAAATGATAGTGTGAAAG
 AATTCATGAAAGCAAAATTACTTATTGGTGTGTTCAATGCGTGGAGCAAC
 AGTCATGATGGCTAGTGGTGAAGAAATTACCTACTCAGGTGTTAATATCA
 TIGAAGAATGCGGTTATTCTGGTGTGGGATGAAATTAAAATTTCAGGCT
 AAAGAGATGTATGGTTACCGACCTTCCCACCTTATATGAGGTTTCAAC
 AATTCATGAAAGGAGGTTTACCGCCCTTTTATTGATGGCTGAAAG
 AACATTGAAAAAGAGATAATTACCGCCCTTTTATTGATGGCTGAAAG
 GATAATTGTTGTTCAACaaGTATGGTTTATGACAACATATAAGCTACAGC
 AGGTAAGGAGGCTTATATGTTAAAGGGCAAAACATGCGAAATCTT
 TTGAAACAGAGCAGAAAATATGAGAAACGTATCTTAGTTTGTAAA
 AATATGAAAAA

SEQ ID NO. 8304**STRAIN H36B**

AGTTTTATTTCCACGTTGCCAAGTTGAGATGATAAAATCCTTAT
 TCCAAATGGTCAACGTAAGCCTGGAAACTCTTATATGCTTATGATAAAAT
 CTTTGATAAGCTATTAAAGCAAAAATAGAAATGACAACAAAATATA
 AAGCAAGTGTGCTGGTATGTTCTGCTGCTAAGAAAATCTATAAGACAGC
 TGTGTCGTTCATGGTTGGCAATAGCAAGAGAAATATGAGGCTATG
 GTTGGCTGTTCATAAAGTTAGGATAATGTTCTATGCTGCTGACAACATT
 GCACATGGTGAAGTCATGGCAGTTGATAGGCTATGGCTGGAAACGACCG
 CGGAACATTATCAAATGGACAGAAATGATAGTTGATAAGAAATTCA
 GCCAAATTACTTATTGGTGTGTTCAATGGTGGAGCAACAGTCATGATG
 GCTAGTGGTGAAGAAATTACCTAGTCAGGTTGTTAATATCATTGAGATTG
 CGGTTATTCTGGTTGGGATGAAATTAAAATTTCAGGCTAAAGAGATGT
 ATGGTTTACCGACCTTCCCACCTTATATGAGGTTCAACAAATTCTAA
 ATCAGAGCAGCTTCTGTTGAGGAAAGCAAGTAGTGTGCGAAACATTGAA
 AAAGAATAATTACCGCCCTTTTATTGATGGTATAAGGATAATTG
 TTCCAACAAGTATGGTTTATGACAACATATAAGCTACAGCAGGTAAGAAA
 GAGCTTATATTGTAAGGGCAAAACATGCGAAATCTTGAACACAGA
 GCCAGAAAATATGAGAAACGTATCTTAGTTTGTAAAAATATGAAA
 AA

SEQ ID NO. 8305**STRAIN 18RS21**

Table 83: Comparative Sequences relating to SAG0108

GCTAGTTTATTTCCACGTTGCCAAGTCGA
 GATGATAAATCCTTATTCAATGGTCAACGTAAGCCTGGAAACTCTT
 ATATGCTTATGATAAATCCTTGTATAAGCTTAAAGCAAAAATAGAAA
 TGACAAACAAAATAAAGCAAGTGTGCTGGTATGGCTGCTGTTAAG
 AAAACTCATAACAGACAGTGTGCTGGTATGGCTGCTGCTGTTAAG
 GAATATGAGGCAATGGCTGCTGGTATGGCTGCTGCTGCTGCTGCTG
 TTATGCTGACACAATGGCTGCTGGTATGGCTGCTGCTGCTGCTGCTG
 TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 TGATAAGAATTCATCAAGCCAATTACTTATTGGTGTTCAGGGTG
 GAGAACACAGTGTGCTGCTGGTATGGCTGCTGCTGCTGCTGCTGCTG
 AATATCATTGAAGATTGGTGTATTCTAGTGTGGATGAAATTAAAATT
 TCAGGCTAAGAGATGTATGGTTACCGCCTCCACTCTTATATGAAG
 TTTCACAAATTCTAAAATCAGAGCAGGTTTCGTATGGACAAgCAAGT
 AGTGTGAAACATTGAAAAGAATAATTACCGCCCTTTTATTGAGGTT
 TGATAAGGATAATTGGTGTCCAAAGTATGGTTATGACAACATAAAG
 CTACAGCAGGTAAGAAAGAGCTTATATTGTAAGGGGCAAAACATGCG
 AAATCTTGAACAGAGCCAGAAAATATGAGAAACGTATCTCTAGTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8306

STRAIN M732

GCTAGTTTATTTCCACGTTGCCAAGTCGA
 GATGATAAATCCTTATTCAATGGTCAACGTAAGCCTGGAAACTCTT
 ATATGCTTATGATAAATCCTTGTATAAGCTTAAAGCAAAAATAGAAA
 TGACAAACAAAATAAAGCAAGTGTGCTGGTATGGCTGCTGCTGCTAAG
 AAAACTCATAACAGACAGTGTGCTGGTATGGCTGCTGCTGCTGCTG
 GAATATGAGGCAATGGCTGCTGGTATGGCTGCTGCTGCTGCTGCTG
 TTATGCTGACACAATGGCTGCTGGTATGGCTGCTGCTGCTGCTGCTG
 TATGGCTGGAACGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 GGATAAGAATTCATCAAGCCAATTCTTATTGGTGTTCAGGGTG
 GACCAACAGTGTGCTGCTGGTATGGCTGCTGCTGCTGCTGCTG
 AATATCATTGAAGATTGGTGTATTCTAGTGTGGATGAAATTAAAATT
 TCAGGCTAAGAGATGTATGGTTACCGCCTCCACTCTTATATGAAG
 TTTCACAAATTCTAAAATCAGAGCAGGTTTCGTATGGACAAgCAAGT
 AGTGTGAAACATTGAAAAGAATAATTACCGCCCTTTTATTGAGGTT
 TGATAAGGATAATTGGTGTCCAAAGTATGGTTATGACAACATAAAG
 CTACAGCAGGTAAGAAAGAGCTTATATTGTAAGGGGCAAAACATGCG
 AAATCTTGAACAGAGCCAGAAAATATGAGAAACGTATCTCTAGTT
 TTTGAAAAAATATGAAAAA

SEQ ID NO. 8307

STRAIN COH1

GCTAGTTTATTTCCACGTTGCCAAGTC
 GAGATGATAAATCCTTATTCAATGGTCAACGTAAGCCTGGAAACTCT
 TTATATGCTTATGATAAATCCTTGTATAAGCTTAAAGCAAAAATAGA
 AATGtCAAACAAAATAAAGCAAGTGTGCTGGTATGGCTGCTGCTA
 AGAAAACCTATAAGACAGTGTGCTGGTATGGCTGCTGCTGCTA
 GAAGATATGAAGGCATAATGGCTGCTGGTATGGCTGCTGCTGCTG
 TCTTATGCTGACAACATTGACATGGTAAAGTGTGCTGCTGCTGCTG
 GTCTGGCTGAAACGACCCGAGAACATTATCAAATGGACAGAAATGATA
 GTGCTGAAAGAATTCATGCTGCTGGTATGGCTGCTGCTGCTGCTG
 TGGAGCAACAGTCATGATGGCTAGTGTGCTGCTGCTGCTGCTG
 TTAAATATCATTGAAGAATGGTGTATTCTAGTGTGGGATgAATTAAA
 TTTCAGGCTAAGAGAGATGTATGGCTTACCGCCCTCCACTCTTATATGA
 AGTTCAACAAATTCTAAAATCAGAGCAGGTTTCGTATGGACAAAGCA
 GTAGTGTGAAACATTGAAAAGAATAATTACCGCCCTTTTATTGAT
 GTGATAAGGATAATTGGTGTCCAAACAGTATGGTTATGACAACATAA
 AGCTACAGCAGGTAAGAAAGAGCTTATATTGTAAGGGGCAAAACATG
 CGAAATCTTGAACAGAGCCAGAAAATATGAGAAACGTATCTCTAGT
 TTTTGAACATTGAAAAAATATGAAAAA

SEQ ID NO. 8308

STRAIN M781

GCTAGTTTATTTCCACGTTGCCAAGTC
 AGATGATAAATCCTTATTCAATGGTCAACGTAAGCCTGGAAACTCT
 TATATGCTTATGATAAATCCTTGTATAAGCTTAAAGCAAAAATAGA
 ATGACAACAAAATAAAGCAAGTGTGCTGGTATGGCTGCTGCTA
 GAAAACCTATAAGACAGTGTGCTGGCTGCTGCTGCTGCTGCTG
 AGAATATGAAGGCATAATGGCTGCTGGCTGCTGCTGCTGCTG
 CTATGCTGACAACATTGACATGGTAAAGTGTGCTGCTGCTGCTG
 CTATGGCTGAAACGACCCGAGAACATTATCAAATGGACAGAAATGATA
 TGATAAGAATTCATGACAGGTTTCGTATGGCTGCTGCTGCTGCTG
 GGAGCAACAGTCATGATGGCTAGTGTGCTGCTGCTGCTGCTG
 TAATATCATTGAAGATTGGTGTATTCTAGTGTGGGATgAATTAAAAT
 TTTCAGGcTAAAGAGATGTATGGTTACCGCCCTCCACTCTTATATGA
 GTTCAAcAATTCTAAAATCAGAGCAGGTTTCGTATGGACAgCAAG
 TAGTGTGAAACATTGAAAAGAATAATTACCGCCCTTTTATTGAG
 GTGATAAGGATAATTGGTGTCCAAACAGTATGGTTATGACAACATAA
 GCTACAGCAGGTAAGAAAGAGCTTATATTGTAAGGGGCAAAACATG
 CGAAATCTTGAACAGAGCCAGAAAATATGAGAAACGTATCTCTAGT
 TTTTGAACATTGAAAAAATATGAAAAA

SEQ ID NO. 8309

Table 83: Comparative Sequences relating to SAG0108

STRAIN CJB110
GCTAGTTTATTTCCACGTTGCCAAGTTCGAG
ATGATAATCCTTATTCTAAATGGTCAACGTAAGCCTGGAAACTCTTTA
TATGCTTATGATAATCCTTGTATAAGCTATTAAAGCAAAAATAGAAAT
GACAAACCAAAATATAAGCAAGTGTGTTGGTATGTTCTGCTGCTAAGA
AAACTCATAAAGACAGCTTGTGCTTGTGCTTGCCTGAAATGCAAGAG
AATATGAAGGCATATGGTGGCTTGTCTAAAGTCTAGGATACAATGTTCT
TATGCTGACAATATTGACATGGTGAAGTCATGGCGAGTGTGATAGGCT
ATGGCTGGAACGACCGCGAGAACATTATCAAAATGGACAGAAATGATAGT
GATAAGAACATTCCATCAAGGAAATTACTTATGGTGGTTCATGGTGG
ACCAACAGTCATGAGCTGTGTTGGTGAAGAAATTACTCTAGTCAGGTGTTA
ATATCATTGAAGATTGCGTTATTCTAGTGTGGGATgAAATTAAATT
CAGCTAAAGAGATGTATGGTTTACAGGCCCTCCACCTTCTATGAAAGT
TTCAACAAATTCTAAATTCAAGAGCAGGTTTCTGCTATGGACAAgCAAGTA
gTGTGCAACAAATTGCAAAAAGAAATAATTACACGCCCTTCTTATCATGGT
GATAAGGATAATTGGTGTCCAACAATGATGGTTTATGACAACATAAAGC
TACAGCAGGTAAGAAAGACGTTTATGTTGAAAGGGCAAAACATGCGA
AATCTTGTGAAACAGGGCAGAAAAATATGAGAACAGTATCTAGTTT
ITGAAAAAAATGAAAAA

SEQ ID NO. 8310

STRAIN 1169NT

GCTAGTTTATTTTCCACGTTGCCAAGTCGA
GATGATTAACATTCTTTATTCAGATAAGCTGGAAACTCTT
ATATGCTTATGATAAAATCCTTGTAGAACGCTTAAAGCAAAAATAGAAA
TGACAAACCaaATATAAGCAAGTGTGGTATGTCCTGCTGCTAAG
AAAATCTCATAAAGCACGGCTGGCTGTAGTTGGAAATAGCAAGA
GAATATGAAGGCATATGGTGGCTGTTCTATAGTTAGGATAATGTT
TTATACCTGCAACATATTGCACTGGTGAAGTCATGGGAGTTGATAGG
TATGGCTGGAACGACCGCGAGAACATTATCAAATGGAAGAACATGATAGT
TGATAAGAAATCCATAGACCCAAATTCTTTATGGTGTGTTCAATGGT
GAGAACACAGTCATGATGGCTAGTGGTGAAGAAATTACCTAGTCAGGTGTT
AATATCATGGAAAGATTGCGTTATTCTAGTGTGGATgAATTAAAATT
TCAGGCTAAAGAGATGTTAGGTTtACAGCCTCCCACTtTTATATGAAG
TTTCAACATTCTAAATTACAGAGCAGGTTTCTGTTAGGACAAGCAGT
AGTGTAGAACAAATTGAAAAGAAATAATTACAGGCCCTTCTTATTCTAGG
TGATAAGGATAATTCTGTTCAACAAGTATGGTTATGACAACCTATAAAAG
CTACAGCAGGTAAGAAAGAGCTTATATTGTAAGGGGAAACATGCG
AAATCTTITGAAAGAGCCAGAAAATATGAGAAACGTATCTCTAGTTT
TTGAAAAAATGAAAAA

SEQ ID NO. 8311

STRAIN JM9130013

GCTAGTTTATTTTCCACGTTGCCAAGTCG
AGATGATAAAATCCTTTATTCAAATGTCACCAAGCCTGGAAACTCTT
TATATGCTTATGATAAAATCTTGTATAAGCTTAAAGCaaaaATGAA
ATGCAACAAAATATAAGCAAGTGTCTGTATGTTCTGCTGTAA
GAAAATCTATAAGACAGCIGTTGCTGTATCATGGTTTGCGAATAGCAAAG
AGAATATGAAGGCATATGCTTGGCTTCTATAAGTAGGATACATAAGT
CTTATGGCTGACAATTGTCACATGGTGAAGTCATGGCAGGTGTGATAGG
CTATGGCTGGAACGACCCCGAGAACATATCaAAATGGACAGAAATGATAG
TTGATAAGAATCCATACGCCCCAAATTCTTATTTGGTTTCAATGGGT
GGAGCAACAGTCATGATGGCTGATGGTAAAAAACTACAGTCAGGTGTT
TAATATCATGTAAGAGATTGGCTTATTCTAGTGTGTTGGGATgAATTAaaaAT
TTCAAGGCTAAAGAGATGTATGGTTACCGCCCTCCACTCTTATGAA
GTTTCAACAAATTCTAAATCAGAGCGGTTTCTGCTATGGACAAGCAGA
TAGTGTGCAACAAATGAAAAGAATATTCTACAGCCCTTCTTATTCTGATG
GTGATAAGGATAATTCTGTTCCAACAGTATGGTTATGACAACATAAAA
GCTACAGCAGGTAAGAAAGAGCTTTATTTGTAAGGGCCAAAACATGC
GAAATCTTCTTAAACAGGCCAGAAAATATGAGAAACGTATCTCTAGTT
TTTTGAAAATGAAA

PRETTY OF: /biotmp/msa286608.2{*} February 24, 2003 06:26 ..

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msa286608.2{662_COH1} 1
msa286608.2{662_M732}
msa286608.2{662_M781}
msa286608.2{662_A909}
msa286608.2{662_H36B}
msa286608.2{662_090}
msa286608.2{662_CJB110}
msa286608.2{662_18RS21}
msa286608.2{662_2603} atgaaaaaga ttgcattatc aaagtttatt aaaaatgattg ttgttattt
msa286608.2{662_JM9130013}
msa286608.2{662_1169NT} Consensus
***** 100
msa286608.2{662_COH1} 51
msa286608.2{662_M732}
msa286608.2{662_M781}

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Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_A909}	-----	-----	-----	-----	-----	-----
msa286608.2{662_H36B}	-----	-----	--agtttta	tttttccac	gttgcacaag	
msa286608.2{662_090}	-----	-----	g	ctagtttta	tttttccac	gttgcacaag
msa286608.2{662_CJB110}	-----	-----	g	ctagtttta	tttttccac	gttgcacaag
msa286608.2{662_18RS21}	-----	-----	g	ctagtttta	tttttccac	gttgcacaag
msa286608.2{662_2603}	gttttaatt	agttagcag	ctagtttta	tttttccac	gttgcacaag	
msa286608.2{662_JM9130013}	-----	-----	g	ctagtttta	tttttccac	gttgcacaag
msa286608.2{662_1169NT}	-----	-----	g	ctagtttta	tttttccac	gttgcacaag
Consensus	*****	*****	-----	-----	-----	
	101				150	
msa286608.2{662_COH1}	ttcgagatga	taAATCCTTT	ATTCAAATG	GTCAACGTAA	GCCTGGAAAC	
msa286608.2{662_M732}	ttcgagatga	taAATCCTTT	ATTCAAATG	GTCAACGTAA	GCCTGGAAAC	
msa286608.2{662_M781}	ttcgagatga	taAATCCTTT	ATTCAAATG	GTCAACGTAA	GCCTGGAAAC	
msa286608.2{662_A909}	-----	--AATCCTTT	ATTCAAATG	GTCAACGTAA	GCCTGGAAAC	
msa286608.2{662_H36B}	ttcgagatga	taAATCCTTT	ATTCAAATG	GTCAACGTAA	GCCTGGAAAC	
msa286608.2{662_090}	ttcgagatga	taAATCCTTT	ATTCAAATG	GTCAACGTAA	GCCTGGAAAC	
msa286608.2{662_CJB110}	ttcgagatga	taAATCCTTT	ATTCAAATG	GTCAACGTAA	GCCTGGAAAC	
msa286608.2{662_18RS21}	ttcgagatga	taAATCCTTT	ATTCAAATG	GTCAACGTAA	GCCTGGAAAC	
msa286608.2{662_2603}	ttcgagatga	taAATCCTTT	ATTCAAATG	GTCAACGTAA	GCCTGGAAAC	
msa286608.2{662_JM9130013}	ttcgagatga	taAATCCTTT	ATTCAAATG	GTCAACGTAA	GCCTGGAAAC	
msa286608.2{662_1169NT}	ttcgagatga	taAATCCTTT	ATTCAAATG	GTCAACGTAA	GCCTGGAAAC	
Consensus	*****	*****	-----	-----	*****	
	151				200	
msa286608.2{662_COH1}	TCTTATATG	CTTATGATAA	ATCCTTGAT	AAGCTATTAA	AGCAAAAAAT	
msa286608.2{662_M732}	TCTTATATG	CTTATGATAA	ATCCTTGAT	AAGCTATTAA	AGCAAAAAAT	
msa286608.2{662_M781}	TCTTATATG	CTTATGATAA	ATCCTTGAT	AAGCTATTAA	AGCAAAAAAT	
msa286608.2{662_A909}	TCTTATATG	CTTATGATAA	ATCCTTGAT	AAGCTATTAA	AGCAAAAAAT	
msa286608.2{662_H36B}	TCTTATATG	CTTATGATAA	ATCCTTGAT	AAGCTATTAA	AGCAAAAAAT	
msa286608.2{662_090}	TCTTATATG	CTTATGATAA	ATCCTTGAT	AAGCTATTAA	AGCAAAAAAT	
msa286608.2{662_CJB110}	TCTTATATG	CTTATGATAA	ATCCTTGAT	AAGCTATTAA	AGCAAAAAAT	
msa286608.2{662_18RS21}	TCTTATATG	CTTATGATAA	ATCCTTGAT	AAGCTATTAA	AGCAAAAAAT	
msa286608.2{662_2603}	TCTTATATG	CTTATGATAA	ATCCTTGAT	AAGCTATTAA	AGCAAAAAAT	
msa286608.2{662_JM9130013}	TCTTATATG	CTTATGATAA	ATCCTTGAT	AAGCTATTAA	AGCAAAAAAT	
msa286608.2{662_1169NT}	TCTTATATG	CTTATGATAA	ATCCTTGAT	AAGCTATTAA	AGCAAAAAAT	
Consensus	*****	*****	*****	*****	*****	
	201				250	
msa286608.2{662_COH1}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCTGCTG	
msa286608.2{662_M732}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCTGCTG	
msa286608.2{662_M781}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCTGCTG	
msa286608.2{662_A909}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCTGCTG	
msa286608.2{662_H36B}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCTGCTG	
msa286608.2{662_090}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCTGCTG	
msa286608.2{662_CJB110}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCTGCTG	
msa286608.2{662_18RS21}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCTGCTG	
msa286608.2{662_2603}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCTGCTG	
msa286608.2{662_JM9130013}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCTGCTG	
msa286608.2{662_1169NT}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCTGCTG	
Consensus	*****	*****	*****	*****	*****	
	251				300	
msa286608.2{662_COH1}	CTAAGAAAAC	TCATAAGACA	GtTGTTGTCG	TTCATGGTTT	TGCGAATAGC	
msa286608.2{662_M732}	CTAAGAAAAC	TCATAAGACA	GtTGTTGTCG	TTCATGGTTT	TGCGAATAGC	
msa286608.2{662_M781}	CTAAGAAAAC	TCATAAGACA	GtTGTTGTCG	TTCATGGTTT	TGCGAATAGC	
msa286608.2{662_A909}	CTAAGAAAAC	TCATAAGACA	GtTGTTGTCG	TTCATGGTTT	TGCGAATAGC	
msa286608.2{662_H36B}	CTAAGAAAAC	TCATAAGACA	GtTGTTGTCG	TTCATGGTTT	TGCGAATAGC	
msa286608.2{662_090}	CTAAGAAAAC	TCATAAGACA	GtTGTTGTCG	TTCATGGTTT	TGCGAATAGC	
msa286608.2{662_CJB110}	CTAAGAAAAC	TCATAAGACA	GtTGTTGTCG	TTCATGGTTT	TGCGAATAGC	
msa286608.2{662_18RS21}	tTAAGAAAAC	TCATAAGACA	GtTGTTGTCG	TTCATGGTTT	TGCGAATAGC	
msa286608.2{662_2603}	tTAAGAAAAC	TCATAAGACA	GtTGTTGTCG	TTCATGGTTT	TGCGAATAGC	
msa286608.2{662_JM9130013}	tTAAGAAAAC	TCATAAGACA	GtTGTTGTCG	TTCATGGTTT	TGCGAATAGC	
msa286608.2{662_1169NT}	tTAAGAAAAC	TCATAAGACA	GtTGTTGTCG	TTCATGGTTT	TGCGAATAGC	
Consensus	*****	*****	*****	*****	*****	
	301				350	
msa286608.2{662_COH1}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAAGT	TAGGATACAA	
msa286608.2{662_M732}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAAGT	TAGGATACAA	
msa286608.2{662_M781}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAAGT	TAGGATACAA	
msa286608.2{662_A909}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAAGT	TAGGATACAA	
msa286608.2{662_H36B}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAAGT	TAGGATACAA	
msa286608.2{662_090}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAAGT	TAGGATACAA	
msa286608.2{662_CJB110}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAAGT	TAGGATACAA	
msa286608.2{662_18RS21}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAAGT	TAGGATACAA	
msa286608.2{662_2603}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAAGT	TAGGATACAA	
msa286608.2{662_JM9130013}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAAGT	TAGGATACAA	
msa286608.2{662_1169NT}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAAGT	TAGGATACAA	
Consensus	*****	*****	*****	*****	*****	
	351				400	
msa286608.2{662_COH1}	TGTTCTTATG	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA	
msa286608.2{662_M732}	TGTTCTTATG	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA	

Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_M781}	TGTTCTTATG	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_A909}	TGTTCTTATG	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_H36B}	TGTTCTTATG	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_090}	TGTTCTTATG	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_CJB110}	TGTTCTTATG	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_18RS21}	TGTTCTTATG	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_2603}	TGTTCTTATG	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_JM9130013}	TGTTCTTATG	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_1169NT}	TGTTCTTATG	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
Consensus	*****	*****	*****	*****	*****
	401				450
msa286608.2{662_COH1}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACAA	TTATCAAATG	GACAGAAATG
msa286608.2{662_M732}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACAA	TTATCAAATG	GACAGAAATG
msa286608.2{662_M781}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACAA	TTATCAAATG	GACAGAAATG
msa286608.2{662_A909}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACAA	TTATCAAATG	GACAGAAATG
msa286608.2{662_H36B}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACAA	TTATCAAATG	GACAGAAATG
msa286608.2{662_090}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACAA	TTATCAAATG	GACAGAAATG
msa286608.2{662_CJB110}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACAA	TTATCAAATG	GACAGAAATG
msa286608.2{662_18RS21}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACAA	TTATCAAATG	GACAGAAATG
msa286608.2{662_2603}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACAA	TTATCAAATG	GACAGAAATG
msa286608.2{662_JM9130013}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACAA	TTATCAAATG	GACAGAAATG
msa286608.2{662_1169NT}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACAA	TTATCAAATG	GACAGAAATG
Consensus	*****	*****	*****	*****	*****
	451				500
msa286608.2{662_COH1}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTCAAT
msa286608.2{662_M732}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTCAAT
msa286608.2{662_M781}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTCAAT
msa286608.2{662_A909}	ATAGTtGATA	AGAATTcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTCAAT
msa286608.2{662_H36B}	ATAGTtGATA	AGAATTcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTCAAT
msa286608.2{662_090}	ATAGTtGATA	AGAATTcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTCAAT
msa286608.2{662_CJB110}	ATAGTtGATA	AGAATTcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTCAAT
msa286608.2{662_18RS21}	ATAGTtGATA	AGAATTcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTCAAT
msa286608.2{662_2603}	ATAGTtGATA	AGAATTcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTCAAT
msa286608.2{662_JM9130013}	ATAGTtGATA	AGAATTcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTCAAT
msa286608.2{662_1169NT}	ATAGTtGATA	AGAATTcCATC	AAGCCAAATT	ACTTTATTTG	GTGTTCAAT
Consensus	*****	*****	*****	*****	*****
	501				550
msa286608.2{662_COH1}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAAATTA	CCTAGTCAGG
msa286608.2{662_M732}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAAATTA	CCTAGTCAGG
msa286608.2{662_M781}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAAATTA	CCTAGTCAGG
msa286608.2{662_A909}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAAATTA	CCTAGTCAGG
msa286608.2{662_H36B}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAAATTA	CCTAGTCAGG
msa286608.2{662_090}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAAATTA	CCTAGTCAGG
msa286608.2{662_CJB110}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAAATTA	CCTAGTCAGG
msa286608.2{662_18RS21}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAAATTA	CCTAGTCAGG
msa286608.2{662_2603}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAAATTA	CCTAGTCAGG
msa286608.2{662_JM9130013}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAAATTA	CCTAGTCAGG
msa286608.2{662_1169NT}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAAATTA	CCTAGTCAGG
Consensus	*****	*****	*****	*****	*****
	551				600
msa286608.2{662_COH1}	TTGTTAATAT	CATTGAAGAT	TGtGGTTATT	CTaGTGTTTG	GGATGAATTAA
msa286608.2{662_M732}	TTGTTAATAT	CATTGAAGAT	TGtGGTTATT	CTaGTGTTTG	GGATGAATTAA
msa286608.2{662_M781}	TTGTTAATAT	CATTGAAGAT	TGtGGTTATT	CTaGTGTTTG	GGATGAATTAA
msa286608.2{662_A909}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTgGTGTTTG	GGATGAATTAA
msa286608.2{662_H36B}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTgGTGTTTG	GGATGAATTAA
msa286608.2{662_090}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTG	GGATGAATTAA
msa286608.2{662_CJB110}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTG	GGATGAATTAA
msa286608.2{662_18RS21}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTG	GGATGAATTAA
msa286608.2{662_2603}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTG	GGATGAATTAA
msa286608.2{662_JM9130013}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTG	GGATGAATTAA
msa286608.2{662_1169NT}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTG	GGATGAATTAA
Consensus	*****	*****	*****	*****	*****
	601				650
msa286608.2{662_COH1}	AAATTCAGG	CTAAAGAGAT	GTATGGTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_M732}	AAATTCAGG	CTAAAGAGAT	GTATGGTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_M781}	AAATTCAGG	CTAAAGAGAT	GTATGGTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_A909}	AAATTCAGG	CTAAAGAGAT	GTATGGTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_H36B}	AAATTCAGG	CTAAAGAGAT	GTATGGTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_090}	AAATTCAGG	CTAAAGAGAT	GTATGGTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_CJB110}	AAATTCAGG	CTAAAGAGAT	GTATGGTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_18RS21}	AAATTCAGG	CTAAAGAGAT	GTATGGTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_2603}	AAATTCAGG	CTAAAGAGAT	GTATGGTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_JM9130013}	AAATTCAGG	CTAAAGAGAT	GTATGGTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_1169NT}	AAATTCAGG	CTAAAGAGAT	GTATGGTTA	CCAGCCTTCC	CACTCTTATA
Consensus	*****	*****	*****	*****	*****
	651				700
msa286608.2{662_COH1}	TGAAGTTCA	ACAATTCTA	AAATCAGAGC	AGGTTTTCG	TATGGACAAG

Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_M732}	TGAAGTTCA ACAATTCATA AAATCAGAGC AGGTTTTCG TATGGACAAG	701	750
msa286608.2{662_M781}	TGAAGTTCA ACAATTCATA AAATCAGAGC AGGTTTTCG TATGGACAAG	msa286608.2{662_A909}	msa286608.2{662_H36B}
msa286608.2{662_A909}	TGAAGTTCA ACAATTCATA AAATCAGAGC AGGTTTTCG TATGGACAAG	TGAAGTTCA ACAATTCATA AAATCAGAGC AGGTTTTCG TATGGACAAG	TGAAGTTCA ACAATTCATA AAATCAGAGC AGGTTTTCG TATGGACAAG
msa286608.2{662_090}	TGAAGTTCA ACAATTCATA AAATCAGAGC AGGTTTTCG TATGGACAAG	msa286608.2{662_CJB110}	msa286608.2{662_18RS21}
msa286608.2{662_CJB110}	TGAAGTTCA ACAATTCATA AAATCAGAGC AGGTTTTCG TATGGACAAG	msa286608.2{662_18RS21}	msa286608.2{662_2603}
msa286608.2{662_18RS21}	TGAAGTTCA ACAATTCATA AAATCAGAGC AGGTTTTCG TATGGACAAG	msa286608.2{662_JM9130013}	msa286608.2{662_1169NT}
msa286608.2{662_JM9130013}	TGAAGTTCA ACAATTCATA AAATCAGAGC AGGTTTTCG TATGGACAAG	Consensus	*****
msa286608.2{662_1169NT}	*****	Consensus	*****
msa286608.2{662_COH1}	CAAGTAGTGT CGAACATTG AAAAGAATA ATTACCGAG CCTCTTTATT	751	800
msa286608.2{662_M732}	CAAGTAGTGT CGAACATTG AAAAGAATA ATTACCGAG CCTCTTTATT	msa286608.2{662_M781}	msa286608.2{662_A909}
msa286608.2{662_M781}	CAAGTAGTGT CGAACATTG AAAAGAATA ATTACCGAG CCTCTTTATT	TGAAGTTCA ACAATTCATA AAATCAGAGC AGGTTTTCG TATGGACAAG	TGAAGTTCA ACAATTCATA AAATCAGAGC AGGTTTTCG TATGGACAAG
msa286608.2{662_A909}	CAAGTAGTGT CGAACATTG AAAAGAATA ATTACCGAG CCTCTTTATT	msa286608.2{662_H36B}	msa286608.2{662_090}
msa286608.2{662_H36B}	CAAGTAGTGT CGAACATTG AAAAGAATA ATTACCGAG CCTCTTTATT	msa286608.2{662_CJB110}	msa286608.2{662_18RS21}
msa286608.2{662_090}	CAAGTAGTGT CGAACATTG AAAAGAATA ATTACCGAG CCTCTTTATT	msa286608.2{662_18RS21}	msa286608.2{662_2603}
msa286608.2{662_CJB110}	CAAGTAGTGT CGAACATTG AAAAGAATA ATTACCGAG CCTCTTTATT	msa286608.2{662_JM9130013}	msa286608.2{662_1169NT}
msa286608.2{662_18RS21}	CAAGTAGTGT CGAACATTG AAAAGAATA ATTACCGAG CCTCTTTATT	msa286608.2{662_JM9130013}	msa286608.2{662_1169NT}
msa286608.2{662_JM9130013}	CAAGTAGTGT CGAACATTG AAAAGAATA ATTACCGAG CCTCTTTATT	Consensus	*****
msa286608.2{662_1169NT}	*****	Consensus	*****
msa286608.2{662_COH1}	CATGGTGATA AGGATAATTG TGTTCCAACA AGTATGGTTT ATGACAACTA	801	850
msa286608.2{662_M732}	CATGGTGATA AGGATAATTG TGTTCCAACA AGTATGGTTT ATGACAACTA	msa286608.2{662_M781}	msa286608.2{662_A909}
msa286608.2{662_M781}	CATGGTGATA AGGATAATTG TGTTCCAACA AGTATGGTTT ATGACAACTA	TGAAGCTACA GCAGGTAAGA AAGAGCTTAA TATTGTAAAA GGGGCAAAAC	TAAAGCTACA GCAGGTAAGA AAGAGCTTAA TATTGTAAAA GGGGCAAAAC
msa286608.2{662_A909}	CATGGTGATA AGGATAATTG TGTTCCAACA AGTATGGTTT ATGACAACTA	msa286608.2{662_H36B}	msa286608.2{662_090}
msa286608.2{662_H36B}	CATGGTGATA AGGATAATTG TGTTCCAACA AGTATGGTTT ATGACAACTA	msa286608.2{662_CJB110}	msa286608.2{662_18RS21}
msa286608.2{662_090}	CATGGTGATA AGGATAATTG TGTTCCAACA AGTATGGTTT ATGACAACTA	msa286608.2{662_18RS21}	msa286608.2{662_2603}
msa286608.2{662_CJB110}	CATGGTGATA AGGATAATTG TGTTCCAACA AGTATGGTTT ATGACAACTA	msa286608.2{662_JM9130013}	msa286608.2{662_1169NT}
msa286608.2{662_18RS21}	CATGGTGATA AGGATAATTG TGTTCCAACA AGTATGGTTT ATGACAACTA	msa286608.2{662_JM9130013}	msa286608.2{662_1169NT}
msa286608.2{662_JM9130013}	CATGGTGATA AGGATAATTG TGTTCCAACA AGTATGGTTT ATGACAACTA	msa286608.2{662_1169NT}	msa286608.2{662_1169NT}
msa286608.2{662_1169NT}	*****	Consensus	*****
msa286608.2{662_COH1}	TAAAGCTACA GCAGGTAAGA AAGAGCTTAA TATTGTAAAA GGGGCAAAAC	851	900
msa286608.2{662_M732}	TAAAGCTACA GCAGGTAAGA AAGAGCTTAA TATTGTAAAA GGGGCAAAAC	msa286608.2{662_M781}	msa286608.2{662_A909}
msa286608.2{662_M781}	TAAAGCTACA GCAGGTAAGA AAGAGCTTAA TATTGTAAAA GGGGCAAAAC	TAAAGCTACA GCAGGTAAGA AAGAGCTTAA TATTGTAAAA GGGGCAAAAC	TAAAGCTACA GCAGGTAAGA AAGAGCTTAA TATTGTAAAA GGGGCAAAAC
msa286608.2{662_A909}	TAAAGCTACA GCAGGTAAGA AAGAGCTTAA TATTGTAAAA GGGGCAAAAC	msa286608.2{662_H36B}	msa286608.2{662_090}
msa286608.2{662_H36B}	TAAAGCTACA GCAGGTAAGA AAGAGCTTAA TATTGTAAAA GGGGCAAAAC	msa286608.2{662_CJB110}	msa286608.2{662_18RS21}
msa286608.2{662_090}	TAAAGCTACA GCAGGTAAGA AAGAGCTTAA TATTGTAAAA GGGGCAAAAC	msa286608.2{662_18RS21}	msa286608.2{662_2603}
msa286608.2{662_CJB110}	TAAAGCTACA GCAGGTAAGA AAGAGCTTAA TATTGTAAAA GGGGCAAAAC	msa286608.2{662_JM9130013}	msa286608.2{662_1169NT}
msa286608.2{662_18RS21}	TAAAGCTACA GCAGGTAAGA AAGAGCTTAA TATTGTAAAA GGGGCAAAAC	msa286608.2{662_JM9130013}	msa286608.2{662_1169NT}
msa286608.2{662_JM9130013}	TAAAGCTACA GCAGGTAAGA AAGAGCTTAA TATTGTAAAA GGGGCAAAAC	msa286608.2{662_1169NT}	msa286608.2{662_1169NT}
msa286608.2{662_1169NT}	*****	Consensus	*****
msa286608.2{662_COH1}	AGTTTTTGTG AAAAATATGA AAAA	901	924
msa286608.2{662_M732}	AGTTTTTGTG AAAAATATGA AAAA	msa286608.2{662_M781}	msa286608.2{662_A909}
msa286608.2{662_M781}	AGTTTTTGTG AAAAATATGA AAAA	msa286608.2{662_H36B}	msa286608.2{662_090}
msa286608.2{662_A909}	AGTTTTTGTG AAAAATATGA AAAA	msa286608.2{662_CJB110}	msa286608.2{662_18RS21}
msa286608.2{662_H36B}	AGTTTTTGTG AAAAATATGA AAAA	msa286608.2{662_2603}	msa286608.2{662_JM9130013}
msa286608.2{662_090}	AGTTTTTGTG AAAAATATGA AAAA	msa286608.2{662_JM9130013}	msa286608.2{662_1169NT}
msa286608.2{662_CJB110}	AGTTTTTGTG AAAAATATGA AAAA	msa286608.2{662_18RS21}	msa286608.2{662_1169NT}
msa286608.2{662_18RS21}	AGTTTTTGTG AAAAATATGA AAAA	msa286608.2{662_2603}	msa286608.2{662_JM9130013}
msa286608.2{662_2603}	AGTTTTTGTG AAAAATATGA AAAA	msa286608.2{662_JM9130013}	msa286608.2{662_1169NT}
msa286608.2{662_JM9130013}	AGTTTTTGTG AAAAATATGA AAAA	msa286608.2{662_1169NT}	msa286608.2{662_1169NT}
msa286608.2{662_1169NT}	*****	Consensus	*****

SEQ ID NO. 8312

Table 83: Comparative Sequences relating to SAG0108

STRAIN 2603 frame: 1

MKKIRLSKF1KMIIVVILFL1SVAASFYFFHVAQVRDDKSF1SNGQRKPGNSLYAYDKSF
 KLLQK1EMTNQNIKQVAWYVPAVKKTHKTAVVHGANSKENMKAYGWLPHKLGYNVLM
 PDNIAHGESHGQLIGYGWNDRENI1IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKL
 PSQVNNIIEDCGYSSVWDELKFQAKEMYGLPAFPPLLYEVSTISKIRAGFSYQGQASSVEQ
 KKNLNLPAFL1HGDKDNFVPTSMVYDNYKATAGKKELYIVKGAKHAKSFETEPEKYEK
 SFLKKYEK

SEQ ID NO. 8313

STRAIN 090 frame: 1

ASFYFFFHVAQVRDDKSF1SNGQRKPGNSLYAYDKSF1KQ1EMTNQNIKQVAWYVPA
 AKKTHKTAVVVGFGANSKENMKAYGWLPHKLGYNVLMFDNIAHGESHGQLIGYGWNDREN
 I1IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVNNIIEDCGYSSVWDELKFQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGQASSVEQLKNNLPAFL1HGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8314

STRAIN A909 frame: 3

SF1SNGQRKPGNSLYAYDKSF1KQ1EMTNQNIKQVAWYVPAAKKTHKTAVVHGFA
 NSKE1NMKAYGWLPHKLGYNVLMFDNIAHGESHGQLIGYGWNDRENI1IKWTEMIVDKN
 SSQITLFGVSMGGATVMMASGEKLPSQVNNIIEDCGYSSVWDELKFQ
 VSTISKIRAGFSYQGQASSVEQLKNNLPAFL1HGDKDNFVPTSMVYDNYKATAGKK
 ELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8315

STRAIN H36B frame: 1

ASFYFFFHVAQVRDDKSF1SNGQRKPGNSLYAYDKSF1KQ1EMTNQNIKQVAWYVPA
 KKTHKTAVVVGFGANSKENMKAYGWLPHKLGYNVLMFDNIAHGESHGQLIGYGWNDREN
 I1IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVNNIIEDCGYSSVWDELKFQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGQASSVEQLKNNLPAFL1HGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8316

STRAIN 18RS21 frame: 1

ASFYFFFHVAQVRDDKSF1SNGQRKPGNSLYAYDKSF1KQ1EMTNQNIKQVAWYVPA
 VKKTHKTAVVVGFGANSKENMKAYGWLPHKLGYNVLMFDNIAHGESHGQLIGYGWNDREN
 I1IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVNNIIEDCGYSSVWDELKFQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGQASSVEQLKNNLPAFL1HGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8317

STRAIN M732 frame: 1

ASFYFFFHVAQVRDDKSF1SNGQRKPGNSLYAYDKSF1KQ1EMTNQNIKQVAWYVPA
 AKKTHKTAVVVGFGANSKENMKAYGWLPHKLGYNVLMFDNIAHGESHGQLIGYGWNDREN
 I1IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVNNIIEDCGYSSVWDELKFQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGQASSVEQLKNNLPAFL1HGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8318

STRAIN COHI frame: 1

ASFYFFFHVAQVRDDKSF1SNGQRKPGNSLYAYDKSF1KQ1EMTNQNIKQVAWYVPA
 AKKTHKTAVVVGFGANSKENMKAYGWLPHKLGYNVLMFDNIAHGESHGQLIGYGWNDREN
 I1IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVNNIIEDCGYSSVWDELKFQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGQASSVEQLKNNLPAFL1HGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8319

STRAIN M781 frame: 1

ASFYFFFHVAQVRDDKSF1SNGQRKPGNSLYAYDKSF1KQ1EMTNQNIKQVAWYVPA
 AKKTHKTAVVVGFGANSKENMKAYGWLPHKLGYNVLMFDNIAHGESHGQLIGYGWNDREN
 I1IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVNNIIEDCGYSSVWDELKFQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGQASSVEQLKNNLPAFL1HGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8320

STRAIN CJB110 frame: 1

ASFYFFFHVAQVRDDKSF1SNGQRKPGNSLYAYDKSF1KQ1EMTNQNIKQVAWYVPA
 AKKTHKTAVVVGFGANSKENMKAYGWLPHKLGYNVLMFDNIAHGESHGQLIGYGWNDREN
 I1IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVNNIIEDCGYSSVWDELKFQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGQASSVEQLKNNLPAFL1HGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8321

STRAIN 1169NT frame: 1

ASFYFFFHVAQVRDDKSF1SNGQRKPGNSLYAYDKSF1KQ1EMTNQNIKQVAWYVPA
 AKKTHKTAVVVGFGANSKENMKAYGWLPHKLGYNVLMFDNIAHGESHGQLIGYGWNDREN
 I1IKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPSQVNNIIEDCGYSSVWDELKFQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGQASSVEQLKNNLPAFL1HGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISSFLKKYEK

SEQ ID NO. 8322

Table 83: Comparative Sequences relating to SAG0108

STRAIN JM9130013 frame: 1
 ASFYFFFVAQVRDDKSFISNGQRKPGNSLYAYDKSF DKLKQKIEMTNQN1 KQVAWYVPA
 VKTTHKTAVVVHGFANSKENMKGWLFHKLGYNVLMPDNIAHGESHGQLIGYGWNDRN
 IIKWTEMIVDKNPSSQITLFGVSMGGATVMMASGEKLPQVNNIIEDCGYSSVWDELKFO
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGASSVEQLKKNNLPALFIHGDKDNFVPTSMV
 YDNYKATAGKKELEYIVKGAKHAKSFETEPEKYEKRISSFLKYEK

PRETTY of: /biotmp/msa286876.2{*} February 24, 2003 06:46 ..

						50
msa286876.2{662_A909}	-----	-----	-----	-----	SF	ISNGQRKPGN
msa286876.2{662_H36B}	-----	-----	-----	SFYFFF	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_COH1}	-----	-----	-----	ASFYFFF	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_M732}	-----	-----	-----	ASFYFFF	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_M781}	-----	-----	-----	ASFYFFF	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_18RS21}	-----	-----	-----	ASFYFFF	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_2603}	mkkirlskf1	kmivvifl1	svaAFYFFF	VAQVRDDKSF	ISNGQRKPGN	
msa286876.2{662_JM9130013}	-----	-----	-----	ASFYFFF	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_090}	-----	-----	-----	ASFYFFF	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_CJB110}	-----	-----	-----	ASFYFFF	VAQVRDDKSF	ISNGQRKPGN
msa286876.2{662_1169NT}	-----	-----	-----	ASFYFFF	VAQVRDDKSF	ISNGQRKPGN
Consensus	*****	*****	*****	*****	*****	*****
						100
msa286876.2{662_A909}	SLIAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAaKKTHKT	aVVVHGFANS	
msa286876.2{662_H36B}	SLIAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAaKKTHKT	aVVVHGFANS	
msa286876.2{662_COH1}	SLIAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAaKKTHKT	vVVVHGFANS	
msa286876.2{662_M732}	SLIAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAaKKTHKT	vVVVHGFANS	
msa286876.2{662_M781}	SLIAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAaKKTHKT	vVVVHGFANS	
msa286876.2{662_18RS21}	SLIAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAvKKTHKT	aVVVHGFANS	
msa286876.2{662_2603}	SLIAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAvKKTHKT	aVVVHGFANS	
msa286876.2{662_JM9130013}	SLIAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAvKKTHKT	aVVVHGFANS	
msa286876.2{662_090}	SLIAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAaKKTHKT	aVVVHGFANS	
msa286876.2{662_CJB110}	SLIAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAaKKTHKT	aVVVHGFANS	
msa286876.2{662_1169NT}	SLIAYDKSFD	KLLKQKIEMT	NQNIKQVAWY	VPAaKKTHKT	aVVVHGFANS	
Consensus	*****	*****	*****	*****	*****	*****
						150
msa286876.2{662_A909}	KENMKAYGWL	FHKLGYNVLm	PDNIAHGESh	GQLIGYGWND	RENIIKWTEM	
msa286876.2{662_H36B}	KENMKAYGWL	FHKLGYNVLm	PDNIAHGESh	GQLIGYGWND	RENIIKWTEM	
msa286876.2{662_COH1}	KENMKAYGWL	FHKLGYNVLm	PDNIAHGESh	GQLIGYGWND	RENIIKWTEM	
msa286876.2{662_M732}	KENMKAYGWL	FHKLGYNVLm	PDNIAHGESh	GQLIGYGWND	RENIIKWTEM	
msa286876.2{662_M781}	KENMKAYGWL	FHKLGYNVLm	PDNIAHGESh	GQLIGYGWND	RENIIKWTEM	
msa286876.2{662_18RS21}	KENMKAYGWL	FHKLGYNVLm	PDNIAHGESh	GQLIGYGWND	RENIIKWTEM	
msa286876.2{662_2603}	KENMKAYGWL	FHKLGYNVLm	PDNIAHGESh	GQLIGYGWND	RENIIKWTEM	
msa286876.2{662_JM9130013}	KENMKAYGWL	FHKLGYNVLm	PDNIAHGESh	GQLIGYGWND	RENIIKWTEM	
msa286876.2{662_090}	KENMKAYGWL	FHKLGYNVLm	PDNIAHGESh	GQLIGYGWND	RENIIKWTEM	
msa286876.2{662_CJB110}	KENMKAYGWL	FHKLGYNVLm	PDNIAHGESh	GQLIGYGWND	RENIIKWTEM	
msa286876.2{662_1169NT}	KENMKAYGWL	FHKLGYNVLm	PDNIAHGESh	GQLIGYGWND	RENIIKWTEM	
Consensus	*****	*****	*****	*****	*****	*****
						200
msa286876.2{662_A909}	IVDKNsSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVNNIIED	CGYSSVWDEL	
msa286876.2{662_H36B}	IVDKNsSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVNNIIED	CGYSSVWDEL	
msa286876.2{662_COH1}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVNNIIED	CGYSSVWDEL	
msa286876.2{662_M732}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVNNIIED	CGYSSVWDEL	
msa286876.2{662_M781}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVNNIIED	CGYSSVWDEL	
msa286876.2{662_18RS21}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVNNIIED	CGYSSVWDEL	
msa286876.2{662_2603}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVNNIIED	CGYSSVWDEL	
msa286876.2{662_JM9130013}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVNNIIED	CGYSSVWDEL	
msa286876.2{662_090}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVNNIIED	CGYSSVWDEL	
msa286876.2{662_CJB110}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVNNIIED	CGYSSVWDEL	
msa286876.2{662_1169NT}	IVDKNpSSQI	TLFGVSMGGA	TVMMASGEKL	PSQVNNIIED	CGYSSVWDEL	
Consensus	*****	*****	*****	*****	*****	*****
						250
msa286876.2{662_A909}	KFQAKEMYGL	PAFPPLLYEVs	TISKIRAGFS	YQQASSVEQL	KKNNLPALFI	
msa286876.2{662_H36B}	KFQAKEMYGL	PAFPPLLYEVs	TISKIRAGFS	YQQASSVEQL	KKNNLPALFI	
msa286876.2{662_COH1}	KFQAKEMYGL	PAFPPLLYEVs	TISKIRAGFS	YQQASSVEQL	KKNNLPALFI	
msa286876.2{662_M732}	KFQAKEMYGL	PAFPPLLYEVs	TISKIRAGFS	YQQASSVEQL	KKNNLPALFI	
msa286876.2{662_M781}	KFQAKEMYGL	PAFPPLLYEVs	TISKIRAGFS	YQQASSVEQL	KKNNLPALFI	
msa286876.2{662_18RS21}	KFQAKEMYGL	PAFPPLLYEVs	TISKIRAGFS	YQQASSVEQL	KKNNLPALFI	
msa286876.2{662_2603}	KFQAKEMYGL	PAFPPLLYEVs	TISKIRAGFS	YQQASSVEQL	KKNNLPALFI	
msa286876.2{662_JM9130013}	KFQAKEMYGL	PAFPPLLYEVs	TISKIRAGFS	YQQASSVEQL	KKNNLPALFI	
msa286876.2{662_090}	KFQAKEMYGL	PAFPPLLYEVs	TISKIRAGFS	YQQASSVEQL	KKNNLPALFI	
msa286876.2{662_CJB110}	KFQAKEMYGL	PAFPPLLYEVs	TISKIRAGFS	YQQASSVEQL	KKNNLPALFI	
msa286876.2{662_1169NT}	KFQAKEMYGL	PAFPPLLYEVs	TISKIRAGFS	YQQASSVEQL	KKNNLPALFI	
Consensus	*****	*****	*****	*****	*****	*****
						300
msa286876.2{662_A909}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS	
msa286876.2{662_H36B}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS	
msa286876.2{662_COH1}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS	

Table 83: Comparative Sequences relating to SAG0108

msa286876.2{662_M732}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_M781}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_18RS21}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_2603}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_JM9130013}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_090}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_CJB110}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
msa286876.2{662_1169NT}	HGDKDNFVPT	SMVYDNYKAT	AGKKELYIVK	GAKHAKSFET	EPEKYEKRIS
Consensus	*****	*****	*****	*****	*****
msa286876.2{662_A909}	SFLKKYEK	301			
msa286876.2{662_H36B}	SFLKKYEK				
msa286876.2{662_COH1}	SFLKKYEK				
msa286876.2{662_M732}	SFLKKYEK				
msa286876.2{662_M781}	SFLKKYEK				
msa286876.2{662_18RS21}	SFLKKYEK				
msa286876.2{662_2603}	SFLKKYEK				
msa286876.2{662_JM9130013}	SFLKKYEK				
msa286876.2{662_090}	SFLKKYEK				
msa286876.2{662_CJB110}	SFLKKYEK				
msa286876.2{662_1169NT}	SFLKKYEK				
Consensus	*****				

Table 84: Comparative Sequences relating to SAG0267**SEQ ID NO. 8401****STRAIN 2603**

ATGATGAAAGTTTAGCCTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACTAAAC
 AATATGGAATGTTAGCAGTGTCACTATCAATATCAAAAAGAATCATAGCATTAAATTG
 ATCGCAGGATTGATTTTAATGCAATATTGATTTAGGAAACCTCAAGGATTTGGACCGT
 ATCGTAGTACGAGGGCTTACGCTTACGCTGTAGCTGTAGCTGTACAGCA
 AAAATGCTAGCTTACGCTTAAAGATTGACTTATGGAGATCTAGCTGTACGCC
 ACAAATGGATTTCAGAAAATGATTATTGGTACCACTTATAGATGCACGACGTAATAAT
 GTTATGTTGTTCTAAATGTTAGGATCTAGTTAAACAGACTGTACACTTCTCTT
 GAGAAGGCTTACAAGAGTGGGAAATAAGCAATGTCATTGTCGGAGAGGTTGCA
 GCATTITGATCAGATAAGAAAGCCTTACCATGCTAAATTACAGAAACTTACCT
 TGCGCAGTACGCAATTGGCGCAAGGACAAAAAATGAAAGCCTTAATGTAGATGCGTT
 GTTCACGATACTTAAACGTTGAGCTGAGGAAAATTGGTAAACCAACTGTGAA
 ACGAATACAGAAGAATATTAAGAGAGTT

SEQ ID NO. 8402**STRAIN 090**

AAAGTTTAGCCTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACT
 AAACAAATGGAATGTTAGCAGTGTCACTATCAATATCAAAAAGAATC
 ATAGCATTAAATTGATGCCAGCCATTGATTTTAAATGCAATCAATTGAT
 TTAGAACCTCAAGATTGGACCGTATCGTAGTGGCAGAGGGTCCAGGATC
 TTATACGGGCTACGCTAGCTGTGCTACAGCAAAATGCTAGCTTATA
 CGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACGCTTAAACAAAT
 CGATTTCAGAAAATGATTGTTGCTTACCACTTATAGATCACGACGTTA
 CAATGTTTATGTTGTTCTAAAAATGGTGTACTGTTAAACCAGACT
 GTCACACTTCTGGAAGACTTACAGGAGGTGGGAAATAAGCCAAT
 GTTCATTITGTCGGAGAGGTTGCAAGCATTGATCAGATTAAAGAAC
 CTTACACATGCTAAAATTACAGAAACTTACCTTGTGCGTGGCAATTG
 GCGCAAAAGGACAAAAAATGAAAGCCTTAATGTAGATGCCATTGTTCA
 CGATACTTAAACGTTGAGCTGAGGAAAATTGGTAAACCAACTG
 TGAAACGAAT

SEQ ID NO. 8403**STRAIN A909**

AAAGTTTAGCCTTGATACTTCAAGCAAAGCACTATCAG
 TGCGCTGACTAAACAATATGGAATGTTAGCAGTGTCACTATCAATATC
 AAAAAGAATCATGCTTAAATTGATGCCAGCCATTGATTTTAAATGCA
 ATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GTCCAGGATCTTACGGGCTTACGTTAGCTGTAGCTGTACAGCAAAATG
 CTAGCTTACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 TTTAACAAATGGATTTCAGAAAATGATTATTGGTACCACTTATAGAT
 CACGACGTAACAATGTTATGTTGTTCTATCAAATGGAGATACTGTT
 AAACCGAGCTGACACTTCTTGAAGAAGTCTTACAAGAGGTGGGAA
 TAAGCCAATGTCATTITGTCGGAGAGGTTGCAAGCATTGTTGACCA
 tTAAGAAAGTTTACCATGCTAAAATTACAGAAACTTACCTTGTGCA
 GCGCAATTGGCGCAAGGACAAAAAATGAAAGCCTTAATGTAGATGC
 GTTGTCCACGATACTTAAACGTTGAGCTGAGGAAAATTGGTAA
 GAAACCACTGTGAAACGAATACAGAAGAATATTAAGAGAGTT

SEQ ID NO. 8404**STRAIN H36B**

AAAGTTTAGCCTTGATACTTCAAGCAAAGCACTATCAG
 TGCGCTGACTAAACAATATGGAATGTTAGCAGTGTCACTATCAATATC
 AAAAAGAATCATGCTTAAATTGATGCCAGCCATTGATTTTAAATGCA
 ATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GTTCAGGATCTTACGGGCTTACGTTAGCTGTAGCTGTACAGCAAAAT
 GCTAGCTTACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTAACAAATGGATTTCAGAAAATGATTATTGGTACCACTTATAGAT
 GCACGACGTAACAATGTTATGTTGTTCTATCAAATGGAGATACTGTT
 TAAACCGAGCTGACACTTCTTGAAGAAGTCTTACAAGAGGTGGGAA
 ATAAGCCAATGTCATTITGTCGGAGAGGTTGCAAGCATTGTTGACCA
 ATTAAGAAAAGTTTACCATGCTAAAATTACAGAAACTTACCTTGTGCA
 AGTGGCAATTGGCGCAAGGACAAAAAATGAAAGCCTTAATGTAGATG
 CGTTGTCCACGATACTTAAACGTTGAGCTGAGGAAAATTGGTAA
 AGAAACCACTGTGAAACGAATACAGAAGAATATTAAGAGAGTT

SEQ ID NO. 8405**STRAIN 18RS21**

AAAGTTTAGCCTTGATACTTCAAGCAAAGCACTATCAG
 TGCGCTGACTAAACAATATGGAATGTTAGCAGTGTCACTATCAATATC
 AAAAAGAATCATGCTTAAATTGATGCCAGCCATTGATTTTAAATGCA
 ATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GTTCAGGATCTTACGGGCTTACGTTAGCTGTAGCTGTACAGCAAAAT
 GCTAGCTTACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
 CTTAACAAATGGATTTCAGAAAATGATTATTGGTACCACTTATAGAT
 GCACGACGTAATAATGTTATGTTGTTCTATCAAATGGTGTACTGTT
 TAAACCGAGCTGACACTTCTTGAAGAAGTCTTACAAGAGGTGGGAA
 ATAAGCCAATGTCATTITGTCGGAGAGGTTGCAAGCATTGTTGACCA
 ATTAAGAAAAGCCTTACCATGCTAAAATTACAGAAACTTACCTTGTGCA
 AGTGGCAATTGGCGCAAGGACAAAAAATGAAAGCCTTAATGTAGATG
 CGTTGTCCACGATACTTAAACGTTGAGCTGAGGAAAATTGGTAA
 GAAACCACTGTGAAACGAATACAGAAGAATATTAAGAGAGTT

Table 84: Comparative Sequences relating to SAG0267**SEQ ID NO. 8406**

STRAIN M732

AAAGTTTAGCCTTGATACTCAAGCAAAGCACTATCA
 GTGGCTGACTAAACAATATGGAATGTTAGCGACTGTCACTATCAATAT
 CAAAAAGAATCATAGCATTAAATTGATGCCAGCCATTGATTTTAAATGC
 AATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GGTCCAGGATCTTACGGCTTACGTGTAGCTGTGCTACAGAAAAAT
 GCTAGCTTACGGCTTACGTGTAGCTGTGCTACAGAAAAAT
 CTTTAACAAATGGATTTCAGAAAATGATTGTTGCTACCACTTATAGAT
 GCACGACGTAACATGTTATGTTGCTTCTATCAAATGGTGTACTGT
 TAAACCAAGACTGTCAACACTTCTTGAAGAAGTCTTACAAGAGGTGGGA
 ATAAAGCCAATGTTCTTGTGGAGAGGTGCAAGCATTGGATCAG
 ATTAAGAAAGCCTTACACATGCTAAAATTACAGAAAACCTTACCTTGTC
 AGTAGCAATTGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGTAGAnn
 CGTTGTTCCACGATACTTAAACGTGTTGAAGCTGAGGAAAATTGGGTTA
 AAAAACCAACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8407

STRAIN COH1

AAAGTTTAGCCTTGATACTCAAGCAAAGCAC
 TATCAGTGGCTGACTAAACAATATGGAATGTTAGCGACTGTCACTATC
 AATATCAAAAAGAATCATAGCATTAAATTGATGCCAGCCATTGATTTTAA
 AATGCAATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAG
 CAGAGGGTCCAGGATCTTACGGCTTACGTGTAGCTGTGCTACAGCA
 AAAATGCTAGCTTACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCT
 GTACGCTTAAACAAATGGATTTCAGAAAATGATTGTTGGTACCACTTA
 TAGATGCACGACGTAACATGTTATGTTGCTTCTATCAAATGGTGT
 ACTGTTAAACCAAGACTGTCAACACTTCTTGAAGAAGTCTTACAAGAGGT
 GGGGATAAAAGCCAATGTTCTTGTGGAGAGGTGCAAGCATTGGAT
 ATCAGATTAAGAAAGCCTTACACATGCTAAAATTACAGAAAACCTTACCT
 TGTCAGTAGCAATTGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGT
 AGATGGGTTGTTCCACGATACTTAAACGTGTTGAAGCTGAGGAAAATT
 GTTAAAAAACCAACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8408

STRAIN M781

AAAGTTTAGCCTTGATACTCAAGCAAAGCACTA
 TCAGTGGCTGACTAAACAATATGGAATGTTAGCGACTGTCACTATCAA
 TATCAAAAAGAATCATAGCATTAAATTGATGCCAGCCATTGATTTTAA
 TGCATTAATGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGTATCA
 GAGGGTCCAGGATCTTACGGCTTACGTGTAGCTGTGCTACAGCAA
 AATGCTAGCTTACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTG
 ACGCTTAAACAAATGGATTTCAGAAAATGATTGTTGGTACCACTTATA
 GATGCACGACGTAACATGTTATGTTGCTTCTATCAAATGGTGTAC
 TGTAAACCAAGACTGTCAACACTTCTTGAAGAAGTCTTACAAGAGGTGG
 GGAATAAAAGCCAATGTTCTTGTGGAGAGGTGCAAGCATTGGAT
 CAGATTAAGAAAGCCTTACACATGCTAAAATTACAGAAAACCTTACCTTG
 TGTCAGTAGCAATTGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGT
 ATGCGTTGTTCCACGATACTTAAACGTGTTGAAGCTGAGGAAAATTGG
 TTAAAAAACCAACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8409

STRAIN CJB110

AAAGTTTAGCCTTGATACTCAAGCAAAGCACTATCA
 GTGGCTGACTAAACAATATGGAATGTTAGCGACTGTCACTATCAATAT
 CAAAAAGAATCATAGCATTAAATTGATGCCAGCCATTGATTTTAAATGC
 AATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GGTCCAGGATCTTACGGCTTACGTGTAGCTGTGCTACAGAAAAAT
 GCTAGCTTACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTA
 CTTTAACAAATGGATTTCAGAAAATGATTGTTGCTACCACTTATAGAT
 GCACGACGTAACATGTTATGTTGCTTCTATCAAATGGTGTACTGT
 TAAACCAAGACTGTCAACACTTCTTGAAGAAGTCTTACAAGAGGTGGGA
 ATAAAGCCAATGTTCTTGTGGAGAGGTGCAAGCATTGGATCAG
 ATTAAGAAAGCCTTACACATGCTAAAATTACAGAAAACCTTACCTTGTC
 AGTGGCAATTGGCGCAAAGGACAAAAAATGAAAAGCGTTAATGTAGATG
 CGTTGTTCCACGATACTTAAACGAGTGTGAAGCTGAGGAAAATTGGGTTA
 AAAAACCAACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO. 8410

STRAIN 1169NT

AAAGTTTAGCCTTGATACTCAAGCAAAGCACTATCA
 GTGGCTGACTAAACAATATGGAATGTTAGCGACTGTCACTATCAATAT
 CAAAAAGAATCATAGCATTAAATTGATGCCAGCCATTGATTTTAAATGC
 AATCAATTGATTAGAACCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GGTCCAGGATCTTACGGCTTACGTGTAGCTGTGCTACAGAAAAAT
 GCTAGCTTACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTA
 CTTTAACAAATGGATTTCAGAAAATGATTGTTGCTACCACTTATAGAT
 GCACGACGTAACATGTTATGTTGCTTCTATCAAATGGTGTACTGT
 TAAACCAAGACTGTCAACACTTCTTGAAGAAGTCTTACAAGAGGTGGGA
 ATAAAGCCAATGTTCTTGTGGAGAGGTGCAAGCATTGGATCAG
 ATTAAGAAAGCCTTACACATGCTAAAATTACAGAAAACCTTACCTTGTC

Table 84: Comparative Sequences relating to SAG0267

AGTGGCAATTGGCGCAAAGGACAAAAATGGAAAGCCTTAATGTAGATG
CGTTTGTCCACGATACTTAAACGTGTGAAGCTGAGGAAAATTGGTTA
AAAAAACACTGTGAAACGAATACAGAAGAATATAAGAGAGTT

SEQ ID NO. 8411

STRAIN JM9130013

AAAGTTTAGCCTTGTACTTAAACATGGAAATGTTAGCGACTGTCACTATCAATAT
CAAAAGAACATCATAGCATTAAATTGATGCCAGCCATTGATTTTTAATGCA
AATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTACTAGCAGAG
GGTCAGGATCTTACGGCTTACGGCTTACGCTAGCTGTGCTACGAAAGAT
GCTAGCTTACCGCTTAAAGATTGACTTGTGGAGTATCTAGCTGTACG
CTTAAACAAATGGATTTCAGAAAATGATTATTGCTACCCATTATAGAT
GCACGACGTAACATGTTATGTTGGTTCTATCAAATGGAGATACTGT
TAAACCAACTGTCACACTCTCTTGAAAGTCTTACAAGAGGTGGGA
ATAAAGGCAATTGGCGCAAAGGACAAAAATGAAAAGCCTTAATGTAGATG
AGTGGCAATTGGCGCAAAGGACAAAAATGAAAAGCCTTAATGTAGATG
CGTTTGTCCACGATACTTAAACGTGTGAAGCTGAGGAAAATTGGTTA
AGAAACACTGTGAAACGAATACAGAAGAATATAAGAGAGTT

PRETTY of: /biotmp/msa521675.2{*} March 10, 2003 08:34 ..

	1	50
msa521675.2{69_A909}	-----AAAG TTTTAGCCTT TGACTTCA AGCAAGCAC TATCAGTGGC	
msa521675.2{69_H36B}	-----AAAG TTTTAGCCTT TGACTTCA AGCAAGCAC TATCAGTGGC	
msa521675.2{69_JM9130013}	-----AAAG TTTTAGCCTT TGACTTCA AGCAAGCAC TATCAGTGGC	
msa521675.2{69_1169NT}	-----AAAG TTTTAGCCTT TGACTTCA AGCAAGCAC TATCAGTGGC	
msa521675.2{69_090}	-----AAAG TTTTAGCCTT TGACTTCA AGCAAGCAC TATCAGTGGC	
msa521675.2{69_CBE110}	-----AAAG TTTTAGCCTT TGACTTCA AGCAAGCAC TATCAGTGGC	
msa521675.2{69_18RS21}	-----AAAG TTTTAGCCTT TGACTTCA AGCAAGCAC TATCAGTGGC	
msa521675.2{69_2603}	atgatgAAAG TTTTAGCCTT TGACTTCA AGCAAGCAC TATCAGTGGC	
msa521675.2{69_COH1}	-----AAAG TTTTAGCCTT TGACTTCA AGCAAGCAC TATCAGTGGC	
msa521675.2{69_M732}	-----AAAG TTTTAGCCTT TGACTTCA AGCAAGCAC TATCAGTGGC	
msa521675.2{69_M781}	-----AAAG TTTTAGCCTT TGACTTCA AGCAAGCAC TATCAGTGGC	
Consensus	*****	*****
	51	100
msa521675.2{69_A909}	TGTACTAAC AATATGGAAT GTT TAGGCAC TGTCACTATC AATATCAAAA	
msa521675.2{69_H36B}	TGTACTAAC AATATGGAAT GTT TAGGCAC TGTCACTATC AATATCAAAA	
msa521675.2{69_JM9130013}	TGTACTAAC AATATGGAAT GTT TAGGCAC TGTCACTATC AATATCAAAA	
msa521675.2{69_1169NT}	TGTACTAAC AATATGGAAT GTT TAGGCAC TGTCACTATC AATATCAAAA	
msa521675.2{69_090}	TGTACTAAC AATATGGAAT GTT TAGGCAC TGTCACTATC AATATCAAAA	
msa521675.2{69_CBE110}	TGTACTAAC AATATGGAAT GTT TAGGCAC TGTCACTATC AATATCAAAA	
msa521675.2{69_18RS21}	TGTACTAAC AATATGGAAT GTT TAGGCAC TGTCACTATC AATATCAAAA	
msa521675.2{69_2603}	TGTACTAAC AATATGGAAT GTT TAGGCAC TGTCACTATC AATATCAAAA	
msa521675.2{69_COH1}	TGTACTAAC AATATGGAAT GTT TAGGCAC TGTCACTATC AATATCAAAA	
msa521675.2{69_M732}	TGTACTAAC AATATGGAAT GTT TAGGCAC TGTCACTATC AATATCAAAA	
msa521675.2{69_M781}	TGTACTAAC AATATGGAAT GTT TAGGCAC TGTCACTATC AATATCAAAA	
Consensus	*****	*****
	101	150
msa521675.2{69_A909}	AGAATCATAG CATTAAATTG ATGCCAGCCA TTGATTTTT AATGCAATCA	
msa521675.2{69_H36B}	AGAATCATAG CATTAAATTG ATGCCAGCCA TTGATTTTT AATGCAATCA	
msa521675.2{69_JM9130013}	AGAATCATAG CATTAAATTG ATGCCAGCCA TTGATTTTT AATGCAATCA	
msa521675.2{69_1169NT}	AGAATCATAG CATTAAATTG ATGCCAGCCA TTGATTTTT AATGCAATCA	
msa521675.2{69_090}	AGAATCATAG CATTAAATTG ATGCCAGCCA TTGATTTTT AATGCAATCA	
msa521675.2{69_CBE110}	AGAATCATAG CATTAAATTG ATGCCAGCCA TTGATTTTT AATGCAATCA	
msa521675.2{69_18RS21}	AGAATCATAG CATTAAATTG ATGCCAGCCA TTGATTTTT AATGCAATCA	
msa521675.2{69_2603}	AGAATCATAG CATTAAATTG ATGCCAGCCA TTGATTTTT AATGCAATCA	
msa521675.2{69_COH1}	AGAATCATAG CATTAAATTG ATGCCAGCCA TTGATTTTT AATGCAATCA	
msa521675.2{69_M732}	AGAATCATAG CATTAAATTG ATGCCAGCCA TTGATTTTT AATGCAATCA	
msa521675.2{69_M781}	AGAATCATAG CATTAAATTG ATGCCAGCCA TTGATTTTT AATGCAATCA	
Consensus	*****	*****
	151	200
msa521675.2{69_A909}	ATGATTTAG AACCTCAAGA TTGGACCGT ATCGTAGTTag CAGAGGGTCC	
msa521675.2{69_H36B}	ATGATTTAG AACCTCAAGA TTGGACCGT ATCGTAGTTag CAGAGGGTCC	
msa521675.2{69_JM9130013}	ATGATTTAG AACCTCAAGA TTGGACCGT ATCGTAGTTag CAGAGGGTCC	
msa521675.2{69_1169NT}	ATGATTTAG AACCTCAAGA TTGGACCGT ATCGTAGTTag CAGAGGGTCC	
msa521675.2{69_090}	ATGATTTAG AACCTCAAGA TTGGACCGT ATCGTAGTTag CAGAGGGTCC	
msa521675.2{69_CBE110}	ATGATTTAG AACCTCAAGA TTGGACCGT ATCGTAGTTag CAGAGGGTCC	
msa521675.2{69_18RS21}	ATGATTTAG AACCTCAAGA TTGGACCGT ATCGTAGTTag CAGAGGGTCC	
msa521675.2{69_2603}	ATGATTTAG AACCTCAAGA TTGGACCGT ATCGTAGTTag CAGAGGGTCC	
msa521675.2{69_COH1}	ATGATTTAG AACCTCAAGA TTGGACCGT ATCGTAGTTag CAGAGGGTCC	
msa521675.2{69_M732}	ATGATTTAG AACCTCAAGA TTGGACCGT ATCGTAGTTag CAGAGGGTCC	
msa521675.2{69_M781}	ATGATTTAG AACCTCAAGA TTGGACCGT ATCGTAGTTag CAGAGGGTCC	
Consensus	*****	*****
	201	250
msa521675.2{69_A909}	AGGATCTTAC CGGGCTTAC GTGTAGCTGT TGCTACAGCA AAAATGCTAG	
msa521675.2{69_H36B}	AGGATCTTAC CGGGCTTAC GTGTAGCTGT TGCTACAGCA AAAATGCTAG	

Table 84: Comparative Sequences relating to SAG0267

msa521675.2{69_JM9130013}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_1169NT}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_090}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_CJB110}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_18RS21}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_2603}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_COH1}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_M732}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_M781}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
Consensus	*****	*****	*****	*****	*****
	251			300	
msa521675.2{69_A909}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_H36B}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_JM9130013}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_1169NT}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_090}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_CJB110}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_18RS21}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_2603}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_COH1}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_M732}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_M781}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
Consensus	*****	*****	*****	*****	*****
	301			350	
msa521675.2{69_A909}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_H36B}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_JM9130013}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_1169NT}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_090}	ACAAATGGAT	TTTCAGAAAA	TGATTTgTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_CJB110}	ACAAATGGAT	TTTCAGAAAA	TGATTTgTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_18RS21}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_2603}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_COH1}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_M732}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
msa521675.2{69_M781}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACTTA	TAGATGCACG
Consensus	*****	*****	*****	*****	*****
	351			400	
msa521675.2{69_A909}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAC
msa521675.2{69_H36B}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAC
msa521675.2{69_JM9130013}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAC
msa521675.2{69_1169NT}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAC
msa521675.2{69_090}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAC
msa521675.2{69_CJB110}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAC
msa521675.2{69_18RS21}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAC
msa521675.2{69_2603}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAC
msa521675.2{69_COH1}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAC
msa521675.2{69_M732}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAC
msa521675.2{69_M781}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAC
Consensus	*****	*****	*****	*****	*****
	401			450	
msa521675.2{69_A909}	CAGACTGTCA	CACTTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAAATAAA
msa521675.2{69_H36B}	CAGACTGTCA	CACTTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAAATAAA
msa521675.2{69_JM9130013}	CAGACTGTCA	CACTTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAAATAAA
msa521675.2{69_1169NT}	CAGACTGTCA	CACTTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAAATAAA
msa521675.2{69_090}	CAGACTGTCA	CACTTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAAATAAA
msa521675.2{69_CJB110}	CAGACTGTCA	CACTTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAAATAAA
msa521675.2{69_18RS21}	CAGACTGTCA	CACTTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAAATAAA
msa521675.2{69_2603}	CAGACTGTCA	CACTTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAAATAAA
msa521675.2{69_COH1}	CAGACTGTCA	CACTTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAAATAAA
msa521675.2{69_M732}	CAGACTGTCA	CACTTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAAATAAA
msa521675.2{69_M781}	CAGACTGTCA	CACTTCTCTT	GAAGAAGTCT	TACAAGAGGT	GGGGAAATAAA
Consensus	*****	*****	*****	*****	*****
	451			500	
msa521675.2{69_A909}	GCCAAATGTT	ATTTTGTCGG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
msa521675.2{69_H36B}	GCCAAATGTT	ATTTTGTCGG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
msa521675.2{69_JM9130013}	GCCAAATGTT	ATTTTGTCGG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
msa521675.2{69_1169NT}	GCCAAATGTT	ATTTTGTCGG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
msa521675.2{69_090}	GCCAAATGTT	ATTTTGTCGG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
msa521675.2{69_CJB110}	GCCAAATGTT	ATTTTGTCGG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
msa521675.2{69_18RS21}	GCCAAATGTT	ATTTTGTCGG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
msa521675.2{69_2603}	GCCAAATGTT	ATTTTGTCGG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
msa521675.2{69_COH1}	GCCAAATGTT	ATTTTGTCGG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
msa521675.2{69_M732}	GCCAAATGTT	ATTTTGTCGG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
msa521675.2{69_M781}	GCCAAATGTT	ATTTTGTCGG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
Consensus	*****	*****	*****	*****	*****
	501			550	
msa521675.2{69_A909}	GAAAGTTTA	CCACATGCTA	AAATTACAGA	AACTTACCT	TGTGCAGTgG

Table 84: Comparative Sequences relating to SAG0267

msa521675.2{69_H36B}	GAAAGttTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_JM9130013}	GAAAGttTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_1169NT}	GAAAGctTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_090}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_CJB110}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_18RS21}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTaG
msa521675.2{69_2603}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTaG
msa521675.2{69_COH1}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTaG
msa521675.2{69_M732}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTaG
msa521675.2{69_M781}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTaG
Consensus	*****	*****	*****	*****	*****
	551				600
msa521675.2{69_A909}	CAATTGGCG	CAAAGGACAA	AAAATGaAAA	GCGTTAACGT	AGAtgcGTTT
msa521675.2{69_H36B}	CAATTGGCG	CAAAGGACAA	AAAATGaAAA	GCGTTAACGT	AGAtgcGTTT
msa521675.2{69_JM9130013}	CAATTGGCG	CAAAGGACAA	AAAATGaAAA	GCGTTAACGT	AGAtgcGTTT
msa521675.2{69_1169NT}	CAATTGGCG	CAAAGGACAA	AAAATGgAAA	GCGTTAACGT	AGAtgcGTTT
msa521675.2{69_090}	CAATTGGCG	CAAAGGACAA	AAAATGgAAA	GCGTTAACGT	AGAtgcGTTT
msa521675.2{69_CJB110}	CAATTGGCG	CAAAGGACAA	AAAATGgAAA	GCGTTAACGT	AGAtgcGTTT
msa521675.2{69_18RS21}	CAATTGGCG	CAAAGGACAA	AAAATGgAAA	GCGTTAACGT	AGAtgcGTTT
msa521675.2{69_2603}	CAATTGGCG	CAAAGGACAA	AAAATGgAAA	GCGTTAACGT	AGAtgcGTTT
msa521675.2{69_COH1}	CAATTGGCG	CAAAGGACAA	AAAATGgAAA	GCGTTAACGT	AGAtgcGTTT
msa521675.2{69_M732}	CAATTGGCG	CAAAGGACAA	AAAATGgAAA	GCGTTAACGT	AGAnncGTTT
msa521675.2{69_M781}	CAATTGGCG	CAAAGGACAA	AAAATGgAAA	GCGTTAACGT	AGAtgcGTTT
Consensus	*****	*****	*****	*****	*****
	601				650
msa521675.2{69_A909}	GTTCACCGAT	ACTTAAACG	tGTGAAGCT	GAGGAAATT	GTAAgAAA
msa521675.2{69_H36B}	GTTCACCGAT	ACTTAAACG	tGTGAAGCT	GAGGAAATT	GTAAgAAA
msa521675.2{69_JM9130013}	GTTCACCGAT	ACTTAAACG	tGTGAAGCT	GAGGAAATT	GTAAgAAA
msa521675.2{69_1169NT}	GTTCACCGAT	ACTTAAACG	tGTGAAGCT	GAGGAAATT	GTAAaAAA
msa521675.2{69_090}	GTTCACCGAT	ACTTAAACG	tGTGAAGCT	GAGGAAATT	GTAAaAAA
msa521675.2{69_CJB110}	GTTCACCGAT	ACTTAAACG	tGTGAAGCT	GAGGAAATT	GTAAaAAA
msa521675.2{69_18RS21}	GTTCACCGAT	ACTTAAACG	tGTGAAGCT	GAGGAAATT	GTAAaAAA
msa521675.2{69_2603}	GTTCACCGAT	ACTTAAACG	tGTGAAGCT	GAGGAAATT	GTAAaAAA
msa521675.2{69_COH1}	GTTCACCGAT	ACTTAAACG	tGTGAAGCT	GAGGAAATT	GTAAaAAA
msa521675.2{69_M732}	GTTCACCGAT	ACTTAAACG	tGTGAAGCT	GAGGAAATT	GTAAaAAA
msa521675.2{69_M781}	GTTCACCGAT	ACTTAAACG	tGTGAAGCT	GAGGAAATT	GTAAaAAA
Consensus	*****	*****	*****	*****	*****
	651				690
msa521675.2{69_A909}	CCACTGTGAA	ACGAAT----	-----	-----	-----
msa521675.2{69_H36B}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_JM9130013}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_1169NT}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_090}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_CJB110}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_18RS21}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_2603}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_COH1}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_M732}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
msa521675.2{69_M781}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 8412

STRAIN 2603 frame: 1

MMKVLAFDTSSKALSVAVLNNECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRLIV
 VAEKGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNGKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 CAVAIGRKQKMKSVNVDAFVPRYLKRVEAEEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8413

STRAIN 090 frame: 1

KVLAFDTSSKALSVAVLNNECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRLIV
 VAEKGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNGKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 CAVAIGRKQKMKSVNVDAFVPRYLKRVEAEEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8414

STRAIN A909 frame: 1

KVLAFDTSSKALSVAVLNNECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRLIV
 VAEKGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNGKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 CAVAIGRKQKMKSVNVDAFVPRYLKRVEAEEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8415

STRAIN H36B frame: 1

KVLAFDTSSKALSVAVLNNECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRLIV
 VAEKGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLQEVGNGKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 CAVAIGRKQKMKSVNVDAFVPRYLKRVEAEEENWLKNHCETNTEEYIKRV

SEQ ID NO. 8416

Table 84: Comparative Sequences relating to SAG0267

STRAIN 18RS21 frame: 1
 KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDIV
 VAECPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTINGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLOEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKQKMKSVNVDAFPVPRYLKRVEAENWLKNHCETNTTEEYIKRV

SEQ ID NO. 8417

STRAIN M732 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDIV
 VAECPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTINGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLOEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKQKMKSVNVDAFPVPRYLKRVEAENWLKNHCETNTTEEYIKRV

SEQ ID NO. 8418

STRAIN COH1 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDIV
 VAECPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTINGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLOEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKQKMKSVNVDAFPVPRYLKRVEAENWLKNHCETNTTEEYIKRV

SEQ ID NO. 8419

STRAIN M781 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDIV
 VAECPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTINGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLOEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKQKMKSVNVDAFPVPRYLKRVEAENWLKNHCETNTTEEYIKRV

SEQ ID NO. 8420

STRAIN CJB110 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDIV
 VAECPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTINGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLOEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKQKMKSVNVDAFPVPRYLKRVEAENWLKNHCETNTTEEYIKRV

SEQ ID NO. 8421

STRAIN 1169NT frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDIV
 VAECPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTINGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLOEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKQKMKSVNVDAFPVPRYLKRVEAENWLKNHCETNTTEEYIKRV

SEQ ID NO. 8422

STRAIN JM9130013 frame: 1

KVLAFTSSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDIV
 VAECPGSYTGLRVAVATAKMLAYTLKIDLVGVSSLYALTINGFSENDLLVPLIDARRNNVY
 VGFYQNGDTVKPDCHTSLEEVLOEVGNKANVHFVGEVAFFDQIKKALPHAKITETLPCA
 VAIGRKQKMKSVNVDAFPVPRYLKRVEAENWLKNHCETNTTEEYIKRV

PRETTY of: /biotmp/msa521982.2{*} March 10, 2003 08:40 ..

	1		50
msa521982.2{69_A909}	--KVLAFTDS SKALSVAVLN NMECLATVTI	NIKKNHSINL	MPAIDFLMQS
msa521982.2{69_H36B}	--KVLAFTDS SKALSVAVLN NMECLATVTI	NIKKNHSINL	MPAIDFLMQS
msa521982.2{69_JM9130013}	--KVLAFTDS SKALSVAVLN NMECLATVTI	NIKKNHSINL	MPAIDFLMQS
msa521982.2{69_090}	--KVLAFTDS SKALSVAVLN NMECLATVTI	NIKKNHSINL	MPAIDFLMQS
msa521982.2{69_COH110}	--KVLAFTDS SKALSVAVLN NMECLATVTI	NIKKNHSINL	MPAIDFLMQS
msa521982.2{69_18RS21}	--KVLAFTDS SKALSVAVLN NMECLATVTI	NIKKNHSINL	MPAIDFLMQS
msa521982.2{69_2603}	--KVLAFTDS SKALSVAVLN NMECLATVTI	NIKKNHSINL	MPAIDFLMQS
msa521982.2{69_COH1}	--KVLAFTDS SKALSVAVLN NMECLATVTI	NIKKNHSINL	MPAIDFLMQS
msa521982.2{69_M781}	--KVLAFTDS SKALSVAVLN NMECLATVTI	NIKKNHSINL	MPAIDFLMQS
msa521982.2{69_1169NT}	--KVLAFTDS SKALSVAVLN NMECLATVTI	NIKKNHSINL	MPAIDFLMQS
msa521982.2{69_M732}	--KVLAFTDS SKALSVAVLN NMECLATVTI	NIKKNHSINL	MPAIDFLMQS
Consensus	*****	*****	*****
	51		100
msa521982.2{69_A909}	IDLEPQDLDR IIVVaEGPGSY	TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_H36B}	IDLEPQDLDR IIVVaEGPGSY	TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_JM9130013}	IDLEPQDLDR IIVVaEGPGSY	TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_090}	IDLEPQDLDR IIVVaEGPGSY	TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_COH110}	IDLEPQDLDR IIVVaEGPGSY	TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_18RS21}	IDLEPQDLDR IIVVaEGPGSY	TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_2603}	IDLEPQDLDR IIVVaEGPGSY	TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_COH1}	IDLEPQDLDR IIVVaEGPGSY	TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_M781}	IDLEPQDLDR IIVVaEGPGSY	TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_1169NT}	IDLEPQDLDR IIVVaEGPGSY	TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
msa521982.2{69_M732}	IDLEPQDLDR IIVVaEGPGSY	TGLRVAVATA	KMLAYTLKID LVGVSSLYAL
Consensus	*****	*****	*****
	101		150
msa521982.2{69_A909}	TNGFSENDLL VPLIDARRNN	VYVGFYQNGD	TVKPDCHTS
msa521982.2{69_H36B}	TNGFSENDLL VPLIDARRNN	VYVGFYQNGD	TVKPDCHTS
		EEVLQEVGNK	EEVLQEVGNK

Table 84: Comparative Sequences relating to SAG0267

msa521982.2{69_JM9130013}	TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVEGNK
msa521982.2{69_090}	TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVEGNK
msa521982.2{69_CJB110}	TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVEGNK
msa521982.2{69_18RS21}	TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVEGNK
msa521982.2{69_2603}	TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVEGNK
msa521982.2{69_COH1}	TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVEGNK
msa521982.2{69_M781}	TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVEGNK
msa521982.2{69_1169NT}	TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVEGNK
msa521982.2{69_M732}	TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPDCHTSL EEVLQEVEGNK
Consensus	***** * ***** * ***** * *****
	***** * ***** * ***** * *****
	151
msa521982.2{69_A909}	ANVHFVGEVA AFvDQIKKvL PHAKITETLP CAVAIGRKQ KMkSVNVdaF
msa521982.2{69_H36B}	ANVHFVGEVA AFvDQIKKvL PHAKITETLP CAVAIGRKQ KMkSVNVdaF
msa521982.2{69_JM9130013}	ANVHFVGEVA AFvDQIKKvL PHAKITETLP CAVAIGRKQ KMkSVNVdaF
msa521982.2{69_090}	ANVHFVGEVA AFFDQIKKKal PHAKITETLP CAVAIGRKQ KMMeSVNVdaF
msa521982.2{69_CJB110}	ANVHFVGEVA AFFDQIKKKal PHAKITETLP CAVAIGRKQ KMMeSVNVdaF
msa521982.2{69_18RS21}	ANVHFVGEVA AFFDQIKKaL PHAKITETLP CAVAIGRKQ KMkSVNVdaF
msa521982.2{69_2603}	ANVHFVGEVA AFFDQIKKaL PHAKITETLP CAVAIGRKQ KMkSVNVdaF
msa521982.2{69_COH1}	ANVHFVGEVA AFFDQIKKaL PHAKITETLP CAVAIGRKQ KMkSVNVdaF
msa521982.2{69_M781}	ANVHFVGEVA AFFDQIKKaL PHAKITETLP CAVAIGRKQ KMkSVNVdaF
msa521982.2{69_1169NT}	ANVHFVGEVA AFvDQIKKaL PHAKITETLP CAVAIGRKQ KMMeSVNVdaF
msa521982.2{69_M732}	ANVHFVGEVA AFvDQIKKaL PHAKITETLP CAVAIGRKQ KMkSVNVxxF
Consensus	***** * ***** * ***** * *****
	***** * ***** * ***** * *****
	200
msa521982.2{69_A909}	VPRYLKRVEA EENWLrNHCE TN-----
msa521982.2{69_H36B}	VPRYLKRVEA EENWLrNHCE TNTEEYIKRV
msa521982.2{69_JM9130013}	VPRYLKRVEA EENWLrNHCE TNTEEYIKRV
msa521982.2{69_090}	VPRYLKRVEA EENWLkNHCE TN-----
msa521982.2{69_CJB110}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_18RS21}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_2603}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_COH1}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_M781}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_1169NT}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_M732}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
Consensus	***** * ***** * *****
	***** * ***** * *****
	201
msa521982.2{69_A909}	VPRYLKRVEA EENWLrNHCE TN-----
msa521982.2{69_H36B}	VPRYLKRVEA EENWLrNHCE TNTEEYIKRV
msa521982.2{69_JM9130013}	VPRYLKRVEA EENWLrNHCE TNTEEYIKRV
msa521982.2{69_090}	VPRYLKRVEA EENWLkNHCE TN-----
msa521982.2{69_CJB110}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_18RS21}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_2603}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_COH1}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_M781}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_1169NT}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_M732}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
Consensus	***** * ***** * *****
	***** * ***** * *****
	230
msa521982.2{69_A909}	VPRYLKRVEA EENWLrNHCE TN-----
msa521982.2{69_H36B}	VPRYLKRVEA EENWLrNHCE TNTEEYIKRV
msa521982.2{69_JM9130013}	VPRYLKRVEA EENWLrNHCE TNTEEYIKRV
msa521982.2{69_090}	VPRYLKRVEA EENWLkNHCE TN-----
msa521982.2{69_CJB110}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_18RS21}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_2603}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_COH1}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_M781}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_1169NT}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
msa521982.2{69_M732}	VPRYLKRVEA EENWLkNHCE TNTEEYIKRV
Consensus	***** * ***** * *****
	***** * ***** * *****

Table 85: Comparative Sequences relating to SAG1361**SEQ ID NO. 8501****STRAIN 2603**

atgagtaaacgacaaaatttaggaatttagtaaaaaaggagaattatacagggctcta
 gtggactaattgttagtaataggcgcttttatggtacaatctcaacctaataagat
 gcagtaaaaactaactacaagttttatgttagagaaggaaagtgttcgtccacta
 ctttgacaggaaaagctaaaggctaatcaagaacagttgtatgtatgtcaataaaa
 ggttaatcgacggactgtcagatcaaagggtgataaaatcacagctggcagcgtt
 gttcaatatacgatacaacaactgcacaagcagcctacgcacactgtaatcgta
 aaatggatcggcgtcagatataatctaaagacaacaggaaagtcttcacgtatgg
 aatgtatcaatcttcatcacaaggacaaggactcaatcgactgtgtgcgacg
 aatcgtctacagcaaaaattatcaaaatgtcaagctaatgtcatacaacacaactt
 caaattgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtat
 aatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtat
 gatccatcggatcaaaaacttagtcaatgtatgtatgtatgtatgtatgtatgtat
 gtacaaggaacatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtat
 ataaaatctaaatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtat
 tattcagaagcagaacaaacaataactgatctatgtatgtatgtatgtatgtatgtat
 aatataaaatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtat
 gtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtat
 gatataaaatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtat
 gtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtatgtat
 caaatcgtgtactaatccaaatggatggatggatggatggatggatggatggatggat
 gatcaatcgtatcttaactctaataagaaatcagatgtatgtatgtatgtatgtatgtat
 gatcaatcgtatcttaactctaataagaaatcagatgtatgtatgtatgtatgtatgtat

SEQ ID NO. 8502**STRAIN 090**

TTTTTATGGCTACAATCTAACCTAATAAGAGTCAGTAAAACACTAA
 CAAAGTTTTATGTGTTAGAGAAGGAAGTGTTCTGCCTCAACTCTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTTATTTGATGCTAAT
 AAAGGTAAATCGAGCAACTGTCAAGCTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCACTAGTTCAATATGATAACAAACGTCAACAGCAGCTACG
 AACTGTCAATCGTCAATTAAATAAAGTAGGCCGTCAAGTTATAATCTA
 AGACAACAGGAAGCTTCAAGCTATGGAATTAAGTCAATCTCTTC
 ATCATCACAAGGACAAGGACTCAATCGACTAGTGGTGGCACGAACTGTC
 TACAGCAAATTATCAAAGTCAAGCTAATGCTTCAATCACAAACAAACTT
 CAAGATGAAATGATGCTTATGAGATGCACAGGCAGAAGTAAATAAAGC
 ACAAAAAGCATGATGATACGTGTTATTACAAAGTGCCTTATCAGGGACAG
 TTGTTGAAGTTAATAGTGTATATTGATCCAGCTCAAAACTAGTCAGTA
 CTGTCATGAGCTAACAGTCAAGGTTAAACTCCAAGTCAACAGGAAACGATGAG
 TGAGTATGATTGGCTAATGTTAAAAAAAGACCAGGGCTGTTAAAATAAAAT
 CTAAGGTCTATCCCTGACAAGGAATGGGAAGCTAAAATTTCATATATCTCA
 AATTATCCAGAAGCAGAAACAAACAATGACTCTAATAACGGCTCTAG
 TGCTGTAATTATAATATAAAGTAGATATTACTAGCCCTCTCGATGCA
 TAAAACAGGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTATTGCTTACAAGTTCTGTGATAAAACAAAGATAATAAACACTTTG
 TGGGTATACATGTTACAATGTTACAATGTTACAATGTTACAAGTCAAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTITATCAGGTTGAAGGCA
 GGACAAATCGGGTTACTAATCCAAGTAAACCTTCAAGGATGGCAAA
 AATTGATAATATTGAATCAATCGATTTAATCTAATAAGAAATCAGAGG

SEQ ID NO. 8503**STRAIN A909**

TTTTTATGGTACAATCTAACCTAATAAGAGTCAGTAAAACACTAA
 CTACAAGTTTTAATGTGTTAGAGAAGGAAGTGTTCTGCCTCAACTCTTT
 TGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTTATTTGATGCT
 AATAAAAGCTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCAC
 AGCTGGTCAGCAGTTAGTCAATATGATAACAAACACTGCACAAGCAGCCT
 ACAGACACTGCTAATCTCAATTAAATAAAGTAGCGCTCAGATTAATAAT
 CTTAAAGACAACAGGAAGTCCTCAGCTATGGAATCAAGTGTATCAATCTTC
 ATCATCATCACAAGGACAAGGGCTCAATCGACTAGTGGTGGCACGAAATC
 GTCTACAGCAAATTATCAAAGTCAGTCAATGCTTCAATCACAAACAA
 CTCAGGAAATTGTAATGCTTATGCAAGATGCAAGGAAAGTAAATAA
 AGCACAAAAGCATTGAAATGACTGTTATTAACAGTGAAGTATCAGGGA
 CAGTTGTTGAAGTTAATAGTGTATTTGATCAGCTTCAAAACTAGTC
 GTACTGTCCATGTAGCAACTGAGGGTAAACTCCAAGTACAAGGAAACGAT
 GAGTGTAGTATGATTGGCTAATGTTAAAAGACCCAGTCTGTTAAATAA
 AATCTAAGGTCTATCTGACAAGGAATGGGAAGGTAAAATTTCATATATC
 TCAAATTATCCAGAAGCAGAAACAAACAACTGACTCTAATAACGGCTC
 TAGTGCTGTAATTATAAATAAAGTAGATATTACTAGCCCTCTCGATG
 CTTAAACAAACAGTTTACTGTTACTGAGTGAAGTAGTTAATGGAGATAAG
 CACCTTATTGTTCTACAAGTCTGTGACAACAAAGATAATAAACACTT
 TGTTGGGTATACAATGATTCTAATGTTAAATTTCCAAGTGAAGTC
 AAATTGCTAAGGCTGATGCTAAGACACAAGAAATTATCAGGTTGAAA
 GCAGGACAAATCGGGTTACTAATCCAAGCAAAACCTTCAAGGATGGC
 AAAAATTGATAATATTGAATCAATAGATCTAAGTCTAATAAGAAATCAG
 AGGTGAAA

SEQ ID NO. 8504**STRAIN H36B**

TTTTTATGGGTACAATCTAACCTAATAAGAGTCAGTAAAACACTAA
 CAAAGTTTTAATGTGTTAGAGAAGGAAGTGTTCTGCCTCAACTCTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTTATTTGATGCTAAT
 AAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC

Table 85: Comparative Sequences relating to SAG1361

TGGTCAGCAGTTAGTTCAATATGATAACAACAACTGCACAAGCAGCCTACG
 AACACTGCTAATCGTCAATTAAAGTAGCCGCTCAGATTAAATAATCTA
 AAGACAACAGGAAGTCITCCAGCTATGGATCAAGTGATCAATCTTCATC
 ATCATCACAGGACAAGGGACTCAATCGACTAGTGGTGCAGCAATCGTC
 TACAGCAAATTAATCAAAGTCAGCTAATGCTTCAATACAACCAACAACTT
 CAAGATTGAGTATGCTTATGAGATGCAAGGCCAGAAGTAAATAAAGC
 ACAAAAAGCATGATGATGACTCTTATTACAAGTGACCTATCAGGACAG
 TTGTTGAAGTTAATAGTGTATTTGATCCAGCTCAAAACTAGTCAGTA
 CTGTCATGCTAGCAACTGAGGAAACTCCAGTACAAGGAACGGATGAG
 TGAGTATGATTGGCTAATGTAACAAAAGCAGGCTGTTAAATAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTTAAATTCTATATCTCA
 AATTATCCAGAACAGCAACAAACAATGACTCTAAACGGCTCTAG
 TGCTGTAATTATAAATGATGACTCTGTTATTACAAGTGACCTATCAGGACAG
 TAAAACAAGGTTTACCGTATGTTGAAGTAAATGAGATAAGCAC
 CTIATTGTTCTACAGTAACTGGTATACTGAGGAAACGGATGAG
 TTGGTAAACGCTGATGCTAAGACACAAGAAATTATCAGGTTGAAAGCA
 GGACAAATCGTAGTTACTAATCCAAGTAAAGCTTCAGGATGGCAAA
 ATTGATAATATTGAATCAATCGATCTAAGTCTAATAAGAAATCAGAG
 TG

SEQ ID NO. 8505**STRAIN 18RS21**

TTTTATGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAACTAACTA
 CAAAGTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTTGATTTGATGCTAAT
 AAAGGTAATCGGCAACTGTTACAGTTAAAGTGGGTGATAAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATAACAACAACTGCACAGCAGCCTACG
 ACACGTGCTAATCGTCAATTAAATAAAGTAGCCGCGTCAGATTAAATCTA
 AAGACAACAGGAAGTCITCCAGCTATGGATCAAGTGATCAATCTTC
 ATCATCACAGGACAAGGGACTCAATCGACTAGTGGTGCAGCAATCGTC
 TACAGCAAATTAATCAAAGTCAGCTAATGCTTCAATACAACCAACAACTT
 CAAGATTGAGTATGCTTATGAGATGCAAGGCCAGAAGTAAATAAAGC
 ACAAAAAGCATGATGATGACTCTTATTACAAGTGACCTATCAGGACAG
 TTGTTGAAGTTAATAGTGTATTTGATCCAGCTCAAAACTAGTCAGTA
 CTGTCATGCTAGCAACTGAGGAAACTCCAGTACAAGGAACGGATGAG
 TGAGTATGATTGGCTAATGTTAAACAGCAGGCTGTTAAATAAAT
 CTAAGGTCTATCCTGACAAGGAATGGGAAGGTTAAATTCTATATCTCA
 AATTATCCAGAACAGCAACAAACATGACTCTAAACGGCTCTAG
 TGCTGTAATTATAAATGATGACTCTGAGGATGCAAGGCCAGAAGTAAAGC
 TTGGTATACATGTTACGTTAAATTTCCAAGGTGAAGTCAAA
 TTGGTAAACGCTGATGCTAAGACACAAGAAATTATCAGGTTGAAAGCA
 GGACAAATCGGGTTACTAATCCAAGTAAACCTTCAGGATGGCAAA
 ATTGATAATATTGAATCAATCGATCTAAGTCTAATAAGAAATCAGAG
 TGAA

SEQ ID NO. 8506**STRAIN M732**

TTTTATGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAACTAATT
 CAAAGTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTGA
 CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTTGATTTGATGCTAAT
 AAAGGTAATCGGCAACTGTTACAGTTAAAGTGGGTGATAAAAATCACAGC
 TGGTCAGCAGTTAGTTCAATATGATAACAACAACTGCACAGCAGCCTACG
 ACACGTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAAATCTA
 AAGACAACAGGAGTTTCAGCTATGGATCAAGTGATCAATCTTCATC
 ATCATCACAGGACAAGGGACTCAATCGACTAGTGGTGCAGCAATCGTC
 TACAGCAAATTAATCAAAGTCAGCTAATGCTTCAATACAACCAACAACTT
 CAAGATTGAGTATGCTTATGAGGATGCAAGGCCAGAAGTAAATAAAGC
 ACAAAAAGCATGATGACTGTTATTACAAGTGACGTTACAGGGACAG
 TTGTTGAAGTTAATAGTGTATTTGATCCAGCTCAAAACTAGTCAGTA
 CTGTCATGCTAGCAACTGAGGAAACTCCAGTACAAGGAACGGATGAG
 TGAGTATGATTGTTAAAGGCTAATGTTAAAAGATCAGGCTGTTAAATAAAGC
 CTAGGTCTATCCTGACAAGGAATGGGAAGGTTAAATTCTATATCTCA
 ATTATCCAGAACAGCAACAAACATGACTCTAATAACGGCTCTAG
 TGCTGTAATTATAAATATAAAGTGTATTTGAGCTACAGCCCTCTCGATGCTA
 TAAACACAGGTTTACCGTATGTTGAAGTTAATGGGAGATAAGCAC
 CTIATTGTCCTACAGTTCTGATGTTAAACAAAGATAATAACACTTTG
 TTGGGTATACAATGTTCTGTTAAAGGTTACAGGTTGAAAGCA
 GGACAAATCGGGTTACTAATCCAAGCAAACCTTCAGGATGGCAAA
 ATTGATAATATTGAATCAATCGATCTAAGTCTAATAAGAAATCAGAG
 TGAA

SEQ ID NO. 8507**STRAIN COH1**

TTTTATGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAAC
 TAATTACAAAGTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTC
 TTTGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTTGATTTGAT
 GCTAATAAAAGGTAATCGGAGCAACTGTTACAGTTAAAGTGGGTGATAAAAAT
 CAAGCTGGTCAAGCAACTGTTACAGTTAAATGATAACAACACTGCACAG
 CCTACGACACTGCTAATCGTCAATTAAATAAAGTAGCGCGTCAGATTAA
 ATTCTAAAGACAACAGGAGTTCCAGCTATGGAATCAAGTGTCAATC

Table 85: Comparative Sequences relating to SAG1361

TTCATCATCATACAAGGACAAGGGACTCAATCGACTAGTGGTGCACGA
 ATCGCTCACAGAAAATTATCAAAGCTAACGCTAATGCTTCATACAACCAA
 CAATCTCAGGAAAGTGAATGATGCTTATGCAGATGCACAGGGAGAAGTAAA
 TAAAGCACAAAAGCATTGAATGTACTCTTATTACAAGTGACGTATCAG
 GGACAGTTGTTGAAGTTAATAGTGATAATTGATCCAGCTTCAAAACTAGT
 CAAGTACTTGCATGAGCAACTGAAGGTAACCTCAAGTACAAGGAAC
 GATGAGTGAGTATGATTGGCTTATGTTAAAAAGATCAGGGCTTAA
 TAAATCTAAGGTCTATCCTGACAAGGAATGGAAGGTTAAATTTCATAT
 ATCTAAATTCTCCAGAACAGCAAGAACAAACTGACTCTAATAAACGG
 CTCTAGTGCTGAAATTATAAAACTAGATAATTACTAGCCTCTCG
 ATGCATTAAACAAAGGTTTACCGTATCAGTGAAAGTAGTTAATGGAGAT
 AAGCACCTTATTGTCCTACAACTTCTGTGATAAAACAAAGATAATAAACCA
 CTTGGTGGGTATACAATGATGTTAAATTCAGGTTAAAGTTCCAAGGTTGAAG
 TCAAAATTGGTAAAGCTGATGCTAACAGAACAGAAATTTCAGGTTG
 AAAGCAGGACAATCGTGGTTACTAATCCAAGCAAAACTTCAAGGATGG
 GCAAAATTGATAATATTGAATCAATCGATCTAAGCTAATAAGAAAT
 CAGAGGTGAA

SEQ ID NO. 8507

STRAIN M781

TTTTATGGTACAATCTCAACCTAATAAGAGTGCACTAAACTAATTA
 CAAAGTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTGA
 CAGGAAAAGCTAACGGCTAATCAAGAACAGTATGTTGATTTTGATGCTAAT
 AAAGGTAAATCGAGCAACTGTTAACGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTCAATATGATACAAACAACGTACAAGCAGCCTACG
 ACACTGCTAACGCTAACCTAAATAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAACAGGGAGTTTCCACCTATGGAATCAAGTGATCAATCTCATC
 ATCATCACAGGACAAGGGACTAACGACTAGTGGTGCAGAACATGTC
 TACAGAAAATTATCAAAGTCAAGCTAACGTTACATCAACCAACAACTT
 CAAGATTTGAATGATGCTTATGCGAGATGCAAGGAGTAAATTCATATCTCA
 AATTATCCAGAACAGCAAGAACAAACATGACTCTAACGCGCTCTAG
 TGCTGTTAAATTATAAAACTAGATATTACTAGCCTCTCGATGCT
 TAAAACAGGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTAATTGTCCTACAACTTCTGTGATAAAACAGATAATAAACACTTTGT
 TTGGTGTAAATGATTCTAACGTTAAATTCAGGTTGAAGTCAGGTTAAAGCA
 TTGGTAAAGCTGATGCTAACAGAACAGAAATTTCAGGTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGCAAAACTTCAAGGATGGGCAAA
 AATTGATAATATTGAATCAATCGATCTAAGCTAATAAGAAATCAGAGG
 TGAA

SEQ ID NO. 8508

STRAIN CJB110

TTTTATGGTACAATCTCAACCTAATAAGAGTGCACTAAACTAACTA
 CAAAGTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTGA
 CAGGAAAAGCTAACGGCTAATCAAGAACAGTATGTTGATTTTGATGCTAAT
 AAAGGTAAATCGAGCAACTGTTAACGTTAAAGTGGGTGATAAAATCACAGC
 TGGTCAGCAGTTAGTCAATATGATACAAACAACGTACAAGCAGCCTACG
 ACACTGCTAACGCTAACCTAAATAAGTAGCGCGTCAGATTAATAATCTA
 AAGACAACAGGGAGTCTCCAGCTATGGAATTAGTGATCAATCTCTTC
 ATCATCACAGGACAAGGGACTAACGACTAGTGGTGCAGAACATGTC
 TACAGAAAATTATCAAAGTCAAGCTAACGTTACATCAACCAACAACTT
 CAAGATTTGAATGATGCTTATGCGAGATGCAAGGAGTAAATAAAGC
 ACAAAAGCATGAAATGACTGTATTACAAAGTGACTPATCAGGGACAG
 TTGGTGAAGTTAATGTTGATATTGATCCAGCTAACGTTAAACAGGAGTGAAGT
 CTGTCATGCTAGCAAGGAAACTGAGGTTAACCTCAAGTACAAGGAAACGATGAG
 TGAGTATGATTGGCTAATGTTAAAGGACAGGCTGTTAAATAAAG
 CTAAGGTCTATCTGACAAGGAATGGGAAGGTTAAATTCTATATCTCA
 AATTATCCAGAACAGCAAAACAAACTGACTCTAACGCGCTCTAG
 TGCTGTTAAATTATAAAATTAAGTAGATATTACTAGCCTCTCGATGCT
 TAAAACAAGGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTTAATTGTCCTACAAAGTTCTGTGATAAAACAGATAATAAACACTTTGT
 TTGGTGTAAATGATTCTAACGTTAAATTCAGGTTGAAGTCAGGTTAAAGCA
 TTGGTAAAGCTGATGCTAACAGAACAGAAATTTCAGGTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGTAAAACCTTCAGGATGGGCAAA
 AATTGATAATATTGAATCAATCGATCTAAGCTAATAAGAAATCAGAGG
 TGAA

SEQ ID NO. 8509

STRAIN 1169NT

TTTTATGGTACAATCTCAACCTAATAAGAGTGCACTAAACTA
 AACTACAAAGTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCT
 TTGACAGGAAAAGCTAACGGCTAATCAAGAACAGTATGTTGATTTTGATG
 CTAATAAAAGCTAACGCAACTGTCACAGTTAAAGTGGGTGATAAAATC
 ACAGCTGGTCAGCTAACGTTACATGATACAAACAACGTACAAGCAGC
 CTACGGACACTGCTAACGTTAAATAAAAGTAGCGCGTCAGATTAATA
 ATCTAAAGAACACAGGAAACTTCCAGCTATGGAATCAAGTGATCAATCT
 TCTTCATCATCACAGAACAGGGACTAACGACTAGTGGTGCAGCAA
 TCGTCTACAGCAAATTATCAAAGCTAACGTTACATGCTTCATACAACCAAC

Table 85: Comparative Sequences relating to SAG1361

AACTTCAAGATTGAATGATGCTTATGCAGATGCACAGGGAGAAGTAAT
 AAAGCACAAAAGCATTGAATGATGACTGTATTACAAGTGACGTATCAGG
 GACAGTTGTGAAGTTAATAGTGTATTGATCCAGCTTCAAAAAGTAGTC
 AAGTACTTGTCACTGTAGCAACTGAAGGAAACTCCAAGTACAAGGAACG
 ATGAGTGACTATGATTTGGCTAATGTTAAAAAGACCAGGCTGTTAAAT
 AAAATCTAAGGCTATCCTGACAAGGAATGGGAAGGTTAAATTCATATA
 TCTCAAATTATCCAGAACAGCAAGCAGAACAAACATGACTCTAAACGGC
 TCTAGTGTGTTAAATTATAAATATAAAGTAGATATTACTAGGCCCTCTCGA
 TGCAATTAAAACAGGTTTACCGTATCAGTGAAGTACTTAATGGAGATA
 AGCACCTTATTGTCCTACAAGTCTGTGATAAACAAAGATAATAAACAC
 TTGTTGGTATAACATGATCTAATCTAAATTCCTAAAGTGAAGT
 CAAAATTGCTAAAGCTGATGCTAAGACACAAGAAATTTCAGGTTGA
 AAGCAGGACAAATCGTGGTTACTAATCCAAGTAAAACCTCAAGGATGG
 CAAAATGATAATATTGAATCAATCGATCTAACTCTAATAAGAAATC
 AGAGGTGAA

SEQ ID NO. 8510

STRAIN JM9130013

TTTTTATGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAACTAACTA
 CAAAGTTTTAATGTTAGAGAAGGAAGTGTTCGTCTCAACTTTTG
 CAGGAAAAGCTAAGGCTAATCAGAACAGTATGTGTATTGATGCTAAT
 AAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGGTATAAAATCACAGC
 TGGTGCAGCAGTTCAATGATACACAACTGCACAGCAGCCTACG
 AACACTGCTAATCGTCAATTAAATAAGTAGCGCGTCAAGTTAAATCTA
 AAGACAAACAGGAAGTCTTCAGCTATGGAATCAAGTGTATCACTTCATC
 ATCATCACAAAGGACAAGGGCTCAATCGACTAGTGGTGCAGGAATCGTC
 TACAGCAGAAATTATCAAGCTCAAGCTAATGCTCATACAAACCAACACTT
 CAAGATTGATGATGCTTATGAGATGCAAGGAGAAGTAAATAAAGC
 ACAAAAGCATGATGATACTGTTATTGATCAAGTGACGTATCAGGAGACAG
 TTGTTGAAGTTAATGATATTGATCAGCTTCAAAAAGTAGTCAAGTA
 CTGTCATGAGCAACTGAGGGTAAACTCCAAGTACAAGGAAACGATGAG
 TGAGTATGATTGGCTAATGTTAAAAAGACCAGTCGTTAAATAAAAAT
 CTAAGGTCTATCTGACAAGGAATGGGAAGTGTAAATTTTCAATATCTCA
 AATTATCCAGAACAGCAAGAACAAACATGACTCTAATAACGGCTCTAG
 TGCTGTAATTTATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCT
 TAAACAAGGTTACTGATCAGTTGAAGTAGTTAATGGAGATAAGCAC
 CTATTGTTCTACAAGTTCTGACAACAAAGATAATAAACACTTTGT
 TTGGGTATACAATGATTCTAATCGTAAATTCTCAAAGTGAAGTCAAA
 TTGGTAAAGCTGATGCTAAGACACAAGAAATTTCAGGTTGAAAGCA
 GGACAAATCGTGGTTACTAATCCAAGCAAACCTTCAGGATGGGCAAAA
 ATTGATAATATTGAATCAATGATCTTAAAGTCTAATAAGAAATCAGAG
 TGAAA

PRETTY of: /biotmp/msa363690.2{*} March 31, 2003 07:01 ..

	1	50
msa363690.2{690_COH1}	-----	-----
msa363690.2{690_M732}	-----	-----
msa363690.2{690_M781}	-----	-----
msa363690.2{690_090}	-----	-----
msa363690.2{690_CJB110}	-----	-----
msa363690.2{690_1169NT}	-----	-----
msa363690.2{690_18RS21}	-----	-----
msa363690.2{690_2603}	atgagtaaac gacaaaattt aggaattagt aaaaaaggag caattatac	-----
msa363690.2{690_A909}	-----	-----
msa363690.2{690_JM9130013}	-----	-----
msa363690.2{690_H36B}	-----	-----
Consensus	*****	*****
	51	100
msa363690.2{690_COH1}	-----	-----TTT TTATGGGTAC
msa363690.2{690_M732}	-----	-----TTT TTATGGGTAC
msa363690.2{690_M781}	-----	-----TTT TTATGGGTAC
msa363690.2{690_090}	-----	-----TTT TTATGGGTAC
msa363690.2{690_CJB110}	-----	-----TTT TTATGGGTAC
msa363690.2{690_1169NT}	-----	-----TTT TTATGGGTAC
msa363690.2{690_18RS21}	-----	-----TTT TTATGGGTAC
msa363690.2{690_2603}	agggtctca gtggcactaa ttgttagtaat aggtggcTTT TTATGGGTAC	-----TTT TTATGGGTAC
msa363690.2{690_A909}	-----	-----TTT TTATGGGTAC
msa363690.2{690_JM9130013}	-----	-----TTT TTATGGGTAC
msa363690.2{690_H36B}	-----	-----TTT TTATGGGTAC
Consensus	*****	*****
	101	150
msa363690.2{690_COH1}	AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAT TACAA AGTTTTTAAT	-----
msa363690.2{690_M732}	AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAT TACAA AGTTTTTAAT	-----
msa363690.2{690_M781}	AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAT TACAA AGTTTTTAAT	-----
msa363690.2{690_090}	AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAC TACAA AGTTTTTAAT	-----
msa363690.2{690_CJB110}	AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAC TACAA AGTTTTTAAT	-----
msa363690.2{690_1169NT}	AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAC TACAA AGTTTTTAAT	-----
msa363690.2{690_18RS21}	AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAC TACAA AGTTTTTAAT	-----
msa363690.2{690_2603}	AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAAC TACAA AGTTTTTAAT	-----

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_A909}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAACTACAA	AGTTTTTAAT	
msa363690.2{690_JM9130013}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAACTACAA	AGTTTTTAAT	
msa363690.2{690_H36B}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAACTACAA	AGTTTTTAAT	
Consensus	*****	*****	*****	*****	*****	*****
	151				200	
msa363690.2{690_COH1}	GTTAGAGAAC	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_M732}	GTTAGAGAAC	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_M781}	GTTAGAGAAC	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_090}	GTTAGAGAAC	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_CJB110}	GTTAGAGAAC	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_1169NT}	GTTAGAGAAC	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_18RS21}	GTTAGAGAAC	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_2603}	GTTAGAGAAC	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_A909}	GTTAGAGAAC	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_JM9130013}	GTTAGAGAAC	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
msa363690.2{690_H36B}	GTTAGAGAAC	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA	
Consensus	*****	*****	*****	*****	*****	*****
	201				250	
msa363690.2{690_COH1}	GGCTAATCAA	GAACAGTATG	TGTATTTGA	TGCTAATAAa	GGTAATCGAG	
msa363690.2{690_M732}	GGCTAATCAA	GAACAGTATG	TGTATTTGA	TGCTAATAAa	GGTAATCGAG	
msa363690.2{690_M781}	GGCTAATCAA	GAACAGTATG	TGTATTTGA	TGCTAATAAa	GGTAATCGAG	
msa363690.2{690_090}	GGCTAATCAA	GAACAGTATG	TGTATTTGA	TGCTAATAAa	GGTAATCGAG	
msa363690.2{690_CJB110}	GGCTAATCAA	GAACAGTATG	TGTATTTGA	TGCTAATAAa	GGTAATCGAG	
msa363690.2{690_1169NT}	GGCTAATCAA	GAACAGTATG	TGTATTTGA	TGCTAATAAa	GGTAATCGAG	
msa363690.2{690_18RS21}	GGCTAATCAA	GAACAGTATG	TGTATTTGA	TGCTAATAAa	GGTAATCGAG	
msa363690.2{690_2603}	GGCTAATCAA	GAACAGTATG	TGTATTTGA	TGCTAATAAa	GGTAATCGAG	
msa363690.2{690_A909}	GGCTAATCAA	GAACAGTATG	TGTATTTGA	TGCTAATAAa	GGTAATCGAG	
msa363690.2{690_JM9130013}	GGCTAATCAA	GAACAGTATG	TGTATTTGA	TGCTAATAAa	GGTAATCGAG	
msa363690.2{690_H36B}	GGCTAATCAA	GAACAGTATG	TGTATTTGA	TGCTAATAAa	GGTAATCGAG	
Consensus	*****	*****	*****	*****	*****	*****
	251				300	
msa363690.2{690_COH1}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA	
msa363690.2{690_M732}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA	
msa363690.2{690_M781}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA	
msa363690.2{690_090}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA	
msa363690.2{690_CJB110}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA	
msa363690.2{690_1169NT}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA	
msa363690.2{690_18RS21}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA	
msa363690.2{690_2603}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA	
msa363690.2{690_A909}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA	
msa363690.2{690_JM9130013}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA	
msa363690.2{690_H36B}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA	
Consensus	*****	*****	*****	*****	*****	*****
	301				350	
msa363690.2{690_COH1}	GTCAATATG	ATACAACAAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG	
msa363690.2{690_M732}	GTCAATATG	ATACAACAAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG	
msa363690.2{690_M781}	GTCAATATG	ATACAACAAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG	
msa363690.2{690_090}	GTCAATATG	ATACAACAAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG	
msa363690.2{690_CJB110}	GTCAATATG	ATACAACAAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG	
msa363690.2{690_1169NT}	GTCAATATG	ATACAACAAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG	
msa363690.2{690_18RS21}	GTCAATATG	ATACAACAAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG	
msa363690.2{690_2603}	GTCAATATG	ATACAACAAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG	
msa363690.2{690_A909}	GTCAATATG	ATACAACAAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG	
msa363690.2{690_JM9130013}	GTCAATATG	ATACAACAAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG	
msa363690.2{690_H36B}	GTCAATATG	ATACAACAAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG	
Consensus	*****	*****	*****	*****	*****	*****
	351				400	
msa363690.2{690_COH1}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA	
msa363690.2{690_M732}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA	
msa363690.2{690_M781}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA	
msa363690.2{690_090}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA	
msa363690.2{690_CJB110}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA	
msa363690.2{690_1169NT}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA	
msa363690.2{690_18RS21}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA	
msa363690.2{690_2603}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA	
msa363690.2{690_A909}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA	
msa363690.2{690_JM9130013}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA	
msa363690.2{690_H36B}	TCAATTAAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA	
Consensus	*****	*****	*****	*****	*****	*****
	401				450	
msa363690.2{690_COH1}	GTTTCCAGC	TATGGAATCA	AGTGATCAAT	CTTCatCATC	ATCACAAGGA	
msa363690.2{690_M732}	GTTTCCAGC	TATGGAATCA	AGTGATCAAT	CTTCatCATC	ATCACAAGGA	
msa363690.2{690_M781}	GTTTCCAGC	TATGGAATCA	AGTGATCAAT	CTTCatCATC	ATCACAAGGA	
msa363690.2{690_090}	GTTTCCAGC	TATGGAATCA	AGTGATCAAT	CTTCatCATC	ATCACAAGGA	
msa363690.2{690_CJB110}	GTTTCCAGC	TATGGAATCA	AGTGATCAAT	CTTCatCATC	ATCACAAGGA	
msa363690.2{690_1169NT}	GTTTCCAGC	TATGGAATCA	AGTGATCAAT	CTTCatCATC	ATCACAAGGA	
msa363690.2{690_18RS21}	GTTTCCAGC	TATGGAATCA	AGTGATCAAT	CTTCatCATC	ATCACAAGGA	

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_2603}	GTcTTCCAGC	TATGGAATCA	AGTGATCAAT	CTTCatTCATC	ATCACAAAGGA	
msa363690.2{690_A909}	Gtctttccagc	TATGGAATCA	AGTGATCAAT	CTTCatTCATC	ATCACAAAGGA	
msa363690.2{690_JM9130013}	Gtctttccagc	TATGGAATCA	AGTGATCAAT	CTTCatTCATC	ATCACAAAGGA	
msa363690.2{690_H36B}	Gtctttccagc	TATGGAATCA	AGTGATCAAT	CTTCatTCATC	ATCACAAAGGA	
Consensus	*****	*****	*****	*****	*****	
541						500
msa363690.2{690_COH1}	CAAGGGaCTC	AATCGACTAG	TGGTGCAGCAG	AATCGCTAC	AGCAAAATTAA	
msa363690.2{690_M732}	CAAGGGaCTC	AATCGACTAG	TGGTGCAGCAG	AATCGCTAC	AGCAAAATTAA	
msa363690.2{690_M781}	CAAGGGaCTC	AATCGACTAG	TGGTGCAGCAG	AATCGCTAC	AGCAAAATTAA	
msa363690.2{690_090}	CAAGGGaCTC	AATCGACTAG	TGGTGCAGCAG	AATCGCTAC	AGCAAAATTAA	
msa363690.2{690_CJB110}	CAAGGGaCTC	AATCGACTAG	TGGTGCAGCAG	AATCGCTAC	AGCAAAATTAA	
msa363690.2{690_1169NT}	CAAGGGaCTC	AATCGACTAG	TGGTGCAGCAG	AATCGCTAC	AGCAAAATTAA	
msa363690.2{690_18RS21}	CAAGGGaCTC	AATCGACTAG	TGGTGCAGCAG	AATCGCTAC	AGCAAAATTAA	
msa363690.2{690_2603}	CAAGGGaCTC	AATCGACTAG	TGGTGCAGCAG	AATCGCTAC	AGCAAAATTAA	
msa363690.2{690_A909}	CAAGGGaCTC	AATCGACTAG	TGGTGCAGCAG	AATCGCTAC	AGCAAAATTAA	
msa363690.2{690_JM9130013}	CAAGGGaCTC	AATCGACTAG	TGGTGCAGCAG	AATCGCTAC	AGCAAAATTAA	
msa363690.2{690_H36B}	CAAGGGaCTC	AATCGACTAG	TGGTGCAGCAG	AATCGCTAC	AGCAAAATTAA	
Consensus	*****	*****	*****	*****	*****	
501						550
msa363690.2{690_COH1}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTGAAATG	
msa363690.2{690_M732}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTGAAATG	
msa363690.2{690_M781}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTGAAATG	
msa363690.2{690_090}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTGAAATG	
msa363690.2{690_CJB110}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTGAAATG	
msa363690.2{690_1169NT}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTGAAATG	
msa363690.2{690_18RS21}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTGAAATG	
msa363690.2{690_2603}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTGAAATG	
msa363690.2{690_A909}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTGAAATG	
msa363690.2{690_JM9130013}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTGAAATG	
msa363690.2{690_H36B}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACITCAA	GATTGAAATG	
Consensus	*****	*****	*****	*****	*****	
551						600
msa363690.2{690_COH1}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG	
msa363690.2{690_M732}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG	
msa363690.2{690_M781}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG	
msa363690.2{690_090}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG	
msa363690.2{690_CJB110}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG	
msa363690.2{690_1169NT}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG	
msa363690.2{690_18RS21}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG	
msa363690.2{690_2603}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG	
msa363690.2{690_A909}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG	
msa363690.2{690_JM9130013}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG	
msa363690.2{690_H36B}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG	
Consensus	*****	*****	*****	*****	*****	
601						650
msa363690.2{690_COH1}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA	
msa363690.2{690_M732}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA	
msa363690.2{690_M781}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA	
msa363690.2{690_090}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA	
msa363690.2{690_CJB110}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA	
msa363690.2{690_1169NT}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA	
msa363690.2{690_18RS21}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA	
msa363690.2{690_2603}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA	
msa363690.2{690_A909}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA	
msa363690.2{690_JM9130013}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA	
msa363690.2{690_H36B}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA	
Consensus	*****	*****	*****	*****	*****	
651						700
msa363690.2{690_COH1}	TAGTGATATT	GATCCAGCTT	CAAAAACACTAG	TCAAGTACTT	GTCCATGTAG	
msa363690.2{690_M732}	TAGTGATATT	GATCCAGCTT	CAAAAACACTAG	TCAAGTACTT	GTCCATGTAG	
msa363690.2{690_M781}	TAGTGATATT	GATCCAGCTT	CAAAAACACTAG	TCAAGTACTT	GTCCATGTAG	
msa363690.2{690_090}	TAGTGATATT	GATCCAGCTT	CAAAAACACTAG	TCAAGTACTT	GTCCATGTAG	
msa363690.2{690_CJB110}	TAGTGATATT	GATCCAGCTT	CAAAAACACTAG	TCAAGTACTT	GTCCATGTAG	
msa363690.2{690_1169NT}	TAGTGATATT	GATCCAGCTT	CAAAAACACTAG	TCAAGTACTT	GTCCATGTAG	
msa363690.2{690_18RS21}	TAGTGATATT	GATCCAGCTT	CAAAAACACTAG	TCAAGTACTT	GTCCATGTAG	
msa363690.2{690_2603}	TAGTGATATT	GATCCAGCTT	CAAAAACACTAG	TCAAGTACTT	GTCCATGTAG	
msa363690.2{690_A909}	TAGTGATATT	GATCCAGCTT	CAAAAACACTAG	TCAAGTACTT	GTCCATGTAG	
msa363690.2{690_JM9130013}	TAGTGATATT	GATCCAGCTT	CAAAAACACTAG	TCAAGTACTT	GTCCATGTAG	
msa363690.2{690_H36B}	TAGTGATATT	GATCCAGCTT	CAAAAACACTAG	TCAAGTACTT	GTCCATGTAG	
Consensus	*****	*****	*****	*****	*****	
701						750
msa363690.2{690_COH1}	CAACTGAAgg	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTG	
msa363690.2{690_M732}	CAACTGAAgg	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTG	
msa363690.2{690_M781}	CAACTGAAgg	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTG	
msa363690.2{690_090}	CAACTGAAgg	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTG	
msa363690.2{690_CJB110}	CAACTGAAgg	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTG	
msa363690.2{690_1169NT}	CAACTGAAgg	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTG	

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_18RS21}	CAACTGAA GG	TAAA CTCAA	GTACA AGGAA	CGAT GAGTGA	GTAT GATTG
msa363690.2{690_2603}	CAACTGAA GG	TAAA CTCAA	GTACA AGGAA	CGAT GAGTGA	GTAT GATTG
msa363690.2{690_A909}	CAACTGAG GG	TAAA CTCAA	GTACA AGGAA	CGAT GAGTGA	GTAT GATTG
msa363690.2{690_JM9130013}	CAACTGAG GG	TAAA CTCAA	GTACA AGGAA	CGAT GAGTGA	GTAT GATTG
msa363690.2{690_H36B}	CAACTGAA GG	TAAA CTCAA	GTACA AGGAA	CGAT GAGTGA	GTAT GATTG
Consensus	*****	*****	*****	*****	*****
		751			800
msa363690.2{690_COH1}	GCTAAT GTtA	AAAAAGatCA	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_M732}	GCTAAT GTtA	AAAAAGatCA	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_M781}	GCTAAT GTtA	AAAAAGatCA	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_090}	GCTAAT GTtA	AAAAAGACC	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_CJB110}	GCTAAT GTtA	AAAAAGACC	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_1169NT}	GCTAAT GTtA	AAAAAGACC	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_18RS21}	GCTAAT GTtA	AAAAAGACC	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_2603}	GCTAAT GTtA	AAAAAGACC	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_A909}	GCTAAT GTtA	AAAAAGACC	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_JM9130013}	GCTAAT GTtA	AAAAAGACC	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_H36B}	GCTAAT GTtA	AAAAAGACC	GgCTGTTAAA	ATAAAATCTA	AGGTCTATCC
Consensus	*****	*****	*****	*****	*****
		801			850
msa363690.2{690_COH1}	TGACAAGGAA	TGGGAAGGTA	AAATTCATA	TATCTCAAAT	TATCCAGAAC
msa363690.2{690_M732}	TGACAAGGAA	TGGGAAGGTA	AAATTCATA	TATCTCAAAT	TATCCAGAAC
msa363690.2{690_M781}	TGACAAGGAA	TGGGAAGGTA	AAATTCATA	TATCTCAAAT	TATCCAGAAC
msa363690.2{690_090}	TGACAAGGAA	TGGGAAGGTA	AAATTCATA	TATCTCAAAT	TATCCAGAAC
msa363690.2{690_CJB110}	TGACAAGGAA	TGGGAAGGTA	AAATTCATA	TATCTCAAAT	TATCCAGAAC
msa363690.2{690_1169NT}	TGACAAGGAA	TGGGAAGGTA	AAATTCATA	TATCTCAAAT	TATCCAGAAC
msa363690.2{690_18RS21}	TGACAAGGAA	TGGGAAGGTA	AAATTCATA	TATCTCAAAT	TATCCAGAAC
msa363690.2{690_2603}	TGACAAGGAA	TGGGAAGGTA	AAATTCATA	TATCTCAAAT	TATCCAGAAC
msa363690.2{690_A909}	TGACAAGGAA	TGGGAAGGTA	AAATTCATA	TATCTCAAAT	TATCCAGAAC
msa363690.2{690_JM9130013}	TGACAAGGAA	TGGGAAGGTA	AAATTCATA	TATCTCAAAT	TATCCAGAAC
msa363690.2{690_H36B}	TGACAAGGAA	TGGGAAGGTA	AAATTCATA	TATCTCAAAT	TATCCAGAAC
Consensus	*****	*****	*****	*****	*****
		851			900
msa363690.2{690_COH1}	CAGAACGAAA	CAACAA TGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_M732}	CAGAACGAAA	CAACAA TGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_M781}	CAGAACGAAA	CAACAA TGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_090}	CAGAACGAAA	CAACAA TGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_CJB110}	CAGAACGAAA	CAACAA TGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_1169NT}	CAGAACGAAA	CAACAA TGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_18RS21}	CAGAACGAAA	CAACAA TGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_2603}	CAGAACGAAA	CAACAA TGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_A909}	CAGAACGAAA	CAACAA TGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_JM9130013}	CAGAACGAAA	CAACAA TGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
msa363690.2{690_H36B}	CAGAACGAAA	CAACAA TGAC	TCTAATAACG	GCTCTAGTGC	TGTAAATTAT
Consensus	*****	*****	*****	*****	*****
		901			950
msa363690.2{690_COH1}	AAATATAAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTT
msa363690.2{690_M732}	AAATATAAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTT
msa363690.2{690_M781}	AAATATAAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTT
msa363690.2{690_090}	AAATATAAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTT
msa363690.2{690_CJB110}	AAATATAAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTT
msa363690.2{690_1169NT}	AAATATAAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTT
msa363690.2{690_18RS21}	AAATATAAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTT
msa363690.2{690_2603}	AAATATAAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTT
msa363690.2{690_A909}	AAATATAAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTT
msa363690.2{690_JM9130013}	AAATATAAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTT
msa363690.2{690_H36B}	AAATATAAAAG	TAGATATTAC	TAGCCCTCTC	GATGCATTAA	AACAAGGTT
Consensus	*****	*****	*****	*****	*****
		951			1000
msa363690.2{690_COH1}	TACCGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTCCCTA
msa363690.2{690_M732}	TACCGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTCCCTA
msa363690.2{690_M781}	TACCGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTCCCTA
msa363690.2{690_090}	TACCGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTCCCTA
msa363690.2{690_CJB110}	TACCGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTCCCTA
msa363690.2{690_1169NT}	TACCGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTCCCTA
msa363690.2{690_18RS21}	TACCGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTCCCTA
msa363690.2{690_2603}	TACCGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTCCCTA
msa363690.2{690_A909}	TACCGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTCCCTA
msa363690.2{690_JM9130013}	TACCGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTCCCTA
msa363690.2{690_H36B}	TACCGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTCCCTA
Consensus	*****	*****	*****	*****	*****
		1001			1050
msa363690.2{690_COH1}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAT
msa363690.2{690_M732}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAT
msa363690.2{690_M781}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAT
msa363690.2{690_090}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAT
msa363690.2{690_CJB110}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAT

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_1169NT}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_18RS21}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_2603}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_A909}	CAAGTTCTGT	GACAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_JM9130013}	CAAGTTCTGT	GACAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_H36B}	CAAGTTCTGT	GACAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
Consensus	*****	*****	*****	*****	*****
	1051				1100
msa363690.2{690_COH1}	GATTCTAATC	GTAAAATTTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_M732}	GATTCTAATC	GTAAAATTTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_M781}	GATTCTAATC	GTAAAATTTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_090}	GATTCTAATC	GTAAAATTTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_CJB110}	GATTCTAATC	GTAAAATTTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_1169NT}	GATTCTAATC	GTAAAATTTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_18RS21}	GATTCTAATC	GTAAAATTTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_2603}	GATTCTAATC	GTAAAATTTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_A909}	GATTCTAATC	GTAAAATTTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_JM9130013}	GATTCTAATC	GTAAAATTTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
msa363690.2{690_H36B}	GATTCTAATC	GTAAAATTTC	CAAAGTTGAA	GTCAAAATTG	GTAAAGCTGA
Consensus	*****	*****	*****	*****	*****
	1101				1150
msa363690.2{690_COH1}	TGCTAAAGACA	CAAGAAATTTC	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_M732}	TGCTAAAGACA	CAAGAAATTTC	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_M781}	TGCTAAAGACA	CAAGAAATTTC	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_090}	TGCTAAAGACA	CAAGAAATTTC	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_CJB110}	TGCTAAAGACA	CAAGAAATTTC	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_1169NT}	TGCTAAAGACA	CAAGAAATTTC	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_18RS21}	TGCTAAAGACA	CAAGAAATTTC	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_2603}	TGCTAAAGACA	CAAGAAATTTC	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_A909}	TGCTAAAGACA	CAAGAAATTTC	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_JM9130013}	TGCTAAAGACA	CAAGAAATTTC	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
msa363690.2{690_H36B}	TGCTAAAGACA	CAAGAAATTTC	TATCAGGTTT	GAAAGCAGGA	CAAATCGTgG
Consensus	*****	*****	*****	*****	*****
	1151				1200
msa363690.2{690_COH1}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_M732}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_M781}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_090}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_CJB110}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_1169NT}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_18RS21}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_2603}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_A909}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_JM9130013}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_H36B}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
Consensus	*****	*****	*****	*****	*****
	1201				1242
msa363690.2{690_COH1}	GAATCAATCG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_M732}	GAATCAATCG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_M781}	GAATCAATCG	ATCTTAAGTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_090}	GAATCAATCG	ATCTTAACTC	TAATAAGAAA	TCAGAGG~~~	~~
msa363690.2{690_CJB110}	GAATCAATCG	ATCTTAACTC	TAATAAGAAA	TCAGAGgtga	~~
msa363690.2{690_1169NT}	GAATCAATCG	ATCTTAACTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_18RS21}	GAATCAATCG	ATCTTAACTC	TAATAAGAAA	TCAGAG~~~	~~
msa363690.2{690_2603}	GAATCAATCG	ATCTTAACTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_A909}	GAATCAATCG	ATCTTAACTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_JM9130013}	GAATCAATCG	ATCTTAACTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_H36B}	GAATCAATCG	ATCTTAACTC	TAATAAGAAA	TCAGAGgtga	~~
Consensus	*****	*****	*****	*****	**

SEQ ID NO. 8511

STRAIN 2603 frame: 1

MSKRQNLGI SKKGAI ISGLSVALIVVIGFLWVQSOPNKS AVKTNYKVFNVR EGSVSSST
 LLTGAKANQEQQVYFDANKGNRATVTVKVGDKITAGQQLVQYDTTTAQAYDTANRQLN
 KVARQINNLKTTGSLPAMESSDQSSSSQGQGTQSTS GATNRLLQCNQYQS QANASYNQQLQ
 DLNDAYADAQAVNKDAQKALNDT VITSDVSGTVEVNSDIDPASKTSQVLHVATEGKLQ
 VQGTMSEYDLANVKDAQV KIKSKVYPDEWEKGKIS YSNP YPEAEAN NDSNNGSAV NY
 KYKVDITSPLDALKQGFITVSV EVVNGDKHLIVPTSSVINKDNKHFVWVY NDSNRKIS K
 VKIGKADAKTQEILSGLKAGQI VVTNP SKTFKDQKIDNIESIDLNSNKKSEVK

SEQ ID NO. 8512

STRAIN 090 frame: 1

FLWVQSOPNKS AVKTNYKVFNVR EGSVSSSTLLTGAKANQEQQVYFDANKGNRATVTVK
 VGDKITAGOOLVQYDTTTAQAYDTANRQLN KVARQINNLKTTGSLPAMESSDQSSSSO
 GQGTQSTS GATNRLLQCNQYQS QANASYNQQLDNLN DAYADAQAEVNKAQKALNDT VITSDV
 SGTVVEVNSDIDPASKTSQVLHVATEGKLQVQGTMSEYDLANVKDDQAVKIKSKVYPDK
 EWEKGKIS YSNP YPEAEAN NDSNNGSAV NYKYKVDITSPLDALKQGFITVSV EVVNGDKH
 LIVPTSSVINKDNKHFVWVY NDSNRKIS KSKV EKIGKADAKTQEILSGLKAGQIVVTPSK
 TFKDGQKIDNIESIDLNSNKKSEVK

Table 85: Comparative Sequences relating to SAG1361

SEQ ID NO. 8513
 STRAIN A909 frame: 1
 FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQQLVQYDITTAQAAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSQ
 GQGQSTSGATNRLOQNYQSOQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITS
 SGTVVEVNSDIDPASKTSQVLVHATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
 EWEKGKISYIISNPYPEAEANNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVNGDKH
 LIVPTSSVTKDNKHVFVWVYNDNSRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8514
 STRAIN H36B frame: 1
 FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQQLVQYDITTAQAAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRLOQNYQSOQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITS
 SGTVVEVNSDIDPASKTSQVLVHATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
 EWEKGKISYIISNPYPEAEANNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVNGDKH
 LIVPTSSVTKDNKHVFVWVYNDNSRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 AFKDQKIDNIESIDLKSNKKSEV

SEQ ID NO. 8515
 STRAIN 18RS21 frame: 1
 FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQQLVQYDITTAQAAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRLOQNYQSOQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITS
 SGTVVEVNSDIDPASKTSQVLVHATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
 EWEKGKISYIISNPYPEAEANNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVNGDKH
 LIVPTSSVTKDNKHVFVWVYNDNSRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSE

SEQ ID NO. 8516
 STRAIN M732 frame: 1
 FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQQLVQYDITTAQAAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRLOQNYQSOQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITS
 SGTVVEVNSDIDPASKTSQVLVHATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
 EWEKGKISYIISNPYPEAEANNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVNGDKH
 LIVPTSSVTKDNKHVFVWVYNDNSRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSE

SEQ ID NO. 8517
 STRAIN COH1 frame: 1
 FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQQLVQYDITTAQAAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRLOQNYQSOQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITS
 SGTVVEVNSDIDPASKTSQVLVHATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
 EWEKGKISYIISNPYPEAEANNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVNGDKH
 LIVPTSSVTKDNKHVFVWVYNDNSRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSE

SEQ ID NO. 8518
 STRAIN M781 frame: 1
 FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQQLVQYDITTAQAAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRLOQNYQSOQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITS
 SGTVVEVNSDIDPASKTSQVLVHATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
 EWEKGKISYIISNPYPEAEANNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVNGDKH
 LIVPTSSVTKDNKHVFVWVYNDNSRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSE

SEQ ID NO. 8519
 STRAIN M781 frame: 1
 FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQQLVQYDITTAQAAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRLOQNYQSOQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITS
 SGTVVEVNSDIDPASKTSQVLVHATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
 EWEKGKISYIISNPYPEAEANNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVNGDKH
 LIVPTSSVTKDNKHVFVWVYNDNSRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSE

SEQ ID NO. 8520
 STRAIN CJB110 frame: 1
 FLWVQSQPNKSAVKTNYKVFNVREGSVSSSTLLTGAKAKANQEQQYVYFDANKGNRATVTVK
 VGDKITAGQQQLVQYDITTAQAAAYDTANRQLNKVARQINNLKTTGSLPAMESSDQSSSSQ
 GQGTQSTSGATNRLOQNYQSOQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITS
 SGTVVEVNSDIDPASKTSQVLVHATEGKLQVQGTMSEYDLANVKKDQAVKIKSKVYPDK
 EWEKGKISYIISNPYPEAEANNDSNNGSSAVNYKYKVDITSPLDALKQGFTVSVEVNGDKH
 LIVPTSSVTKDNKHVFVWVYNDNSRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLKSNKKSE

SEQ ID NO. 8521

Table 85: Comparative Sequences relating to SAG1361

STRAIN 1169NT frame: 1
 FLWVQSPNKS A V K T N Y K V F N V R E G S V S S T L L T G K A K A N Q E Q V V Y F D A N K G N R A T V T V K
 V G D K I T A G Q Q L V Q Y D T T A Q A A Y D T A N R Q L N K V A R Q I N N L K T T G S L P A M E S S D Q S S S S Q
 G G T Q S T S G A T N R L Q Q N Y Q S Q A N A S Y N Q Q L Q D L N D A Y A D A Q A E V N K A Q K A L N D T V I T S D V
 S G T V V E V N S D I D P A S K T S Q V L V H V A T E G K L Q V Q G T M S E Y D L A N V K K D Q A V K I K S K V Y P D K
 E W E G K I S Y I S N Y P E A B A N N N D S N N G S A V N Y K Y K V D I T S P L D A L K Q G F T V S V E V V N G D K H
 L I V P T S S V I N K D N K H F V W V Y N D S N R K I S K V E V K I G K A D A K T Q E I L S G L K A Q G I V V T N P S K
 T F K D G Q K I D N I E S I D L K S N K K S E V K

SEQ ID NO. 8522

STRAIN JM9130013 frame: 1

FLWVQSPNKS A V K T N Y K V F N V R E G S V S S T L L T G K A K A N Q E Q V V Y F D A N K G N R A T V T V K
 V G D K I T A G Q Q L V Q Y D T T A Q A A Y D T A N R Q L N K V A R Q I N N L K T T G S L P A M E S S D Q S S S S Q
 G Q Q A Q S T S G A T N R L Q Q N Y Q S Q A N A S Y N Q Q L Q D L N D A Y A D A Q A E V N K A Q K A L N D T V I T S D V
 S G T V V E V N S D I D P A S K T S Q V L V H V A T E G K L Q V Q G T M S E Y D L A N V K K D Q V K I K S K V Y P D K
 E W E G K I S Y I S N Y P E A B A N N N D S N N G S A V N Y K Y K V D I T S P L D A L K Q G F T V S V E V V N G D K H
 L I V P T S S V I N K D N K H F V W V Y N D S N R K I S K V E V K I G K A D A K T Q E I L S G L K A Q G I V V T N P S K
 T F K D G Q K I D N I E S I D L K S N K K S E V K

PRETTY of: /biotmp/msa375805.2{*} April 1, 2003 02:58 ..

msa375805.2{690_COH1}	-----	-----	-----	F	LWVQSPNKS	AVKTNYKVFN
msa375805.2{690_M732}	-----	-----	-----	F	LWVQSPNKS	AVKTNYKVFN
msa375805.2{690_M781}	-----	-----	-----	F	LWVQSPNKS	AVKTNYKVFN
msa375805.2{690_090}	-----	-----	-----	F	LWVQSPNKS	AVKTNYKVFN
msa375805.2{690_CJB110}	-----	-----	-----	F	LWVQSPNKS	AVKTNYKVFN
msa375805.2{690_1169NT}	-----	-----	-----	F	LWVQSPNKS	AVKTNYKVFN
msa375805.2{690_18RS21}	-----	-----	-----	F	LWVQSPNKS	AVKTNYKVFN
msa375805.2{690_2603}	mskrqnlgis	kgkaiisgl	valivviggf	F	LWVQSPNKS	AVKTNYKVFN
msa375805.2{690_A909}	-----	-----	-----	F	LWVQSPNKS	AVKTNYKVFN
msa375805.2{690_JM9130013}	-----	-----	-----	F	LWVQSPNKS	AVKTNYKVFN
msa375805.2{690_H36B}	-----	-----	-----	F	LWVQSPNKS	AVKTNYKVFN
Consensus	*****	*****	*****	*****	*****	*****
51						
msa375805.2{690_COH1}	VREGSVSSST	LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL	100
msa375805.2{690_M732}	VREGSVSSST	LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL	
msa375805.2{690_M781}	VREGSVSSST	LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL	
msa375805.2{690_090}	VREGSVSSST	LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL	
msa375805.2{690_CJB110}	VREGSVSSST	LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL	
msa375805.2{690_1169NT}	VREGSVSSST	LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL	
msa375805.2{690_18RS21}	VREGSVSSST	LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL	
msa375805.2{690_2603}	VREGSVSSST	LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL	
msa375805.2{690_A909}	VREGSVSSST	LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL	
msa375805.2{690_JM9130013}	VREGSVSSST	LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL	
msa375805.2{690_H36B}	VREGSVSSST	LLTGKAKANQ	EQYVYFDANK	GNRATVTVKV	GDKITAGQQL	
Consensus	*****	*****	*****	*****	*****	*****
101						
msa375805.2{690_COH1}	VQYDTTTAQA	A Y D T A N R Q L N	K V A R Q I N N L K	T T G S F P A M E s	S D Q S S S S S Q G	150
msa375805.2{690_M732}	VQYDTTTAQA	A Y D T A N R Q L N	K V A R Q I N N L K	T T G S F P A M E s	S D Q S S S S S Q G	
msa375805.2{690_M781}	VQYDTTTAQA	A Y D T A N R Q L N	K V A R Q I N N L K	T T G S F P A M E s	S D Q S S S S S Q G	
msa375805.2{690_090}	VQYDTTTAQA	A Y D T A N R Q L N	K V A R Q I N N L K	T T G S 1 P A M E l	S D Q S S S S S Q G	
msa375805.2{690_CJB110}	VQYDTTTAQA	A Y D T A N R Q L N	K V A R Q I N N L K	T T G S 1 P A M E l	S D Q S S S S S Q G	
msa375805.2{690_1169NT}	VQYDTTTAQA	A Y D T A N R Q L N	K V A R Q I N N L K	T T G S 1 P A M E s	S D Q S S S S S Q G	
msa375805.2{690_18RS21}	VQYDTTTAQA	A Y D T A N R Q L N	K V A R Q I N N L K	T T G S 1 P A M E s	S D Q S S S S S Q G	
msa375805.2{690_2603}	VQYDTTTAQA	A Y D T A N R Q L N	K V A R Q I N N L K	T T G S 1 P A M E s	S D Q S S S S S Q G	
msa375805.2{690_A909}	VQYDTTTAQA	A Y D T A N R Q L N	K V A R Q I N N L K	T T G S 1 P A M E s	S D Q S S S S S Q G	
msa375805.2{690_JM9130013}	VQYDTTTAQA	A Y D T A N R Q L N	K V A R Q I N N L K	T T G S 1 P A M E s	S D Q S S S S S Q G	
msa375805.2{690_H36B}	VQYDTTTAQA	A Y D T A N R Q L N	K V A R Q I N N L K	T T G S 1 P A M E s	S D Q S S S S S Q G	
Consensus	*****	*****	*****	*****	*****	*****
151						
msa375805.2{690_COH1}	Q G T Q S T S G A T	N R L Q Q N Y Q S O	A N A S Y N Q Q L Q	D L N D A Y A D A Q	A E V N K A Q K A L	200
msa375805.2{690_M732}	Q G T Q S T S G A T	N R L Q Q N Y Q S O	A N A S Y N Q Q L Q	D L N D A Y A D A Q	A E V N K A Q K A L	
msa375805.2{690_M781}	Q G T Q S T S G A T	N R L Q Q N Y Q S O	A N A S Y N Q Q L Q	D L N D A Y A D A Q	A E V N K A Q K A L	
msa375805.2{690_090}	Q G T Q S T S G A T	N R L Q Q N Y Q S O	A N A S Y N Q Q L Q	D L N D A Y A D A Q	A E V N K A Q K A L	
msa375805.2{690_CJB110}	Q G T Q S T S G A T	N R L Q Q N Y Q S O	A N A S Y N Q Q L Q	D L N D A Y A D A Q	A E V N K A Q K A L	
msa375805.2{690_1169NT}	Q G T Q S T S G A T	N R L Q Q N Y Q S O	A N A S Y N Q Q L Q	D L N D A Y A D A Q	A E V N K A Q K A L	
msa375805.2{690_18RS21}	Q G T Q S T S G A T	N R L Q Q N Y Q S O	A N A S Y N Q Q L Q	D L N D A Y A D A Q	A E V N K A Q K A L	
msa375805.2{690_2603}	Q G T Q S T S G A T	N R L Q Q N Y Q S O	A N A S Y N Q Q L Q	D L N D A Y A D A Q	A E V N K A Q K A L	
msa375805.2{690_A909}	Q G a Q S T S G A T	N R L Q Q N Y Q S O	A N A S Y N Q Q L Q	D L N D A Y A D A Q	A E V N K A Q K A L	
msa375805.2{690_JM9130013}	Q G a Q S T S G A T	N R L Q Q N Y Q S O	A N A S Y N Q Q L Q	D L N D A Y A D A Q	A E V N K A Q K A L	
msa375805.2{690_H36B}	Q G C Q S T S G A T	N R L Q Q N Y Q S O	A N A S Y N Q Q L Q	D L N D A Y A D A Q	A E V N K A Q K A L	
Consensus	*****	*****	*****	*****	*****	*****
201						
msa375805.2{690_COH1}	N D T V I T S D V S	G T V V E V N S D I	D P A S K T S Q V L	V H V A T E G K L Q	V Q G T M S E Y D L	250
msa375805.2{690_M732}	N D T V I T S D V S	G T V V E V N S D I	D P A S K T S Q V L	V H V A T E G K L Q	V Q G T M S E Y D L	
msa375805.2{690_M781}	N D T V I T S D V S	G T V V E V N S D I	D P A S K T S Q V L	V H V A T E G K L Q	V Q G T M S E Y D L	
msa375805.2{690_090}	N D T V I T S D V S	G T V V E V N S D I	D P A S K T S Q V L	V H V A T E G K L Q	V Q G T M S E Y D L	

Table 85: Comparative Sequences relating to SAG1361

msa375805.2{690_CJB110}	NDTVITSDVS	GTVVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSEYDL
msa375805.2{690_1169NT}	NDTVITSDVS	GTVVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSEYDL
msa375805.2{690_18RS21}	NDTVITSDVS	GTVVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSEYDL
msa375805.2{690_2603}	NDTVITSDVS	GTVVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSEYDL
msa375805.2{690_A909}	NDTVITSDVS	GTVVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSEYDL
msa375805.2{690_JM9130013}	NDTVITSDVS	GTVVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSEYDL
msa375805.2{690_H36B}	NDTVITSDVS	GTVVEVNSDI	DPASKTSQVL	VHVATEGKLQ	VQGTMSEYDL
Consensus	*****	*****	*****	*****	*****
msa375805.2{690_COH1}		251			300
msa375805.2{690_M732}	ANVKKDQaVK	I KSKVYPDKE	WEGKISYIISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_M781}	ANVKKDQaVK	I KSKVYPDKE	WEGKISYIISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_090}	ANVKKDQaVK	I KSKVYPDKE	WEGKISYIISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_CJB110}	ANVKKDQaVK	I KSKVYPDKE	WEGKISYIISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_1169NT}	ANVKKDQaVK	I KSKVYPDKE	WEGKISYIISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_18RS21}	ANVKKDQaVK	I KSKVYPDKE	WEGKISYIISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_2603}	ANVKKDQaVK	I KSKVYPDKE	WEGKISYIISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_A909}	ANVKKDQsVK	I KSKVYPDKE	WEGKISYIISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_JM9130013}	ANVKKDQsVK	I KSKVYPDKE	WEGKISYIISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_H36B}	ANVKKDQaVK	I KSKVYPDKE	WEGKISYIISN	YPEAEANNND	SNNGSSAVNY
Consensus	*****	*****	*****	*****	*****
msa375805.2{690_COH1}		301			350
msa375805.2{690_M732}	KYKVDIRTSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFWWVYN
msa375805.2{690_M781}	KYKVDIRTSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFWWVYN
msa375805.2{690_090}	KYKVDIRTSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFWWVYN
msa375805.2{690_CJB110}	KYKVDIRTSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFWWVYN
msa375805.2{690_1169NT}	KYKVDIRTSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFWWVYN
msa375805.2{690_18RS21}	KYKVDIRTSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFWWVYN
msa375805.2{690_2603}	KYKVDIRTSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFWWVYN
msa375805.2{690_A909}	KYKVDIRTSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFWWVYN
msa375805.2{690_JM9130013}	KYKVDIRTSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFWWVYN
msa375805.2{690_H36B}	KYKVDIRTSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFWWVYN
Consensus	*****	*****	*****	*****	*****
msa375805.2{690_COH1}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_M732}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_M781}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_090}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_CJB110}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_1169NT}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_18RS21}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_2603}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_A909}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_JM9130013}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_H36B}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
Consensus	*****	*****	*****	*****	*****
msa375805.2{690_COH1}		401	414		
msa375805.2{690_M732}	ESIDLkSNKK	SEv-			
msa375805.2{690_M781}	ESIDLkSNKK	SEv-			
msa375805.2{690_090}	ESIDLkSNKK	SEv-			
msa375805.2{690_CJB110}	ESIDLnSNKK	SE--			
msa375805.2{690_1169NT}	ESIDLnSNKK	SEv-			
msa375805.2{690_18RS21}	ESIDLnSNKK	SE--			
msa375805.2{690_2603}	ESIDLnSNKK	SEvK			
msa375805.2{690_A909}	ESIDLkSNKK	SEvK			
msa375805.2{690_JM9130013}	ESIDLkSNKK	SEvK			
msa375805.2{690_H36B}	ESIDLkSNKK	SEv-	***		
Consensus	*****	*****	***		

Table 86: Comparative Sequences relating to SAG1393

SEQ ID NO. 8602
STRAIN 090
GAAGGCTTCACCTATTATGGAAAAATTCCCTGAAAAATCCGAAAAAAGTAAT
TAATTATCACATTCTTACACTGGTATTATAAAACTAGGTCTTAATG
TTCAAGTTACAGTTAGACTTAGAAAAAGATACCCCCGTTTGGTAAG
CAACTGAAAGAAGCTAAAAATTAACTGCTGATGATACAGAACGTTATTGC
CGCACAAAAACCTGATTAACTCATGGTTTCTGATCAAGATCCAAACATCA
ATACTCTGAAAAAAATTGCAACCAACTTTAGTTATAAAATAGGTGCAACAA
AATTATTAGATATGATGCCAGCTTGGGAAAGTATCGGTAAGAAAAA
AGAAGCTAATCAGTGGTTAGCCAATGGAAAACTAAAATCTCGCTGCCA
AAAAAGATTACCCATCTTAAAGCTAACACTACTTTACTATTATG
TTTTTATGATAAAAATATCTTATATGGTAATAATTGGCAGCGCG
TGAGAACATACTATGATTCACTAGGTTATGCTGCCAGAAAAGTC
AAAAAGATGTcTTTAAAAAGGGTGGTTACCGTTTCgCAAGAACGATC
GGTGATTACGTTGGAGATTATGCCCTGTTATAAAACAAAAGCCTAA
AAAAGCAGCTTCatcATTAAAGAAGTGTGCTGGAAGAATTACCAAG
CTGTCatAAAAGGGCACATCATAGAAAGTaaCTACCGACGTGTTTATTC
TCTGACCCCTCATTTAGAAGCTCAATTAAAATCATTTACAAA

SEQ ID NO. 8603
STRAIN A909
GAAGGGCTTACCTATTATGGAAAAATTCCCTG
AAAAATCCTGGAAAAAAAGTAATTAAATTTCACATATTCTTACACTGGATATTTA
TTAAAACTAGGAGTTAATGTTCAAGTTACAGTTAGACTTAGAAAAAGA
TAGCCCCGTTTGGTAAaCACTGAAAGGAGCTAAAAAAATTAACTGTTT
ATGATAACAGAACGATTGCGCACAACCCATGTATTAACTCATGTTT
GATCAAGATCCTAAACATCAAACTCTGCAAAAAAAATTGCACCAACTTGT
TATTAATATGGTCACAAAATTATTAGATAATGATGCCAGCTTGGGGA
AAGTATTGGTAAAGGAAAAAGAGCTAATCAGTGGTTAGCCAATGGAAA
ACTAAAACCTCGCTGCCAAAAGATTACCATATCTTAAACCTCAA
CACTACTTTTACCATATGGATTTTATGATAAAATATCTATTATATG
GTAATAATTGAGCGCGGTGGAGAACTAATCTATGATTCACTAGGTTAT
GCTGGCCCAGAAAAGTCAAAAAGATGTCCTTAAAGGGTGGTTTAC
CGTTTGCAGAACGAGCAATCGGTGATTACGTTGGAGATTATGCCCTTGT
ATATAAACAAAAGCACTAAAAAGCAGCTTCATCACTAAAGAAAGTGAT
GTCAGGAAAGAATTACCAAGCTGCAAAAAGGGCACATCATAGAAAGTAA
CTACGACGCTGTTTATTCTCTGACCCTATCTTAAAGCTCAATTAA
AATCTTACAAA

SEQ ID NO. 8604
 STRAIN H36B
 GAAGGGCTCACCTTATATGGAAAA
 ATTCCTGAAAATCCGAAAAAAGTAATTAAATTACATATTCTTACACTGG
 ATATTATTAACAGTAGGAGTTAATGTTCAAGTTACAGTTAGACTTAG
 AAAAGATAgCCCCGGTTTGGTAagCAGTAAAGGAGCTAAAAAAATTAA
 ACTGCTGATGATAACAGAGCTATTGGCAGCACAAAAACCTGATTAAtCAT
 GGTGTTTGTATCAAgtATCCAACATCAACTCTGAAAAAAATTGCCAACAA
 CTTTAGTTATTAAATATGGTGCAAAATTATTTAGtAtTgATGCCAGCT
 TTGGGGAAGTATTGGTAAAGAAAAAGAAGCTATACTAGTGGTTAGGCCA
 ATGGAAAACAAACTCTCGCTGCCAAAAAGATTACACCATATCTTAA
 GGCTCAACACTTACTTACTATTATAGATTTTATGATAAAATATCTAT
 TTATATGGTAATAATTGGACGCGGtGGAGAACTAATCTATGATtCACT
 AGGTTATGCTGCCCGAAAAAGCTAAAAAAAGATGCTTTAAAAAAAGGGT
 GGTGTTACCGTTTcgCAAGAAGCAATCGGTgATTACGTTGGAGATTATGCC
 CTGTTAATATAACAAACAGACTAAAAAGCAGCTTCACTTAAAGA
 AAGTGTGTTGGAAAGAATTACAGCTGTCAAAAGGGCACATCATAG
 AAAGTAACATACGAGCTTTTATTCTCTGACCCTCTATCTTAAAGCT
 CAATTAAATATTTACAAA

Table 86: Comparative Sequences relating to SAG1393**SEQ ID NO. 8605**

STRAIN 18RS21

GAAGGCTTCACCTTATTATGG
 AAAAATTCTGAAAATCCGAAAAAAAGTAATTAAATTACATATTCTTACAC
 TGGGTATTATTAAAACTAGGTGTTAATGTTCAAGTTACAGTTAGACT
 TAGAAAAAGATAGCCCCGTTTTGGTAAACAACGTGAAAGAGCTAAAAAA
 TTAACGTGCTGATGACAGAACGCTATTGCCGCACAAAACCTGATTAAAT
 CATGGTTCTGATCAAGATCCAACATCAACTCTGAAAAAAATTGAC
 CAACCTTGTATTAAATATGGTGCACAAAATTATTTAGATAATGAC
 GCCTTGGGAAAGTATTCCGGTAAAGAAAAAGAGCTAATCAGTGGGTTAG
 CCAATGGAAAACCTAAACCTCGCTGTCAAAGAAGATTTACACCATATCT
 TAAAGCTTAACACTACTTTACTATTATGGATTTTATGATAAAAATATC
 TATTATATGGTAAATAATTGGACCGGGTGGAGAACTAATCTATGATT
 ACTAGTTATGCTGCCCAAGAAAAAGCTAAAAAGATGCTTTAAAAAG
 GGTGGTTACCGTTTCGCAAGAACGATCGGTGATTACGTTGGAGATTAT
 GCCCTTGTAAATATAACAAAACgACTAAAAAAGCAGCTTCACTTAA
 AGAAAGTGATGCTGGAAGAATTACCGCTGTCAAAAAGGGCACATCA
 TAGAAAGTAACGACGTGTTTATTCTGACCCTCTATCTTTAGAA
 GCTCAATTAAAATCATTACAAA

SEQ ID NO. 8606

STRAIN M732

GAAGGCTTCACCTTATTATGG
 AAAAATTCTGAAAATCCGAAAAAAAGTAATTAAATTACATATTCTTAC
 CTGGGTATTATTAAAACTAGGTGTTAATGTTCAAGTTACAGTTAGAC
 TTAGAAAAAGATAGCCCCGTTTTGGTAAAGCAACTGAAAGAGCTAAAAAA
 ATTAACGTGCTGATGACAGAACGCTATTGCCGCACAAAACCTGATTAA
 TCATGGTTCTGATCAAGATCCAACACATCAACTCTGAAAAAAATTGCA
 CCAACTTGTATTAAATATGGTGCACAAAATTATTTAGATAATGATGCC
 AGCCTTGGGAAAGTATTGGTAAAGAAAAAGCTAATCAGTGGGTT
 GCAATGGAAAACCTCTCGCTGCCCAAAAAGATTTACACCATAT
 TTAAAGCCTAACACTACTTTACTATTATGGATTTTATGATAAAAATA
 TCTATTATATGGTAAATAATTGGACCGGGTGGAGAACTAATCTATGAT
 TCACTAGTTATGCTGCCCAAGAAAAAGCTAAAAAAGATGCTTTAAAAAA
 AGGGGGTTACCGTTTCGCAAGAACGAAATCGGTGATTACGTTGGAGATT
 ATGCCCTGTTAAATATAACAAAACGACTAAAAAAGCAGCTTCACTTAA
 AAGAAAGTGATGCTGGAAGAATTACCGCTGTCAAAAAGGGCACATC
 CATAGAAAGTAACGACGTGTTTATTCTGACCCTCTATCTTTAGA
 AGCTCAATTAAAATCATTACAAA

SEQ ID NO. 8607

STRAIN COH1

GAAGGCTTCACCTTATTATGG
 AAAAATTCTGAAAATCCGAAAAAAAGTAATTAAATTACATATTCTTAC
 ACTGGGTATTATTAAAACTAGGTGTTAATGTTCAAGTTACAGTTAGAC
 CTTAGAAAAAGATAGCCCCGTTTTGGTAAAGCAACTGAAAGAGCTAAAAA
 ATTAACGTGCTGATGACAGAACGCTATTGCCGCACAAAACCTGATTAA
 ATCATGGTTCTGATCAAGATCCAACACATCAACTCTGAAAAAAATTGCA
 ACCAACTTGTATTAAATATGGTGCACAAAATTATTTAGATAATGATGCC
 CAGCCTTGGGAAAGTATTGGTAAAGAAAAAGCTAATCAGTGGGTT
 AGCCAAATGGAAAACCTCTCGCTGCCCAAAAAGATTTACACCATAT
 CTTAAAGCCTAACACTACTTTACTATTATGGATTTTATGATAAAAATA
 TCTATTATATGGTAAATAATTGGACCGGGTGGAGAACTAATCTATGAT
 TCACTAGTTATGCTGCCCAAGAAAAAGCTAAAAAAGATGCTTTAAAAAA
 AGGGGGTTACCGTTTCGCAAGAACGAAATCGGTGATTACGTTGGAGATT
 ATGCCCTGTTAAATATAACAAAACGACTAAAAAAGCAGCTTCACTTAA
 AAGAAAGTGATGCTGGAAGAATTACCGCTGTCAAAAAGGGCACATC
 CATAGAAAGTAACGACGTGTTTATTCTGACCCTCTATCTTTAGA
 AGCTCAATTAAAATCATTACAAA

SEQ ID NO. 8608

STRAIN M781

GAAGGCTTCACCTTATTATGG
 AAAAATTCTGAAAATCCGAAAAAAAGTAATTAAATTACATATTCTTAC
 CTGGGTATTATTAAAACTAGGTGTTAATGTTCAAGTTACAGTTAGAC
 TTAGAAAAAGATAGCCCCGTTTTGGTAAAGCAACTGAAAGAGCTAAAAAA
 ATTAACGTGCTGATGACAGAACGCTATTGCCGCACAAAACCTGATTAA
 TCATGGTTCTGATCAAGATCCAACACATCAACTCTGAAAAAAATTGCA
 CCAACTTGTATTAAATATGGTGCACAAAATTATTTAGATAATGATGCC
 AGCCTTGGGAAAGTATTGGTAAAGAAAAAGCTAATCAGTGGGTT
 GCCAATGGAAAACCTCTCGCTGCCCAAAAAGATTTACACCATATC
 TTAAAGCCTAACACTACTTTACTATTATGGATTTTATGATAAAAATA
 TCTATTATATGGTAAATAATTGGACCGGGTGGAGAACTAATCTATGATT
 CACTAGTTATGCTGCCCAAGAAAAAGCTAAAAAAGATGCTTTAAAAAA
 GGGGGTTACCGTTTCGCAAGAACGAAATCGGTGATTACGTTGGAGATT
 TGCCCTGTTAAATATAACAAAACGACTAAAAAAGCAGCTTCACTTAA

Table 86: Comparative Sequences relating to SAG1393

AAGAAAAGTGTCTGGAAGAATTACAGCTGCAAAAAAGGGCACATC
ATAGAAAGTAACTACGACGTTTATTCCTCTGACCCTCATCTTAGA
AGCTCAATTAAAATCATTTACAAA

SEQ ID NO. 8609

STRAIN CJB110

GAAGGCCTTCACCTATTATGGA
AAAATTCTGAAAATCCGAAAAAAAGTAATTAATTTCATATTCTTACAC
TGGGTATTATTAAGACTAGGTGTTAATGTTCAAGTTACAGTTAGACT
TAGAAAAAGATAGCCCGTTTGTTAGAAGCAACTGAAAGAAGCTAAAAAA
TTAACCTGCTGATGATAAGAGCTATTGCCGCAACAAACCTGATTTAAT
CATGGTATTCTGATCAAGATCCAAACATCAATCTGAAAGAAAATTGAC
CAACCTTGTATTAAATATGGTGCAACAAACATTATTAGATATGATGCCA
GCCCTGGGGAAAGTATTGGTAAAGAAAAAGAAGCTAATCAGTGGGTTAG
CCAATGAAAAGTAAACACTCTCGCTGCCAAAAAGATTTACACCATATCT
TAAAGCTTAACACTACTTTACTATTATGGTATTATGATAAAAATATC
TATTATATGGTAATAATTGGACGCGGTTAGAGACTAATCTGATTC
ACTAGGTATTGCTGCCAGAAAAAGCTCAACAAAGATGCTTTAAAAG
GGTGGTTACCGTTTGCAGAAGCAATCGGTATTACGTTGGAGATTAT
GCCCTGTTAATATAACAAAAGACTAAAAAGCAGCTTCACTTAAAG
AGAAAGTGTCTGGAGAATTACAGCTGCAAAAAGGGCACATCA
TAGAAAGTAACTACGACGTGTTTATTCCTCTGACCCTCATCTTAGAA
GCTCAATTAAAATCATTTACAAA

SEQ ID NO. 8610

STRAIN 1169NT

GAAGGCCTTCACCTATTATGGAAAAAAATT
CCTGAAAATCCGAAAAGTAATTAATTTCATATTCTTACACTGGGTA
TTTATTAAAGACTAGGTGTTAATGTTCAAGTTACAGTTAGACTTAGAAA
AAGATAGCCCGTTTGGTAAGCAACTGAAAGAAGCTAAAAAAATTAAC
GCTGATGATAAGAGCTATTGCCGcACAaaaACCTGATTTAATCATGGT
TTTCGATCAAGATCCAAACATCAATACTCTGAAAGAAAATGCAACCAACTT
TAGTTATAAATATGGTGCACAAAATTATTAGATATGATGCCAGCCTTG
GGGAAAGTATTGGTAAAGAAAAAGaaGCTAATCAGTGGGTTAGCCAATG
GAAAACACTAAAAGCTCGCTGCCAAAAAAAGATTTACACCATATCTTAAAGC
CTAACACTACTTTACTATTATGGATTTTATGATAAAAATATCTATTAA
TATGCTTAATAATTGGACGCGGTTGGAGAACTAATCTATGATTCAGG
TTATGCTGCCCTGAGAAAAGTCACAAAAGATGCTTTAAAAGGGTGGT
TTACCGTTTCgCAAGAAGCAATCGGTATTACGTTGGAGATTATGCCCTT
GTAAATAATAACAAAAGCAGCTAAAAGCAGCTTCATCACTTAAAGAAAAG
TGATGCTGGAGAATTACCGAGCTGCAAAAAGGGCACATCATAGAAA
GTAACTACGACGTGTTTATTCCTCTGACCCTCATCTTAGAAAGCTCAA
TTAAATCATTTACAAA

SEQ ID NO. 8611

STRAIN JM9130013

GAAGGCCTTCACCTATTATG
GAAAATCCGAAAAGTAATTAATTTCATATTCTTAC
ACTGGATATTATTAAGACTAGGAGTTAATGTTCAAGTTACAGTTAGA
CTTAGAAAAGATAGCCCGTTTGGTAAGCAACTGAAAGGAGCTAAA
AATTAACTGCTGATGACAGAAGCTATTGCCGCAACAAACCTGATTTA
ATCATGGTTTGATCAAGATCCAAACATCAATACTCTGAAAAGAAAATG
ACCAACTTCTGATCAAGATCCAAACATCAATACTCTGAAAAGAAAATG
CAGCTTGGGGAAAGTATTGGTAAAGAAAAAGCAGCTAATCAGTGGGTT
AGGCAATGGAAAAGCTAAACACTCTCGCTGCCAAAAAGATTTACACCATAT
CTTAAACCTAACACTACTTTACCATATTGGATTTTATGATAAAAATA
TCTATTATATGGTAATAATTGGACGCCGGTGGAGAAGCTAATCTATGAT
TCACTAGTTATGCTGCCCTGAGAAAAGTCACAAAAGATGCTTTAAAAG
AGGCTGGTTACCGTTTCgCAAGAAGCAATCGGTGATTACGTTGGAGATT
ATGCCCTGTTAATATAACAAAAGCAGCTAAAAGCAGCTTCATCACTT
AAAGAAAGTGTCTGGAGAATTACCGAGCTGCAAAAAGGGCACAT
CATAGAAAGTAACTACGACGTGTTTATTCCTCTGACCCTCATCTTAG
AAGCTCAATTAAAATCATTTACAAA

PRETTY of: /biotmp/msa521731.2{*} April 28, 2003 08:07 ..

	1	50
msa521731.2{691_090}	-----	
msa521731.2{691_1169NT}	-----	
msa521731.2{691_CJB110}	-----	
msa521731.2{691_COH1}	-----	
msa521731.2{691_M732}	-----	
msa521731.2{691_M781}	-----	
msa521731.2{691_18RS21}	-----	
msa521731.2{691_2603}	atgaaaaaaaa ttggattat tgtcctcaca ctactgacct tcttttgg	

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_A909}	-----	-----	-----	-----	-----
msa521731.2{691_JM9130013}	-----	-----	-----	-----	-----
msa521731.2{691_H36B}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51			100	
msa521731.2{691_090}	-----	-----	-----	-----	-----
msa521731.2{691_1169NT}	-----	-----	-----	-----	-----
msa521731.2{691_CJB110}	-----	-----	-----	-----	-----
msa521731.2{691_COH1}	-----	-----	-----	-----	-----
msa521731.2{691_M732}	-----	-----	-----	-----	-----
msa521731.2{691_M781}	-----	-----	-----	-----	-----
msa521731.2{691_18RS21}	-----	-----	-----	-----	-----
msa521731.2{691_2603}	atcttgcgga	caacaaacta	aacaagaaaag	cactaaaaca	actatttcta
msa521731.2{691_A909}	-----	-----	-----	-----	-----
msa521731.2{691_JM9130013}	-----	-----	-----	-----	-----
msa521731.2{691_H36B}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101			150	
msa521731.2{691_090}	-----	---GAAGGC	TTCACCTATT	ATGGAAAAAAT	TCCTGAAAAT
msa521731.2{691_1169NT}	-----	---GAAGGC	TTCACCTATT	ATGGAAAAAAT	TCCTGAAAAT
msa521731.2{691_CJB110}	-----	---GAAGGC	TTCACCTATT	ATGGAAAAAAT	TCCTGAAAAT
msa521731.2{691_COH1}	-----	---GAAGGC	TTCACCTATT	ATGGAAAAAAT	TCCTGAAAAT
msa521731.2{691_M732}	-----	---GAAGGC	TTCACCTATT	ATGGAAAAAAT	TCCTGAAAAT
msa521731.2{691_M781}	-----	---GAAGGC	TTCACCTATT	ATGGAAAAAAT	TCCTGAAAAT
msa521731.2{691_18RS21}	-----	---GAAGGC	TTCACCTATT	ATGGAAAAAAT	TCCTGAAAAT
msa521731.2{691_2603}	aatgcctaa	aattGAAGGC	TTCACCTATT	ATGGAAAAAAT	TCCTGAAAAT
msa521731.2{691_A909}	-----	---GAAGGC	TTCACCTATT	ATGGAAAAAAT	TCCTGAAAAT
msa521731.2{691_JM9130013}	-----	---GAAGGC	TTCACCTATT	ATGGAAAAAAT	TCCTGAAAAT
msa521731.2{691_H36B}	-----	---GAAGGC	TTCACCTATT	ATGGAAAAAAT	TCCTGAAAAT
Consensus	*****	*****	*****	*****	*****
	151			200	
msa521731.2{691_090}	CCGAAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGGT	ATTTATTAAAA
msa521731.2{691_1169NT}	CCGAAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGGT	ATTTATTAAAA
msa521731.2{691_CJB110}	CCGAAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGGT	ATTTATTAAAA
msa521731.2{691_COH1}	CCGAAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGGT	ATTTATTAAAA
msa521731.2{691_M732}	CCGAAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGGT	ATTTATTAAAA
msa521731.2{691_M781}	CCGAAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGGT	ATTTATTAAAA
msa521731.2{691_18RS21}	CCGAAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGGT	ATTTATTAAAA
msa521731.2{691_2603}	CCGAAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGGT	ATTTATTAAAA
msa521731.2{691_A909}	CCGAAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGGT	ATTTATTAAAA
msa521731.2{691_JM9130013}	CCGAAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGGT	ATTTATTAAAA
msa521731.2{691_H36B}	CCGAAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGGT	ATTTATTAAAA
Consensus	*****	*****	*****	*****	*****
	201			250	
msa521731.2{691_090}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_1169NT}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_CJB110}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_COH1}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_M732}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_M781}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_18RS21}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_2603}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_A909}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_JM9130013}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_H36B}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
Consensus	*****	*****	*****	*****	*****
	251			300	
msa521731.2{691_090}	CCGTTTTGG	TAAGCAACTG	AAAGaAGCTA	AAAAATTAAAC	TGCTGATGAT
msa521731.2{691_1169NT}	CCGTTTTGG	TAAGCAACTG	AAAGaAGCTA	AAAAATTAAAC	TGCTGATGAT
msa521731.2{691_CJB110}	CCGTTTTGG	TAAGCAACTG	AAAGaAGCTA	AAAAATTAAAC	TGCTGATGAT
msa521731.2{691_COH1}	CCGTTTTGG	TAAGCAACTG	AAAGaAGCTA	AAAAATTAAAC	TGCTGATGAT
msa521731.2{691_M732}	CCGTTTTGG	TAAGCAACTG	AAAGaAGCTA	AAAAATTAAAC	TGCTGATGAT
msa521731.2{691_M781}	CCGTTTTGG	TAAGCAACTG	AAAGaAGCTA	AAAAATTAAAC	TGCTGATGAT
msa521731.2{691_18RS21}	CCGTTTTGG	TAAGCAACTG	AAAGaAGCTA	AAAAATTAAAC	TGCTGATGAT
msa521731.2{691_2603}	CCGTTTTGG	TAAGCAACTG	AAAGaAGCTA	AAAAATTAAAC	TGCTGATGAT
msa521731.2{691_A909}	CCGTTTTGG	TAAGCAACTG	AAAGaAGCTA	AAAAATTAAAC	TGCTGATGAT
msa521731.2{691_JM9130013}	CCGTTTTGG	TAAGCAACTG	AAAGaAGCTA	AAAAATTAAAC	TGCTGATGAT
msa521731.2{691_H36B}	CCGTTTTGG	TAAGCAACTG	AAAGaAGCTA	AAAAATTAAAC	TGCTGATGAT
Consensus	*****	***-	***-	*****	*****
	301			350	
msa521731.2{691_090}	ACAGAAGCTA	TTGCCGCACA	AAAAACCTGAT	TTAACATGG	TTTTCGATCA
msa521731.2{691_1169NT}	ACAGAAGCTA	TTGCCGCACA	AAAAACCTGAT	TTAACATGG	TTTTCGATCA

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_CJB110}	ACAGAACGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTcGATCA
msa521731.2{691_COH1}	ACAGAACGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTcGATCA
msa521731.2{691_M732}	ACAGAACGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTcGATCA
msa521731.2{691_M781}	ACAGAACGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTcGATCA
msa521731.2{691_18RS21}	ACAGAACGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTcGATCA
msa521731.2{691_2603}	ACAGAACGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTcGATCA
msa521731.2{691_A909}	ACAGAACGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTtGATCA
msa521731.2{691_JM9130013}	ACAGAACGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTtGATCA
msa521731.2{691_H36B}	ACAGAACGCTA TTGCCGCACA AAAACCTGAT TTAATCATGG TTTTtGATCA
Consensus	***** * ***** * ***** * ***** * ***** * *****
	351
msa521731.2{691_090}	AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCCACCAACT TTAGTTATTAA
msa521731.2{691_1169NT}	AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCCACCAACT TTAGTTATTAA
msa521731.2{691_CJB110}	AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCCACCAACT TTAGTTATTAA
msa521731.2{691_COH1}	AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCCACCAACT TTAGTTATTAA
msa521731.2{691_M732}	AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCCACCAACT TTAGTTATTAA
msa521731.2{691_M781}	AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCCACCAACT TTAGTTATTAA
msa521731.2{691_18RS21}	AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCCACCAACT TTAGTTATTAA
msa521731.2{691_2603}	AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCCACCAACT TTAGTTATTAA
msa521731.2{691_A909}	AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCCACCAACT TTAGTTATTAA
msa521731.2{691_JM9130013}	AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCCACCAACT TTAGTTATTAA
msa521731.2{691_H36B}	AGATCCAAAC ATCAATACTC TGAAAAAAAT TGCCACCAACT TTAGTTATTAA
Consensus	***** * ***** * ***** * ***** * *****
	400
msa521731.2{691_090}	AATATGGTGC ACAAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
msa521731.2{691_1169NT}	AATATGGTGC ACAAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
msa521731.2{691_CJB110}	AATATGGTGC ACAAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
msa521731.2{691_COH1}	AATATGGTGC ACAAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
msa521731.2{691_M732}	AATATGGTGC ACAAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
msa521731.2{691_M781}	AATATGGTGC ACAAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
msa521731.2{691_18RS21}	AATATGGTGC ACAAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
msa521731.2{691_2603}	AATATGGTGC ACAAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
msa521731.2{691_A909}	AATATGGTGC ACAAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
msa521731.2{691_JM9130013}	AATATGGTGC ACAAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
msa521731.2{691_H36B}	AATATGGTGC ACAAAAATTAT TTAGATATGA TGCCAGCcTT GGGGAAAGTA
Consensus	***** * ***** * ***** * ***** * *****
	450
msa521731.2{691_090}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_1169NT}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_CJB110}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_COH1}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_M732}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_M781}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_18RS21}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_2603}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_A909}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_JM9130013}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_H36B}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
Consensus	***** * ***** * ***** * ***** * *****
	500
msa521731.2{691_090}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_1169NT}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_CJB110}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_COH1}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_M732}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_M781}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_18RS21}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_2603}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_A909}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_JM9130013}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
msa521731.2{691_H36B}	TTCGGTAAAG AAAAAGAACG TAATCAGTGG GTTAGCCAAT GGAAACTAA
Consensus	***** * ***** * ***** * ***** * *****
	550
msa521731.2{691_090}	AACTCTCGCT GcCAAAAAAG ATTACACCA TATCTTAAG CCTAACACTA
msa521731.2{691_1169NT}	AACTCTCGCT GcCAAAAAAG ATTACACCA TATCTTAAG CCTAACACTA
msa521731.2{691_CJB110}	AACTCTCGCT GcCAAAAAAG ATTACACCA TATCTTAAG CCTAACACTA
msa521731.2{691_COH1}	AACTCTCGCT GcCAAAAAAG ATTACACCA TATCTTAAG CCTAACACTA
msa521731.2{691_M732}	AACTCTCGCT GcCAAAAAAG ATTACACCA TATCTTAAG CCTAACACTA
msa521731.2{691_M781}	AACTCTCGCT GcCAAAAAAG ATTACACCA TATCTTAAG CCTAACACTA
msa521731.2{691_18RS21}	AACTCTCGCT GtCAAAAAAG ATTACACCA TATCTTAAG CCTAACACTA
msa521731.2{691_2603}	AACTCTCGCT GtCAAAAAAG ATTACACCA TATCTTAAG CCTAACACTA
msa521731.2{691_A909}	AACTCTCGCT GtCAAAAAAG ATTACACCA TATCTTAAG CCTAACACTA
msa521731.2{691_JM9130013}	AACTCTCGCT GtCAAAAAAG ATTACACCA TATCTTAAG CCTAACACTA
msa521731.2{691_H36B}	AACTCTCGCT GtCAAAAAAG ATTACACCA TATCTTAAG CCTAACACTA
Consensus	***** * ***** * ***** * ***** * *****
	600
msa521731.2{691_090}	CTTTTACCAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGTAAT
msa521731.2{691_1169NT}	CTTTTACCAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGTAAT
msa521731.2{691_CJB110}	CTTTTACCAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGTAAT
msa521731.2{691_COH1}	CTTTTACCAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGTAAT
msa521731.2{691_M732}	CTTTTACCAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGTAAT
msa521731.2{691_M781}	CTTTTACCAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGTAAT
msa521731.2{691_18RS21}	CTTTTACCAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGTAAT
msa521731.2{691_2603}	CTTTTACCAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGTAAT
msa521731.2{691_A909}	CTTTTACCAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGTAAT
msa521731.2{691_JM9130013}	CTTTTACCAT TATgGATTTT TATGATAAAA ATATCTATTT ATATGTAAT

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_H36B}	CTTTTACTAT	TATAgATTTT	TATGATAAAA	ATATCTATT	ATATGGTAAT
Consensus					
msa521731.2{691_090}	601	AATTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCACTAG
msa521731.2{691_1169NT}		AATTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCACTAG
msa521731.2{691_CJB110}		AATTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCACTAG
msa521731.2{691_COH1}		AATTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCACTAG
msa521731.2{691_M732}		AATTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCACTAG
msa521731.2{691_M781}		AATTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCACTAG
msa521731.2{691_18RS21}		AATTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCACTAG
msa521731.2{691_2603}		AATTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCACTAG
msa521731.2{691_A909}		AATTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCACTAG
msa521731.2{691_JM9130013}		AATTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCACTAG
msa521731.2{691_H36B}		AATTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCACTAG
Consensus					
msa521731.2{691_090}	700	CCCAGAAAAA	GTCAAAAAAAAG	ATGTCTTTAA	AAAAGGGTGG
msa521731.2{691_1169NT}		CCCAGAAAAA	GTCAAAAAAAAG	ATGTCTTTAA	AAAAGGGTGG
msa521731.2{691_CJB110}		CCCAGAAAAA	GTCAAAAAAAAG	ATGTCTTTAA	AAAAGGGTGG
msa521731.2{691_COH1}		CCCAGAAAAA	GTCAAAAAAAAG	ATGTCTTTAA	AAAAGGGTGG
msa521731.2{691_M732}		CCCAGAAAAA	GTCAAAAAAAAG	ATGTCTTTAA	AAAAGGGTGG
msa521731.2{691_M781}		CCCAGAAAAA	GTCAAAAAAAAG	ATGTCTTTAA	AAAAGGGTGG
msa521731.2{691_18RS21}		CCCAGAAAAA	GTCAAAAAAAAG	ATGTCTTTAA	AAAAGGGTGG
msa521731.2{691_2603}		CCCAGAAAAA	GTCAAAAAAAAG	ATGTCTTTAA	AAAAGGGTGG
msa521731.2{691_A909}		CCCAGAAAAA	GTCAAAAAAAAG	ATGTCTTTAA	AAAAGGGTGG
msa521731.2{691_JM9130013}		CCCAGAAAAA	GTCAAAAAAAAG	ATGTCTTTAA	AAAAGGGTGG
msa521731.2{691_H36B}		CCCAGAAAAA	GTCAAAAAAAAG	ATGTCTTTAA	AAAAGGGTGG
Consensus					
msa521731.2{691_090}	701	CGCAAGAACG	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT
msa521731.2{691_1169NT}		CGCAAGAACG	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT
msa521731.2{691_CJB110}		CGCAAGAACG	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT
msa521731.2{691_COH1}		CGCAAGAACG	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT
msa521731.2{691_M732}		CGCAAGAACG	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT
msa521731.2{691_M781}		CGCAAGAACG	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT
msa521731.2{691_18RS21}		CGCAAGAACG	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT
msa521731.2{691_2603}		CGCAAGAACG	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT
msa521731.2{691_A909}		CGCAAGAACG	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT
msa521731.2{691_JM9130013}		CGCAAGAACG	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT
msa521731.2{691_H36B}		CGCAAGAACG	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT
Consensus					
msa521731.2{691_090}	800	AACAAAACGA	CTAAAAAAAGC	AGCTTCATCA	CTTAAAGAAA
msa521731.2{691_1169NT}		AACAAAACGA	CTAAAAAAAGC	AGCTTCATCA	CTTAAAGAAA
msa521731.2{691_CJB110}		AACAAAACGA	CTAAAAAAAGC	AGCTTCATCA	CTTAAAGAAA
msa521731.2{691_COH1}		AACAAAACGA	CTAAAAAAAGC	AGCTTCATCA	CTTAAAGAAA
msa521731.2{691_M732}		AACAAAACGA	CTAAAAAAAGC	AGCTTCATCA	CTTAAAGAAA
msa521731.2{691_M781}		AACAAAACGA	CTAAAAAAAGC	AGCTTCATCA	CTTAAAGAAA
msa521731.2{691_18RS21}		AACAAAACGA	CTAAAAAAAGC	AGCTTCATCA	CTTAAAGAAA
msa521731.2{691_2603}		AACAAAACGA	CTAAAAAAAGC	AGCTTCATCA	CTTAAAGAAA
msa521731.2{691_A909}		AACAAAACGA	CTAAAAAAAGC	AGCTTCATCA	CTTAAAGAAA
msa521731.2{691_JM9130013}		AACAAAACGA	CTAAAAAAAGC	AGCTTCATCA	CTTAAAGAAA
msa521731.2{691_H36B}		AACAAAACGA	CTAAAAAAAGC	AGCTTCATCA	CTTAAAGAAA
Consensus					
msa521731.2{691_090}	801	GAAGAATTAA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA
msa521731.2{691_1169NT}		GAAGAATTAA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA
msa521731.2{691_CJB110}		GAAGAATTAA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA
msa521731.2{691_COH1}		GAAGAATTAA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA
msa521731.2{691_M732}		GAAGAATTAA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA
msa521731.2{691_M781}		GAAGAATTAA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA
msa521731.2{691_18RS21}		GAAGAATTAA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA
msa521731.2{691_2603}		GAAGAATTAA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA
msa521731.2{691_A909}		GAAGAATTAA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA
msa521731.2{691_JM9130013}		GAAGAATTAA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA
msa521731.2{691_H36B}		GAAGAATTAA	CCAGCTGTCA	AAAAAGGGCA	CATCATAGAA
Consensus					
msa521731.2{691_090}	900	ACGTGTTTTA	TTTCCTCTGAC	CCCTCTATCTT	TAGAAGCTCA
msa521731.2{691_1169NT}		ACGTGTTTTA	TTTCCTCTGAC	CCCTCTATCTT	TAGAAGCTCA
msa521731.2{691_CJB110}		ACGTGTTTTA	TTTCCTCTGAC	CCCTCTATCTT	TAGAAGCTCA
msa521731.2{691_COH1}		ACGTGTTTTA	TTTCCTCTGAC	CCCTCTATCTT	TAGAAGCTCA

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_M732}	ACGTGTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_M781}	ACGTGTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_18RS21}	ACGTGTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_2603}	ACGTGTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_A909}	ACGTGTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_JM9130013}	ACGTGTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_H36B}	ACGTGTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
Consensus	*****	*****	*****	*****	*****
	901		930		
msa521731.2{691_090}	TTTACAAA--	-----	-----		
msa521731.2{691_1169NT}	TTTACAAA--	-----	-----		
msa521731.2{691_CJB110}	TTTACAAA--	-----	-----		
msa521731.2{691_COH1}	TTTACAAA--	-----	-----		
msa521731.2{691_M732}	TTTACAAA--	-----	-----		
msa521731.2{691_M781}	TTTACAAA--	-----	-----		
msa521731.2{691_18RS21}	TTTACAAA--	-----	-----		
msa521731.2{691_2603}	TTTACAAAgg	ctatcaaaga	aaatacaaaat		
msa521731.2{691_A909}	TTTACAAA--	-----	-----		
msa521731.2{691_JM9130013}	TTTACAAA--	-----	-----		
msa521731.2{691_H36B}	TTTACAAA--	-----	-----		
Consensus	*****	*****	*****		

SEQ ID NO. 8612

STRAIN 2603 frame: 1

MKKIGIIVLTLTFFLVSCGQQTQESTKTTISKMPKIEGFTYYGKIPENPKKVINFYYSYTGULLKLGVNVSSYSLDLEKDSPVFGKQLKEAKKLTA
 YTGLLKGVLGVNVSSYLDLEKDSPVFGKQLKEAKKLTDADDTEAIAAAQKPDLIMVFDQDPN
 INTLKKAAPTLVIKYGAQNYLDMMMPALGKVFGKEKEANQWVSQWKTCKTAAKKDLHHLILKPNNTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 YVGDYALVNINKTTKKAASSLKESEDVWKNLPAVKKGHIIESNYDVYFSDPLSLEAQLKSFT
 FTKAIKENTN

SEQ ID NO. 8613

STRAIN 090 frame: 1

EGFTYYGKIPENPKKVINFYYSYTGULLKLGVNVSSYSLDLEKDSPVFGKQLKGAKKLTA
 DDTEAIAAQKPDLIMVFDQDPNINTLKKAAPTLVIKYGAQNYLDMMMPALGKVFGKEKEANQWVSQWKTCKTAAKKDLHHLILKPNNTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKKGWFTVSQEAGDYGVDYALVNINKTTKKAASSLKESEDVWKNLPAVKKGHIIESNYDVYFSDPLSLEAQLKSFT

SEQ ID NO. 8614

STRAIN A909 frame: 1

EGFTYYGKIPENPKKVINFYYSYTGULLKLGVNVSSYSLDLEKDSPVFGKQLKGAKKLTA
 DDTEAIAAQKPDLIMVFDQDPNINTLKKAAPTLVIKYGAQNYLDMMMPALGKVFGKEKEANQWVSQWKTCKTAAKKDLHHLILKPNNTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKKGWFTVSQEAGDYGVDYALVNINKTTKKAASSLKESEDVWKNLPAVKKGHIIESNYDVYFSDPLSLEAQLKSFT

SEQ ID NO. 8615

STRAIN H36B frame: 1

EGFTYYGKIPENPKKVINFYYSYTGULLKLGVNVSSYSLDLEKDSPVFGKQLKGAKKLTA
 DDTEAIAAQKPDLIMVFDQDPNINTLKKAAPTLVIKYGAQNYLDMMMPALGKVFGKEKEANQWVSQWKTCKTAAKKDLHHLILKPNNTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKKGWFTVSQEAGDYGVDYALVNINKTTKKAASSLKESEDVWKNLPAVKKGHIIESNYDVYFSDPLSLEAQLKSFT

SEQ ID NO. 8616

STRAIN 18RS21 frame: 1

EGFTYYGKIPENPKKVINFYYSYTGULLKLGVNVSSYSLDLEKDSPVFGKQLKGAKKLTA
 DDTEAIAAQKPDLIMVFDQDPNINTLKKAAPTLVIKYGAQNYLDMMMPALGKVFGKEKEANQWVSQWKTCKTAAKKDLHHLILKPNNTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKKGWFTVSQEAGDYGVDYALVNINKTTKKAASSLKESEDVWKNLPAVKKGHIIESNYDVYFSDPLSLEAQLKSFT

SEQ ID NO. 8617

STRAIN M732 frame: 1

EGFTYYGKIPENPKKVINFYYSYTGULLKLGVNVSSYSLDLEKDSPVFGKQLKGAKKLTA
 DDTEAIAAQKPDLIMVFDQDPNINTLKKAAPTLVIKYGAQNYLDMMMPALGKVFGKEKEANQWVSQWKTCKTAAKKDLHHLILKPNNTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
 EKVKKDVFKKKGWFTVSQEAGDYGVDYALVNINKTTKKAASSLKESEDVWKNLPAVKKGHIIESNYDVYFSDPLSLEAQLKSFT

SEQ ID NO. 8618

STRAIN COH1 frame: 1

EGFTYYGKIPENPKKVINFYYSYTGULLKLGVNVSSYSLDLEKDSPVFGKQLKGAKKLTA
 DDTEAIAAQKPDLIMVFDQDPNINTLKKAAPTLVIKYGAQNYLDMMMPALGKVFGKEKEAN

Table 86: Comparative Sequences relating to SAG1393

QWVSQLWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFVTSQEAIGDYVGDXALVNINKTTKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8619

STRAIN M781 frame: 1

EGFTYYGKIPENPKVINFTYSYTGYLLKLGVNVSYSLDLEKDSPVFGKQLKEAKKLTA
DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMMPALGVFGKEKEAN
QWVSQLWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFVTSQEAIGDYVGDXALVNINKTTKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8620

STRAIN CJB110 frame: 1

EGFTYYGKIPENPKVINFTYSYTGYLLKLGVNVSYSLDLEKDSPVFGKQLKEAKKLTA
DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMMPALGVFGKEKEAN
QWVSQLWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFVTSQEAIGDYVGDXALVNINKTTKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8621

STRAIN 1169NT frame: 1

EGFTYYGKIPENPKVINFTYSYTGYLLKLGVNVSYSLDLEKDSPVFGKQLKEAKKLTA
DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMMPALGVFGKEKEAN
QWVSQLWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFVTSQEAIGDYVGDXALVNINKTTKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

SEQ ID NO. 8622

STRAIN JM9130013 frame: 1

EGFTYYGKIPENPKVINFTYSYTGYLLKLGVNVSYSLDLEKDSPVFGKQLKEAKKLTA
DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTLVIKYGAQNYLDMMMPALGVFGKEKEAN
QWVSQLWKTTLAAKKDLHHILKPNTTFTIMDFYDKNIYLYGNNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFVTSQEAIGDYVGDXALVNINKTTKAASSLKESDVWKNLPAVKKGHI
IESNYDVFYFSDPLSLEAQLKSFT

PRETTY of: /biotmp/msa522124.2{*} April 28, 2003 08:17 ..

	1	50
msa522124.2{691_090}	-----	EG FTYYGKIPEN
msa522124.2{691_1169NT}	-----	EG FTYYGKIPEN
msa522124.2{691_CJB110}	-----	EG FTYYGKIPEN
msa522124.2{691_COH1}	-----	EG FTYYGKIPEN
msa522124.2{691_M732}	-----	EG FTYYGKIPEN
msa522124.2{691_M781}	-----	EG FTYYGKIPEN
msa522124.2{691_18RS21}	-----	EG FTYYGKIPEN
msa522124.2{691_2603}	mkkigiiivlt lltffflvscg qqtkqestkt tiskmpk iEG	FTYYGKIPEN
msa522124.2{691_A909}	-----	EG FTYYGKIPEN
msa522124.2{691_JM9130013}	-----	EG FTYYGKIPEN
msa522124.2{691_H36B}	-----	EG FTYYGKIPEN
Consensus	*****	*****
	51	100
msa522124.2{691_090}	PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KeAKKL TADD	
msa522124.2{691_1169NT}	PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KeAKKL TADD	
msa522124.2{691_CJB110}	PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KeAKKL TADD	
msa522124.2{691_COH1}	PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KeAKKL TADD	
msa522124.2{691_M732}	PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KeAKKL TADD	
msa522124.2{691_M781}	PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KeAKKL TADD	
msa522124.2{691_18RS21}	PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KeAKKL TADD	
msa522124.2{691_2603}	PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KeAKKL TADD	
msa522124.2{691_A909}	PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KgAKKL TADD	
msa522124.2{691_JM9130013}	PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KgAKKL TADD	
msa522124.2{691_H36B}	PKKVINFTYS YTGYLLKLGV NVSSYSLDLE KDSPVFGKQL KgAKKL TADD	
Consensus	*****	*****
	101	150
msa522124.2{691_090}	TEAIAAAQKPD LIMVFDQDPN INTLKKIAPT LVVKYGAQNY LDMMMPALGV	
msa522124.2{691_1169NT}	TEAIAAAQKPD LIMVFDQDPN INTLKKIAPT LVVKYGAQNY LDMMMPALGV	
msa522124.2{691_CJB110}	TEAIAAAQKPD LIMVFDQDPN INTLKKIAPT LVVKYGAQNY LDMMMPALGV	
msa522124.2{691_COH1}	TEAIAAAQKPD LIMVFDQDPN INTLKKIAPT LVVKYGAQNY LDMMMPALGV	
msa522124.2{691_M732}	TEAIAAAQKPD LIMVFDQDPN INTLKKIAPT LVVKYGAQNY LDMMMPALGV	
msa522124.2{691_M781}	TEAIAAAQKPD LIMVFDQDPN INTLKKIAPT LVVKYGAQNY LDMMMPALGV	
msa522124.2{691_18RS21}	TEAIAAAQKPD LIMVFDQDPN INTLKKIAPT LVVKYGAQNY LDMMMPALGV	
msa522124.2{691_2603}	TEAIAAAQKPD LIMVFDQDPN INTLKKIAPT LVVKYGAQNY LDMMMPALGV	
msa522124.2{691_A909}	TEAIAAAQKPD LIMVFDQDPN INTLKKIAPT LVVKYGAQNY LDMMMPALGV	
msa522124.2{691_JM9130013}	TEAIAAAQKPD LIMVFDQDPN INTLKKIAPT LVVKYGAQNY LDMMMPALGV	

Table 86: Comparative Sequences relating to SAG1393

msa522124.2{691_H36B}	TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMMMPALGKV
Consensus	***** * ***** * ***** * ***** * *****
	151
msa522124.2{691_090}	FGKEKEANQW VSQWKTCKTLA
msa522124.2{691_1169NT}	akKDLHHILk PNTTFTImDF YDKNIYLYGN
msa522124.2{691_CJB110}	FGKEKEANQW VSQWKTCKTLA
msa522124.2{691_COH1}	akKDLHHILk PNTTFTImDF YDKNIYLYGN
msa522124.2{691_M732}	FGKEKEANQW VSQWKTCKTLA
msa522124.2{691_M781}	akKDLHHILk PNTTFTImDF YDKNIYLYGN
msa522124.2{691_18RS21}	FGKEKEANQW VSQWKTCKTLA
msa522124.2{691_2603}	VKKDLHHILk PNTTFTImDF YDKNIYLYGN
msa522124.2{691_A909}	FGKEKEANQW VSQWKTCKTLA
msa522124.2{691_JM9130013}	akKDLHHILk PNTTFTImDF YDKNIYLYGN
msa522124.2{691_H36B}	FGKEKEANQW VSQWKTCKTLA
Consensus	akKDLHHILk PNTTFTImDF YDKNIYLYGN
	***** * ***** - ***** - *****
	200
msa522124.2{691_090}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_1169NT}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_CJB110}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_COH1}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_M732}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_M781}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_18RS21}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_2603}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_A909}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_JM9130013}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_H36B}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
Consensus	***** * ***** * ***** * *****
	201
msa522124.2{691_090}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_1169NT}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_CJB110}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_COH1}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_M732}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_M781}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_18RS21}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_2603}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_A909}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_JM9130013}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
msa522124.2{691_H36B}	NFGRGGELIY DSLGYAAPEK VKKDVFKKGW FTVSQEAIKD YVGDYALVNI
Consensus	***** * ***** * ***** * *****
	251
msa522124.2{691_090}	NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
msa522124.2{691_1169NT}	NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
msa522124.2{691_CJB110}	NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
msa522124.2{691_COH1}	NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
msa522124.2{691_M732}	NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
msa522124.2{691_M781}	NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
msa522124.2{691_18RS21}	NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
msa522124.2{691_2603}	NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
msa522124.2{691_A909}	NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
msa522124.2{691_JM9130013}	NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
msa522124.2{691_H36B}	NKTTKKAASS LKESDVWKNL PAVKKGHIIE SNYDVFYFSD PLSLEAQLKS
Consensus	***** * ***** * ***** * *****
	300
msa522124.2{691_090}	FT-----
msa522124.2{691_1169NT}	FT-----
msa522124.2{691_CJB110}	FT-----
msa522124.2{691_COH1}	FT-----
msa522124.2{691_M732}	FT-----
msa522124.2{691_M781}	FT-----
msa522124.2{691_18RS21}	FT-----
msa522124.2{691_2603}	FTkaikentn
msa522124.2{691_A909}	FT-----
msa522124.2{691_JM9130013}	FT-----
msa522124.2{691_H36B}	FT-----
Consensus	*****
	301 310

Table 87: Comparative Sequences relating to SAG0645**SEQ ID NO. 8701****STRAIN 2603**

ATGAAATTATCGAAGAAGTTTGTGCTGCTGTT
 TAAACATGGTGGCGGGGTCACTGTGAAACCACTAGCTCAGTTGCGACTGGAATGAGT
 ATTGTAAGAGCTCAGAAGTCACAAGAACGCCAGCGAAAACAACAGTAAATATCTAT
 AAATTACAAGCCTAGTTAATTCGAAATTACTCTAAATCGGGTATCGAGAAATAAA
 GACCGGAAAGTAATATCTAAACTATGCTAACTCTGGTGCACATGTAAGGTTGCAAGGT
 GTACAGTTAACGTTAAAGTCAGACGGATATTCTGTTGATGAATTGAAAAAATTG
 ACAACAGTTAGCAGCAGTCAGGAAAGTTGGAACGATTCTTGAGAAGAACGTTGCACTCTA
 CCTCAAAACTATGCTCAAGGTTGGTCTGCGATGCTCTGGATTCAAAGAATCTG
 AGATACCTGTGATCTAGAAGATTAAAGAATTCACTTCAAACTTACAAAGCTTATGCT
 GTACCCGGTTGTTGGAAATTACCGAGTGTCAACTCTACAGGTACAGGTTCTCTGAA
 ATTAATATTGTTAACGAGTTGACTGATGAACCAAAACAGATAAAGATGTTAAA
 AAATTAGGTCAAGCACGATGCAAGGTTAACGATTGAGAATTCAAATGGTTCTGAAA
 TCTACAATCCCTGCCATTAGGTGACTATGAAAAATTGAAATTACTGATAAATTGCA
 GATGGCTTGTATAATGTTGGGAAACAGATTGGTGGCAGAACACTGAATAGA
 GATGAGCACTACACTATTGATGAAACCAACAGTTGATAACCCAAATACATTAAAATTACG
 TTAAACAGAGAAATTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCTTGTAAA
 AATCAAGGCTCTTGTATAAGCTAACATGCAAAACAGATGATGCGGATTGGAAATT
 CCAGTGTCAACTATTAAAGGAGTGTAGGAAAGCAATTGAAAATACTTT
 GAACCTCAATATGACCATCTCTGATAAAAGCTGACAACTCCAAACCATCTAATCTCCA
 AGAAAACCAGAGATTCTACAGTGGTGGGAAACGATTGTAAGAAAGACTCAACAGAAA
 CAAACACTAGGTGGTGTGAGTTGATTGTTGGCTTCTGATGGGACAGCAGTAAAATGG
 ACAGATGCTTATTAAAGCAATACTAAATAAAACATATTGCTGGAGAAGCTGTTACT
 GGGCAACCAATCAAATTGAAATCACATACAGACGGTACGGTTGAGATTAAAGGTTGGCT
 TATGAGTTGAGATGCAAGGAGTACAGCACTAACCTAACAAATTAAAGAAACAAA
 GCACCCAGAAGGTTATGTAATCCCTGATAAAAGAAATTGAGTTACAGTATCACAAACATCT
 TATAATACAAAACCACATGACATCACGGTTGATAGTGTGATGCAACACCTGATACAATT
 AAAAACAAACAAACGTCCTCAATCCCTAACACTGTTGAGTATGGTACGGCTATTTGTC
 GCTATGGTGTGCGGTGATGGCTTTGCTTAAGGGGATGAAGCGTCGACAAAGAT
 AAC

SEQ ID NO. 8702**STRAIN 090**

GCAGAAGTGTACAAGAACGCCAGCGAAAAC
 AGCACTAAATCTATAATTACAAGCTGATAGTTATAAATCGGAAATT
 CTCTAAATGGGTATCGAGATAAAAGCGCGAAGTAATATCTAACTAT
 GTAAACTTGGTCAAACTGTAAGGTTGCAAGGTGTACAGTTAAACG
 TTATAAAGTCAGACGGATATTCTGTTGATGAATTGAAAATTGACAA
 CAGITGAAGCAGCAGATGCAAAAGTTGGAACGATTCTGAGAAGAAGGTGTC
 AGTCTACCTAAAAACTATGCTCAAGGTTGGTGTGATGCTCTGGA
 TTCAAAAGTAATGTGAGATACTTGTATGAGAAGATTAAAGAATT
 CTICAAACATTACCAAAACCTTATGCTGTACGGTTGTTGCAATTACCA
 GTTGTCAACTCTACAGGTACAGGTTCTTCTGTTGAGATTAAAGGTT
 TAAAACGTTGTAACTGATGAACCAAAACAGATAAAGATGTTAAAAT
 TAGGTCAAGGAGTGTACAGGTTATACGATTGGTGAAGAATTCAAATGGTC
 TTGAAATTCACATCCCTGCCAATTAGGTGACTATGAAATTGAAAT
 TACTGATAAAATTGCAAGTGGCTGACTTATAAAATCTGTTGAAAATCA
 AGATTGGTCAAAACACTGAATAGAGATGAGCACTACACTATTGATGA
 CCAACAGTTGATAACCAAAATACATTAAACAGTTAAACCAAGAGAA
 ATTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCTTGTAAAAATC
 AAGATGCTCTGATAAAAGCTACTGCAAAATACAGATGATGCGGATTGG
 GAAATTGCAACTTAAAGCTACTAACATTAATGAAAAGCAGTTTAGGAAAAC
 AATTGAAAATACITGCAACTTCAATATGACCAACTCTCTGATAAGCTG
 ACAATCCAAAACCATCTAATCTCCAAGAAAACAGAAGTCATACTGGT
 GGAAACAGATTGTAAGAAAGACTCAACAGAAAACAACAAACACTAGGTGG
 TGCTGAGTTGTTGGCTCTGATGGGACAGCAGTAAAATGGACAG
 ATGCTCTTATTAAAGCAATACTAAATAAAACTATATTGCTGAGAAGCT
 GITACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGGTGA
 GATTAAGGTTGGCTTATGAGTTGATGCAATGCAAGGTTAAGTAACT
 TAACCTACAAATTAAAGAAACAAAAGCAGAGGTTAAGTAACT
 GATAAGGAATCGAGTTACAGTATCACAAACATCTTATAAATACAAAACC
 AACGACATCACGGTTGATAGTGTGATGCAACACCTGATACAATTAAA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8703**STRAIN A909**

GCAGAAGTGTACAAGAACGCCAGCGAAA
 AACACAGTAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAA
 TTACTTCAATGGGTATCGAGATAAAAGACGGCGAAGTAATATCTAAC
 TATGCTAAACTTGGTCAATGTTAAAGGTTGCAAGGTGTACAGTTAA
 ACGTTATAAAGTCAGACGGATATTCTGTTGATGAATTGAAAATTG
 CAACAGTTGAAACAGCAGATGCAAAAGTTGGAACGATTCTGAGAAGCT
 GTCACTCTACCTCAAAACTAATGCTCAAGGTTGGTGTGATGCTCT
 GGATTCAAAAGTAATGAGACTTGTGAGATTGAGAATTAAAGAATT
 CACCTTCAAAACATTACCAAAAGCTTATGCTGACGGTTCTGAGAATT
 CCAGTTGCTAACTCTACAGGTACAGGTTCTTCTGAAATTAAATTTA
 CCCTAaaACGTTGTAACTGATGAACCAAAACAGATAAAGATGTTAAA
 AATTAGGTCAAGGAGCATGCAAGGTTACAGATTGGTGAAGAATTCAATGG
 TTCTGAAATCTACAATCCCTGCCAATTAGGTGACTATGAAAATTG
 AATTACTGATAAAATTGCAAGTGGCTGACTTATAAAATCTGTTGAAA
 TCAAGATTGGTGTGAAAACACTGAATAGAGATGAGCACTACACTATTGAT
 GAACCAACAGTTGATAACCAAAATACATTAAAATTACGTTAAACCAGA

Table 87: Comparative Sequences relating to SAG0645

GAAATTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCTGGTTAAAA
 ATCAAGATGCTCTTGATAAAACGCTACTGCAAATACAGATGCGGCATT
 TTGGAATTCCAGTTGCATCAACTATTAAAGAAAAGCAGTTTAGGAAA
 AGCAATTGAAAATACCTTGAACCTCAATATGACCATACT CCTGATAAAG
 CTGACAATCCAAAACCCTCAATCTCCAAAGAAAACAGAAGTTCTACT
 GGTGGAAACGATTGTAAGAAAAGACTCAACAGAAAACACAACACTAGG
 TGTTGCTGAGTTGATTTGGCTTCTGATGGGACAGCAGTAAATGGA
 CAGATGCTCTTATTAAAGCGAATACTAAATAAAACTATATTGCTGGAGAA
 GCTGTTACTGGCAACCAATCAAATTGTAAGAAAACAGAAAACACTAGG
 TGAGATTAAAGGTTGGCTTATGCAGTTGATGCGAATGCGAGAGGGTACAG
 CAGTAACCTACAAATTAAAAGAAAACAAAAGCACCAGAAGGTTATGTAATC
 CCTGATAAAGAAATCGAGTTACAGTATCACAAACATCTTATAATACAAA
 ACCAACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAA
 AAAACAACAA

SEQ ID NO. 8704

STRAIN 18RS21

GCAGAAGTGTACAAGAACGCCAGCGAAAAC
 AGCAGTAAATATCTATAAATACAGCTGATAGTTATAAATCGGAAATT
 CTCTTAATGGTGTGAGATAAGACGGCGAAGTAAATCTAACTAT
 GCTAAACTTGGTACAATGTAAAGGTTGCAAGGTGTCAGTTAAACG
 TTATAAAGTCAGAGCGGATATTCTGTTGATGAAATTGAAAAATTGACAA
 CAGTTGAGCAGCAGATGCAAAAGTTGGAACGATTCTGAGAAGGGTGT
 AGTCTACCTCAGGAAACTAATGCTCAAGGTTGGTCGATGCTCTGGA
 TTCAAAAGTAAATGAGATACTTGTATGAGAAGATTAAAGAATTCA
 CTGAAACATTACACCAAAAGCTTATGCTGACCGTTGTTGAAATTACCA
 GTGCTAACTCTACAGGTAACGGTTTCTGAAATTGAAATTATTTACCC
 TAAAAACGGTTAATGATGAAACAAAACAGATAAAAGATGTTAAATAAT
 TAGGTACAGGAGATGCAGGTTATACGATTGTAAGAATTCAAATGGTTC
 TTGAAATCTAACCTGGCCAATTAGGTGACTATGAAAAAATTGAAATT
 TACTGATAAATTGCGAGTGCCTGACTTTAAATCTGTTGAAATTCA
 AGATTGGTTGAAACACTGAAATAGAGATGAGCACTACACTATTGATGAA
 CCAACAGTTGATAACCAAAATCATTTAAACGTTAAACCAAGAA
 ATTAAAGAAAATTGCTGAGCTACTTAAAGGAATGACCTTGTAAATTAC
 AAGATGCTCTGATAAAAGCTACTGCAAATACAGATGATGCGGCATT
 GAAATTCCAGTCACTTAAAGCAACTTAAATGAAAAGCAGTTTGTGAAAGG
 AATTGAAAATACCTTGAACCTCAATATGACCATACTCTGACAAGCTG
 ACAATCCAAAACCATCTAACCTTCAAGAAAACAGAAGTTCTACTGGT
 GGAAACGATTGTAAGAAAAGACTCAACGAAAACAAACACTAGGTGG
 TGCTGAGTTGATTTGGCTCTGATGGGACAGCAGTAAATGGACAG
 ATGCTCTTATTAAAGCAGAACTACTAAATAAAACTATATTGCTGGAGAAGCT
 GTTACTGGCAACCAATCAAATTGAAATCACATACAGCGGTACCTTGA
 GATTAAAGGTTGGCTTATGCAAGTTGCAATGCGAGAGGGTACAGCAG
 TAACCTACAAATTAAAAGAAAACAGCAGAAGGTTATGTAATCTT
 GATAAAAGAAATCGAGTTACAGTATCACAAACATCTTATAATACAAA
 AACTGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAAA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8705

STRAIN M732

GCAGAAGTGTACAAGAACGCCAGCGAAAACACAGT
 AAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACTCTA
 ATGGTGTGAGATAAAAGCAGGGCAAGTAAATATCTAACTATGCTAA
 CTGGTACAATGTTAAAGGTTGCAAGGTGTCAGTTAAACGTTATAA
 AGTCAAGACGGATATTCTGTTGATGAAATTGAAAAATTGACAAACAGT
 AAGCAGCAGATGCAAAGTCTGCAACGATTCTGAGAAGGGTGT
 CCTCAAAACAACTATGCTCAAGGTTGGTCGATGCTCTGGATTCAA
 AAGTAATGAGACTTGTATGAGAAGATTAAAGAATTCACTTCAA
 ACATTACAAAAGCTTATGCTGACCGTTGTTGTTGAAATTACAGTTGCT
 AACCTACAGGTTACAGGTTTCTGAAATTAAATATTACCTTAA
 CGTTGATAACTGATGAAACAAAACAGATAAAAGATGTTAAATTAGGT
 AGGACGATGCGAGTTACGATTGGTGAAGAATTCAAATGGTTGAA
 TCTACAATCCCTGCAAATTAGGTGACTATGAAAAAATTGAAATTACTG
 TAAATTGCGAGATGCTTGCACCTATAAAATCTGTTGAAAATTCAAGATTG
 GTTGCAAAACACTGAAATAGAGATGAGCACTACACTATTGATGAA
 GTTGTAAACCAAATACATTTAAACCGAGAAGGTTAA
 AGAAAATTGCTGAGCTACTTAAAGGAATGACCTTGTAAAAATTCAAGATG
 CTCTGATAAAAGCTACTGCAAATACAGATGATGCGCATTGTTGAAATT
 CCAGTTGCTCATCAACTTAAATGAAAAGCAGTTTGTGAAAGCAATTG
 AAATACTTGGACTTCAATATGACCATACTCTGATAAAGCTGACAATC
 CAAAACCATCTAACCTCCAGAAAACAGAAGGTTCACTACTGGGGAAA
 CGATTGTTAAAGAAAAGACTCAACAGAAAACAAACACTAGGTGGTCTG
 GTTGTGATTGCTGCTGATGGGACAGCAGTAAAATGGACAGATGCTC
 TTATTAAGCGAATACTAATAAAACTATATTGCTGGAGAAGCTGTTACT
 GGGCAACCAATCAAATTGAAATCACATACAGCGGTACGTTGAGATTAA
 AGGTTTGGCTTATGCAAGTTGAGTGCAGAGGGTACAGCAGTAACTT
 ACAAAATTAAAAGAAAACAGCAGAAGGTTATGTAATCCCTGATAAA
 GAATCGAGTTACAGTATCACAAACATCTTATAATACAAA
 CATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAAA
 AACGTCCCTCA

SEQ ID NO. 8706

STRAIN COH1

Table 87: Comparative Sequences relating to SAG0645

'GCAGAAGTGTACAAGAACGCCAGCGAAAC
 AGCAGTAAATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTAA
 CTTnTAATGGTGTATCGAGAATAAAGACGGCGAAGTAATATCTAATCT
 GCTAAACTTGGTGACAATGTAAGGTTGCAAGGTGTCAGTTAACG
 TTATAAAGTCAGAGCGGATATTCTGTGATGAATTGAAAATTGACAA
 CAGTTGAAGCGAGATGCAAAGTGGAACGATTCTGAGAAGAGGTGTC
 AGTCTACCTCAAAAATGCTAAGGTTGCTGATGCTCTCGA
 TCAAAAAGTAATGTGAGATACTTGATGAGAATTAAAGAACATTAC
 CTTCAAAACATTACCAAAAGCTTATGCTGACCGTTGCAAGGTTACCC
 GTTGCTAATCTCACAGGTACAGGTTCTCTGAAATTAAATTACCC
 TAAAAACGGTGTAACTGATGAACCAAAACAGATAAAGATGTTAAAAAAT
 TAGGTCAAGGAGATGCAAGCTATACGATTGGTGAAGAATTCAAATGGTTC
 TTGAATCTAACATCCCTGCAATTAGGTGACTATGAAAAAATTGAAAT
 TACTGATAAATTGCAAGATGGCTGACTTATAAATCTGTTGAAAATCA
 AGATTGGTCAAAACACTGAATAGAGATGAGCACTACACTATTGATGAA
 CCAACAGTGTATAACCAAAATACATTAAAATTACGTTAAACCAAGAGAA
 ATTAAAGAAAATTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAATC
 AAAGATGCTCTGATAAAAGCTACTGCAAATACAGATGATGCGGCAATTG
 GAAATTCCAGTGCATCAACTTAAATGAAAAGCAGTTTAGGAAAAGC
 AATTGAAAATACCTTTGAACTTCAATGACCATACTCTGATAAAGCTG
 ACAATCCAAAACCATCTAACCTTCCAAGAAAACCAGAAGTTCATACTGGT
 GGGAAACAGATTGTAAGAAAGACTCAACAGAAAACACAAACACTAGGG
 TGCTGAGTTGATTGTTGGCTCTGATGGACAGCAGTAAAATGGACAG
 ATGCTCTTAAAGCGAATACTAATAAAACATATATTGCTGGAGAACCT
 GTTACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTGA
 GATTAAAGGTTGGCTTATGCAAGTTGATGCAAGGTTATGTAATCCCT
 GATAAAAGGAATCGAGTTACAGTATCACAAACATCTTATAAATACAAAACC
 AACTGACATCACGGTTGATAGTGTGCTGACACACCTGATACAATTAAA
 ACACAAACGTCCTCA

SEQ ID NO. 8707

STRAIN M781

GCAGAAGTGTACAAGAACGCCAGCGAAACAG
 CAGTAAATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACT
 TCTAATGGTGTATCGAGAATAAAGACGGCGAAGTAATATCTAATCTGC
 TAAACTTGGTGACAATGTAAGGTTGCAAGGTGTCAGTTAACGTT
 ATAAGTCAGACGGATATTCTGTGATGAATTGAAAATTGACAACA
 GTTGAAGCAGCAGATGCAAAGTGGAACGATTCTGAGAAGAGGTGTCAG
 TCTACCTCAAAAACATGCTCAAGGTTGCTGTCATGCTCTGGATT
 CAAAAGTAATGTGAGATACTTGATGAGAATTAAAGAACATTACCT
 TCAACACATTACCAAAAGCTTATGCTGACCGTTGTTGCAATTACAGT
 TGCTAATCTCACAGGTACAGGTTCTGtaATTAAATTACCTTA
 AAAACGGTGTAACTGATGCAACCAAAACAGATAAAGATGTTAAAATTA
 GGTCAAGGACGATGCAAGTTACGATTGGTGAAGAATTCAAATGGTTCTT
 GAAATCTAACATCCCTGCAATTAGGTGACTATGAAAAAATTGAAATTAA
 CTGATAAAATTGCAAGATGGCTTGCATTTATAAATCTGTTGAAAATCAAG
 ATGTTGCAAAACACTGAATAGAGATGAGCACTACACTATTGATGAAAC
 AACAGTGTATAACCAAAATACATTAAAATTACGTTAAACCAAGAGAAAT
 TTAAGAAAATTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAATCAA
 GATGCTCTGATAAAAGCTACTGCAAATACAGATGATGCGGCAATTGGA
 AAATTGCAAGTGTGATCAACTTAAATGAAAAGCAGTTTAGGAAAAGCAA
 TTGAAAATACTTTGAACTTCAATATGACCATACTCCTGATAAAAGCTGAC
 ATTCAAAACCATCTAACCTTCCAAGAAAACAGAAGTTCATACTGG
 GAAACGATTGTAAGAAAGACTCAACAGAACACAAAACACTAGGTGG
 CTGAGTTGATTGTTGGCTCTGATGGGACAGCAGTAAATGGACAGAT
 GCTCTTATTAAAGCAATACTAATAAAACATATTGCTGGAGAACCTGTT
 TACTGGGCAACCAATCAAATTGAAATCACATACAGACGGTACGTTGAGA
 TTAAAGGTTGGCTTATGCAAGTTGCAAGTGGCAAGACGGTACAGCAGTA
 ACTTACAAATTAAAAGAAACAAAAGCACCAGAACAGGTTATGTAATCCCTGA
 TAAAGAAATCGAGTTACAGTATCACAAACATCTTATAAATACAAAACCAA
 CTGACATCACGGTTGATAGTGTGCTGACACACCTGATACAATTAAA
 ACACAAACGTT

SEQ ID NO. 8708

STRAIN CJB110

GCAGAAGTGTACAAGAACGCCAGCGAA
 AACAGCAGTAAATCTATAAATTACAAGCTGATAGTTATAAATTGAAA
 TTACTCTAATGGTGTATCGAGAATAAAGACGGCGAAGTAATATCTAAC
 TATGCTAACCTGGTGACAATGTAAGGTTGCAAGGTGTCAGTTAAC
 ACCTTATAAAGTCAGACGGATAATTCTGTGATGAATTGAAAATTGAA
 CAACAGTTGAGCAGCAGATGCAAAGTGGAACGAAITCTGTAAGAACGGT
 GTCAAGCTACCTCAAAAACATGCTCAAGGTTGGTCTGATGCTCT
 GGATTCAAAAGTAATGTGAGATACTTGTGATGAGAATTAAAGAATT
 CACCTTCAAACATTACCAAAAGCTTATGCTGACCGTTGTTGTTGAAATT
 CCAGTTGCTAATCTACAGGTACAGGTTCCCTTCTGAAATTAAATTGAA
 CCTCTAAAACGTTGTAATCTGATGAACCAAAACAGATAAAGATGTTAAA
 ATTAGGTAGGACGATGCAAGGTTATACGATTGGTGAAGAATTCAAATGG
 TTCTGAAATCTACAATCCCTGCAATTAGTGACTATGAAAAAATTGAA
 ATTACTGATAAAATTGCAAGATGGCTTGCAGTTATAAATCTGTTGGAAA
 TCAAGATTGCTGAAACACTGAATAGAGATGAGCACTACACTATTGAT
 GAACCAACAGTTGATAACCAAAATACATTAATTACGTTAAACCAAGA
 GAAATTAAAGAAATTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAA

Table 87: Comparative Sequences relating to SAG0645

ATCAAGATGCTTGTATAAAGCTACTGCAAATACAGATGATGCCGCATT
 TTGGAAATTCCAGTTGCATCACTTAAATGAAAAAGCAGTTTAGGAAA
 AGCAATIGAAAATCTTTGAACCTCAATGACCATACTCCGTATAAAG
 CTGACAATcCAAACCATCTAATCCTCCAAGAAAACCAGAAGITCATACT
 GTGGGGAAACGAAATTGTAAAGAAAAGACTCAACAGAAAACACAAACACTAGG
 TGGTGTGAGTTGATTGGCTTGTGATGGGACAGCAGTAAATGG
 CAGATGCTCTTAAAGCGAATACTAAATAAAACTATATTGCTGGAGAA
 GCTGTTACTGGCAACCAATCAAATTGAAATCACAATCACAGACGGTACGTT
 TGAGATTAAAGGTTGGCTTATGCACTGAGTTGCAATGAGGGTACAG
 CAGTAACCTACAAATTAAAAGAACAAAGCACCAGAAGGTTATGTAATC
 CCTGATAAAGAAATCGAGTTACAGTATCACAAACATCTATAATCCAAA
 ACCAATGACATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAA
 AAAACACAAACGTCCTTC

SEQ ID NO. 8709

STRAIN JM9130013

GCAGAAGTGTCAAAGAACGCCAGCGAAAACAGCAGTA
 AATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTACTCTAA
 TTGGTGTGAGTTGCAAGATAAAAGCAGGGCAAGTAAATCTAACTATGCTAAAC
 TTGGTGTGACAATGTTAAAGGTTGCAAGGTGTACAGTTAAACGTTATAAA
 GTCAAGACGGATAATTCTGTGATGAAATTGAAAAATTGACACAGTTG
 AGCAGCAGATGCAAAGGTTGAAACGATTCTGAAGAAGGGTGTCACT
 CTCAAAAGAACTAATGTTGGCTGCGATGCTCTGGATTCAA
 AGTAATGTGAGATACTTGTAGTAGAAGATTAAAGAATTCACTTCAA
 CATTACCAAAGTTATGCTGTACCGTTGTTGTTGAAATTACAGTTGCTA
 ACTCTACAGGTTACAGGTTCCCTTGTGAAATTAAATTACCCCTAAAAAC
 GTTGTAACTGTGAAACCAAAACAGATAAAGATGTTAAAAAATTAGGTCA
 GGACGATGCAAGTTACGATTGGTGAAGAATTCAAATGGTTCTGAAAT
 CTAACTCCCTGCCAATTAGCTGACTGAAATTGAAATTACTGAT
 AAATTTGCAAGTGGCTTGACTTATAAAATGTTGAAATTCAAGATTGG
 TTCGAAAACACTGAATAGAGATGAGCACTACACTATTGATGAAACACAG
 TTGATAACCAAAATACATTAACCTTACGTTAAACCCAGAGAAATTAA
 GAAATTGCTGAGCTACTTAAAGGAATGACCTTGTAAATTCAAGATGC
 TCTTGATAAAGGTTACTGCAAATACAGATGTCGGCATTTCGAAATT
 CAGTTGCACTCACTTAAATGAAAAGCAGTTTAGGAAAGCAATTGAA
 ATACATTGCACTTCAATATGACCATACCTCTGATAAAAGCTGACAATCC
 AAAACCATCTAACTCTCAAAGAACCAAGGTTACAGTACTGGGGAAAC
 GATTGTAAAGAAAAGACTCAACAGAAACACAAACACTAGGGTGTGAG
 TTGATTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAGATGCTCT
 TATTAAGCGAATACTAAAAACTATATGCTGGAGAAGCTGTTACTG
 GCGAACCAATCAAATTGAAATCACATACAGACGGTACGTTGAGATTAA
 GGTGTTGGCTTATGCACTGAGTTGCGAATGAGGGTACAGCACTTA
 CAAATTAAAAGAACAAAAGCACCAGAAGGTTATGTAATCCCTGATAAAG
 AAATCGAGTTACAGTATCACAAACATCTTAAATACAAAACCAACTGAC
 ATCACGGTTGATAGTGCTGATGCAACACCTGATACAATTAAAACAACAA
 ACGTCCCTCA

PRETTY of: /biotmp/msa123961.2{*} April 30, 2003 07:17 ..

msa123961.2{80_2603}	1	50
msa123961.2{80_A909}	atgaaaattat cgaagaagtt attgtttcg gctgctgtt taacaatgg	
msa123961.2{80_M732}	-----	-----
msa123961.2{80_090}	-----	-----
msa123961.2{80_COH1}	-----	-----
msa123961.2{80_M781}	-----	-----
msa123961.2{801_JM9130013}	-----	-----
msa123961.2{80_18RS21}	-----	-----
msa123961.2{80h_CJB110}	-----	-----
Consensus	-----	-----
msa123961.2{80_2603}	51	100
msa123961.2{80_A909}	ggccgggtca actgttgaac cagtagctca gtttgcact ggaatgagta	
msa123961.2{80_M732}	-----	-----
msa123961.2{80_090}	-----	-----
msa123961.2{80_COH1}	-----	-----
msa123961.2{80_M781}	-----	-----
msa123961.2{801_JM9130013}	-----	-----
msa123961.2{80_18RS21}	-----	-----
msa123961.2{80h_CJB110}	-----	-----
Consensus	-----	-----
msa123961.2{80_2603}	101	150
msa123961.2{80_A909}	ttgtaagagc tgcagaagtgc tcacaagaac gcccaggcAACaaCAGTA	
msa123961.2{80_M732}	-----	-----
msa123961.2{80_090}	-----	-----
msa123961.2{80_COH1}	-----	-----
msa123961.2{80_M781}	-----	-----
msa123961.2{801_JM9130013}	-----	-----
msa123961.2{80_18RS21}	-----	-----
msa123961.2{80h_CJB110}	-----	-----
Consensus	-----	-----

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80h_CJB110}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAgCAGTA	
Consensus	-----	*****	*****	*****	*****	-----
	151					200
msa123961.2{80_2603}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTctAA	
msa123961.2{80_A909}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTctAA	
msa123961.2{80_M732}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTctAA	
msa123961.2{80_090}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTctAA	
msa123961.2{80_COH1}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTctAA	
msa123961.2{80_M781}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTctAA	
msa123961.2{801_JM9130013}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTctAA	
msa123961.2{80_18RS21}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTctAA	
msa123961.2{80h_CJB110}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATtGGAAA	TTACTTctAA	
Consensus	*****	*****	*****	*****	*****	*****
	201					250
msa123961.2{80_2603}	TGGTGGTATC	GAGAATAAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	
msa123961.2{80_A909}	TGGTGGTATC	GAGAATAAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	
msa123961.2{80_M732}	TGGTGGTATC	GAGAATAAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	
msa123961.2{80_090}	TGGTGGTATC	GAGAATAAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	
msa123961.2{80_COH1}	TGGTGGTATC	GAGAATAAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	
msa123961.2{80_M781}	TGGTGGTATC	GAGAATAAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	
msa123961.2{801_JM9130013}	TGGTGGTATC	GAGAATAAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	
msa123961.2{80_18RS21}	TGGTGGTATC	GAGAATAAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	
msa123961.2{80h_CJB110}	TGGTGGTATC	GAGAATAAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC	
Consensus	*****	*****	*****	*****	*****	*****
	251					300
msa123961.2{80_2603}	TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTAA	ACGTTATAAA	
msa123961.2{80_A909}	TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTAA	ACGTTATAAA	
msa123961.2{80_M732}	TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTAA	ACGTTATAAA	
msa123961.2{80_090}	TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTAA	ACGTTATAAA	
msa123961.2{80_COH1}	TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTAA	ACGTTATAAA	
msa123961.2{80_M781}	TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTAA	ACGTTATAAA	
msa123961.2{801_JM9130013}	TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTAA	ACGTTATAAA	
msa123961.2{80_18RS21}	TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTAA	ACGTTATAAA	
msa123961.2{80h_CJB110}	TTGGTGACAA	TGTAAAAGGT	TTGCAAGGTG	TACAGTTAA	ACGTTATAAA	
Consensus	*****	*****	*****	*****	*****	*****
	301					350
msa123961.2{80_2603}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	
msa123961.2{80_A909}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	
msa123961.2{80_M732}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	
msa123961.2{80_090}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	
msa123961.2{80_COH1}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	
msa123961.2{80_M781}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	
msa123961.2{801_JM9130013}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	
msa123961.2{80_18RS21}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	
msa123961.2{80h_CJB110}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA	
Consensus	*****	*****	*****	*****	*****	*****
	351					400
msa123961.2{80_2603}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	
msa123961.2{80_A909}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	
msa123961.2{80_M732}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	
msa123961.2{80_090}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	
msa123961.2{80_COH1}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	
msa123961.2{80_M781}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	
msa123961.2{801_JM9130013}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	
msa123961.2{80_18RS21}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	
msa123961.2{80h_CJB110}	AGCAGCAGAT	GCAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC	
Consensus	*****	*****	*****	*****	*****	*****
	401					450
msa123961.2{80_2603}	CTCAAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	
msa123961.2{80_A909}	CTCAAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	
msa123961.2{80_M732}	CTCAAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	
msa123961.2{80_090}	CTCAAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	
msa123961.2{80_COH1}	CTCAAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	
msa123961.2{80_M781}	CTCAAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	
msa123961.2{801_JM9130013}	CTCAAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	
msa123961.2{80_18RS21}	CTCAAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	
msa123961.2{80h_CJB110}	CTCAAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA	
Consensus	*****	*****	*****	*****	*****	*****
	451					500
msa123961.2{80_2603}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA	
msa123961.2{80_A909}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA	
msa123961.2{80_M732}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA	
msa123961.2{80_090}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA	
msa123961.2{80_COH1}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA	
msa123961.2{80_M781}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA	
msa123961.2{801_JM9130013}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA	

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_18RS21}	AGTAATGTGA	GATACTTGTA	TGTTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{80h_CJB110}	AGTAATGTGA	GATACTTGTA	TGTTAGAAGAT	TTAAAGAATT	CACCTTCAAA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATT	CCAGTTGCTA
msa123961.2{80_A909}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATT	CCAGTTGCTA
msa123961.2{80_M732}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATT	CCAGTTGCTA
msa123961.2{80_090}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATT	CCAGTTGCTA
msa123961.2{80_COH1}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATT	CCAGTTGCTA
msa123961.2{80_M781}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATT	CCAGTTGCTA
msa123961.2{801_JM9130013}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATT	CCAGTTGCTA
msa123961.2{80_18RS21}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATT	CCAGTTGCTA
msa123961.2{80h_CJB110}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTTGGAATT	CCAGTTGCTA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_A909}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_M732}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_090}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_COH1}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_M781}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{801_JM9130013}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_18RS21}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80h_CJB110}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	GTTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAA	AATTAGGTCA
msa123961.2{80_A909}	GTTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAA	AATTAGGTCA
msa123961.2{80_M732}	GTTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAA	AATTAGGTCA
msa123961.2{80_090}	GTTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAA	AATTAGGTCA
msa123961.2{80_COH1}	GTTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAA	AATTAGGTCA
msa123961.2{80_M781}	GTTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAA	AATTAGGTCA
msa123961.2{801_JM9130013}	GTTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAA	AATTAGGTCA
msa123961.2{80_18RS21}	GTTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAA	AATTAGGTCA
msa123961.2{80h_CJB110}	GTTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAA	AATTAGGTCA
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
msa123961.2{80_A909}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
msa123961.2{80_M732}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
msa123961.2{80_090}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
msa123961.2{80_COH1}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
msa123961.2{80_M781}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
msa123961.2{801_JM9130013}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
msa123961.2{80_18RS21}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
msa123961.2{80h_CJB110}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTG	AATTACTGAT
msa123961.2{80_A909}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTG	AATTACTGAT
msa123961.2{80_M732}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTG	AATTACTGAT
msa123961.2{80_090}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTG	AATTACTGAT
msa123961.2{80_COH1}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTG	AATTACTGAT
msa123961.2{80_M781}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTG	AATTACTGAT
msa123961.2{801_JM9130013}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTG	AATTACTGAT
msa123961.2{80_18RS21}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTG	AATTACTGAT
msa123961.2{80h_CJB110}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTG	AATTACTGAT
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	AAATTTCGAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_A909}	AAATTTCGAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_M732}	AAATTTCGAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_090}	AAATTTCGAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_COH1}	AAATTTCGAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_M781}	AAATTTCGAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{801_JM9130013}	AAATTTCGAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_18RS21}	AAATTTCGAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80h_CJB110}	AAATTTCGAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80_A909}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80_M732}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80_090}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80_COH1}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80_M781}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80h_CJB110}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	501	550			
msa123961.2{80_A909}					
msa123961.2{80_M732}					
msa123961.2{80_090}					
msa123961.2{80_COH1}					
msa123961.2{80_M781}					
msa123961.2{801_JM9130013}					
msa123961.2{80_18RS21}					
msa123961.2{80h_CJB110}					
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	551	600			
msa123961.2{80_A909}					
msa123961.2{80_M732}					
msa123961.2{80_090}					
msa123961.2{80_COH1}					
msa123961.2{80_M781}					
msa123961.2{801_JM9130013}					
msa123961.2{80_18RS21}					
msa123961.2{80h_CJB110}					
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	601	650			
msa123961.2{80_A909}					
msa123961.2{80_M732}					
msa123961.2{80_090}					
msa123961.2{80_COH1}					
msa123961.2{80_M781}					
msa123961.2{801_JM9130013}					
msa123961.2{80_18RS21}					
msa123961.2{80h_CJB110}					
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	651	700			
msa123961.2{80_A909}					
msa123961.2{80_M732}					
msa123961.2{80_090}					
msa123961.2{80_COH1}					
msa123961.2{80_M781}					
msa123961.2{801_JM9130013}					
msa123961.2{80_18RS21}					
msa123961.2{80h_CJB110}					
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	701	750			
msa123961.2{80_A909}					
msa123961.2{80_M732}					
msa123961.2{80_090}					
msa123961.2{80_COH1}					
msa123961.2{80_M781}					
msa123961.2{801_JM9130013}					
msa123961.2{80_18RS21}					
msa123961.2{80h_CJB110}					
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	751	800			
msa123961.2{80_A909}					
msa123961.2{80_M732}					
msa123961.2{80_090}					
msa123961.2{80_COH1}					
msa123961.2{80_M781}					
msa123961.2{801_JM9130013}					
msa123961.2{80_18RS21}					
msa123961.2{80h_CJB110}					
Consensus	*****	*****	*****	*****	*****
msa123961.2{80_2603}	801	850			
msa123961.2{80_A909}					
msa123961.2{80_M732}					
msa123961.2{80_090}					
msa123961.2{80_COH1}					
msa123961.2{80_M781}					
msa123961.2{80h_CJB110}					
Consensus	*****	*****	*****	*****	*****

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{801_JM9130013}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG	
msa123961.2{80_18RS21}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG	
msa123961.2{80h_CJB110}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG	
Consensus	*****	*****	*****	*****	*****	*****
	851				900	
msa123961.2{80_2603}	TTGTATAACCA	AAATACATTA	AAAATTACGT	TTAACCCAGA	GAAATTAAAA	
msa123961.2{80_A909}	TTGTATAACCA	AAATACATTA	AAAATTACGT	TTAACCCAGA	GAAATTAAAA	
msa123961.2{80_M732}	TTGTATAACCA	AAATACATTA	AAAATTACGT	TTAACCCAGA	GAAATTAAAA	
msa123961.2{80_090}	TTGTATAACCA	AAATACATTA	AAAATTACGT	TTAACCCAGA	GAAATTAAAA	
msa123961.2{80_COH1}	TTGTATAACCA	AAATACATTA	AAAATTACGT	TTAACCCAGA	GAAATTAAAA	
msa123961.2{80_M781}	TTGTATAACCA	AAATACATTA	AAAATTACGT	TTAACCCAGA	GAAATTAAAA	
msa123961.2{801_JM9130013}	TTGTATAACCA	AAATACATTA	AAAATTACGT	TTAACCCAGA	GAAATTAAAA	
msa123961.2{80_18RS21}	TTGTATAACCA	AAATACATTA	AAAATTACGT	TTAACCCAGA	GAAATTAAAA	
msa123961.2{80h_CJB110}	TTGTATAACCA	AAATACATTA	AAAATTACGT	TTAACCCAGA	GAAATTAAAA	
Consensus	*****	*****	*****	*****	*****	*****
	901				950	
msa123961.2{80_2603}	GAAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC	
msa123961.2{80_A909}	GAAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC	
msa123961.2{80_M732}	GAAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC	
msa123961.2{80_090}	GAAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC	
msa123961.2{80_COH1}	GAAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC	
msa123961.2{80_M781}	GAAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC	
msa123961.2{801_JM9130013}	GAAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC	
msa123961.2{80_18RS21}	GAAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC	
msa123961.2{80h_CJB110}	GAAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTTAAAA	ATCAAGATGC	
Consensus	*****	*****	*****	*****	*****	*****
	951				1000	
msa123961.2{80_2603}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTTC	
msa123961.2{80_A909}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTTC	
msa123961.2{80_M732}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTTC	
msa123961.2{80_090}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTTC	
msa123961.2{80_COH1}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTTC	
msa123961.2{80_M781}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTTC	
msa123961.2{801_JM9130013}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTTC	
msa123961.2{80_18RS21}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTTC	
msa123961.2{80h_CJB110}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATTT	TTGGAAATTTC	
Consensus	*****	*****	*****	*****	*****	*****
	1001				1050	
msa123961.2{80_2603}	CAGTTGCATC	AACATTAAAT	AAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA	
msa123961.2{80_A909}	CAGTTGCATC	AACATTAAAT	AAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA	
msa123961.2{80_M732}	CAGTTGCATC	AACATTAAAT	AAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA	
msa123961.2{80_090}	CAGTTGCATC	AACATTAAAT	AAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA	
msa123961.2{80_COH1}	CAGTTGCATC	AACATTAAAT	AAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA	
msa123961.2{80_M781}	CAGTTGCATC	AACATTAAAT	AAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA	
msa123961.2{801_JM9130013}	CAGTTGCATC	AACATTAAAT	AAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA	
msa123961.2{80_18RS21}	CAGTTGCATC	AACATTAAAT	AAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA	
msa123961.2{80h_CJB110}	CAGTTGCATC	AACATTAAAT	AAAAAAGCAG	TTTTAGGAAA	AGCAATTGAA	
Consensus	*****	*****	*****	*****	*****	*****
	1051				1100	
msa123961.2{80_2603}	AATACTTTTG	AACTTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC	
msa123961.2{80_A909}	AATACTTTTG	AACTTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC	
msa123961.2{80_M732}	AATACTTTTG	AACTTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC	
msa123961.2{80_090}	AATACTTTTG	AACTTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC	
msa123961.2{80_COH1}	AATACTTTTG	AACTTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC	
msa123961.2{80_M781}	AATACTTTTG	AACTTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC	
msa123961.2{801_JM9130013}	AATACTTTTG	AACTTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC	
msa123961.2{80_18RS21}	AATACTTTTG	AACTTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC	
msa123961.2{80h_CJB110}	AATACTTTTG	AACTTCAATA	TGACCATACT	CCTGATAAAG	CTGACAAATCC	
Consensus	*****	*****	*****	*****	*****	*****
	1101				1150	
msa123961.2{80_2603}	AAAACCATCT	AATCCTCCAA	AAAAACCAGA	AGTTCATACT	GGTGGAAAC	
msa123961.2{80_A909}	AAAACCATCT	AATCCTCCAA	AAAAACCAGA	AGTTCATACT	GGTGGAAAC	
msa123961.2{80_M732}	AAAACCATCT	AATCCTCCAA	AAAAACCAGA	AGTTCATACT	GGTGGAAAC	
msa123961.2{80_090}	AAAACCATCT	AATCCTCCAA	AAAAACCAGA	AGTTCATACT	GGTGGAAAC	
msa123961.2{80_COH1}	AAAACCATCT	AATCCTCCAA	AAAAACCAGA	AGTTCATACT	GGTGGAAAC	
msa123961.2{80_M781}	AAAACCATCT	AATCCTCCAA	AAAAACCAGA	AGTTCATACT	GGTGGAAAC	
msa123961.2{801_JM9130013}	AAAACCATCT	AATCCTCCAA	AAAAACCAGA	AGTTCATACT	GGTGGAAAC	
msa123961.2{80_18RS21}	AAAACCATCT	AATCCTCCAA	AAAAACCAGA	AGTTCATACT	GGTGGAAAC	
msa123961.2{80h_CJB110}	AAAACCATCT	AATCCTCCAA	AAAAACCAGA	AGTTCATACT	GGTGGAAAC	
Consensus	*****	*****	*****	*****	*****	*****
	1151				1200	
msa123961.2{80_2603}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGTGAG	
msa123961.2{80_A909}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGTGAG	
msa123961.2{80_M732}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGTGAG	
msa123961.2{80_090}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGTGAG	
msa123961.2{80_COH1}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGTGAG	

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_M781}	GATTTGTAAA GAAAGACTCA ACAGAAACAC AAACACTAGG TGGTGCTGAG	
msa123961.2{801 JM9130013}	GATTTGTAAA GAAAGACTCA ACAGAAACAC AAACACTAGG TGGTGCTGAG	
msa123961.2{80_18RS21}	GATTTGTAAA GAAAGACTCA ACAGAAACAC AAACACTAGG TGGTGCTGAG	
msa123961.2{80h_CJB110}	GATTTGTAAA GAAAGACTCA ACAGAAACAC AAACACTAGG TGGTGCTGAG	
Consensus	*****	*****
		1201
msa123961.2{80_2603}	TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT	1250
msa123961.2{80_A909}	TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT	
msa123961.2{80_M732}	TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT	
msa123961.2{80_090}	TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT	
msa123961.2{80_COH1}	TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT	
msa123961.2{80_M781}	TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT	
msa123961.2{801 JM9130013}	TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT	
msa123961.2{80_18RS21}	TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT	
msa123961.2{80h_CJB110}	TTTGATTTGT TGGCTTCTGA TGGGACAGCA GTAAAATGGA CAGATGCTCT	
Consensus	*****	*****
		1251
msa123961.2{80_2603}	TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG	1300
msa123961.2{80_A909}	TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG	
msa123961.2{80_M732}	TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG	
msa123961.2{80_090}	TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG	
msa123961.2{80_COH1}	TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG	
msa123961.2{80_M781}	TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG	
msa123961.2{801 JM9130013}	TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG	
msa123961.2{80_18RS21}	TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG	
msa123961.2{80h_CJB110}	TATTAAAGCG AATACTAATA AAAACTATAT TGCTGGAGAA GCTGTTACTG	
Consensus	*****	*****
		1301
msa123961.2{80_2603}	GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA	1350
msa123961.2{80_A909}	GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA	
msa123961.2{80_M732}	GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA	
msa123961.2{80_090}	GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA	
msa123961.2{80_COH1}	GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA	
msa123961.2{80_M781}	GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA	
msa123961.2{801 JM9130013}	GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA	
msa123961.2{80_18RS21}	GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA	
msa123961.2{80h_CJB110}	GGCAACCAAT CAAATTGAAA TCACATACAG ACGGTACGTT TGAGATTAAA	
Consensus	*****	*****
		1351
msa123961.2{80_2603}	GGTTTGGCTT ATGCAGTTGA TCGGAATGCA GAGGGTACAG CAGTAACITTA	1400
msa123961.2{80_A909}	GGTTTGGCTT ATGCAGTTGA TCGGAATGCA GAGGGTACAG CAGTAACITTA	
msa123961.2{80_M732}	GGTTTGGCTT ATGCAGTTGA TCGGAATGCA GAGGGTACAG CAGTAACITTA	
msa123961.2{80_090}	GGTTTGGCTT ATGCAGTTGA TCGGAATGCA GAGGGTACAG CAGTAACITTA	
msa123961.2{80_COH1}	GGTTTGGCTT ATGCAGTTGA TCGGAATGCA GAGGGTACAG CAGTAACITTA	
msa123961.2{80_M781}	GGTTTGGCTT ATGCAGTTGA TCGGAATGCA GAGGGTACAG CAGTAACITTA	
msa123961.2{801 JM9130013}	GGTTTGGCTT ATGCAGTTGA TCGGAATGCA GAGGGTACAG CAGTAACITTA	
msa123961.2{80_18RS21}	GGTTTGGCTT ATGCAGTTGA TCGGAATGCA GAGGGTACAG CAGTAACITTA	
msa123961.2{80h_CJB110}	GGTTTGGCTT ATGCAGTTGA TCGGAATGCA GAGGGTACAG CAGTAACITTA	
Consensus	*****	*****
		1401
msa123961.2{80_2603}	CAAATAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG	1450
msa123961.2{80_A909}	CAAATAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG	
msa123961.2{80_M732}	CAAATAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG	
msa123961.2{80_090}	CAAATAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG	
msa123961.2{80_COH1}	CAAATAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG	
msa123961.2{80_M781}	CAAATAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG	
msa123961.2{801 JM9130013}	CAAATAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG	
msa123961.2{80_18RS21}	CAAATAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG	
msa123961.2{80h_CJB110}	CAAATAAAA GAAACAAAAG CACCAGAAGG TTATGTAATC CCTGATAAAG	
Consensus	*****	*****
		1451
msa123961.2{80_2603}	AAATCGAGTT TACAGTATCA CAAACATCTT ATAATcAAA ACCAACIGAC	1500
msa123961.2{80_A909}	AAATCGAGTT TACAGTATCA CAAACATCTT ATAATcAAA ACCAACIGAC	
msa123961.2{80_M732}	AAATCGAGTT TACAGTATCA CAAACATCTT ATAATcAAA ACCAACIGAC	
msa123961.2{80_090}	AAATCGAGTT TACAGTATCA CAAACATCTT ATAATcAAA ACCAACIGAC	
msa123961.2{80_COH1}	AAATCGAGTT TACAGTATCA CAAACATCTT ATAATcAAA ACCAACIGAC	
msa123961.2{80_M781}	AAATCGAGTT TACAGTATCA CAAACATCTT ATAATcAAA ACCAACIGAC	
msa123961.2{801 JM9130013}	AAATCGAGTT TACAGTATCA CAAACATCTT ATAATcAAA ACCAACIGAC	
msa123961.2{80_18RS21}	AAATCGAGTT TACAGTATCA CAAACATCTT ATAATcAAA ACCAACIGAC	
msa123961.2{80h_CJB110}	AAATCGAGTT TACAGTATCA CAAACATCTT ATAATcAAA ACCAACIGAC	
Consensus	*****	*****
		1501
msa123961.2{80_2603}	ATACCGGTT ATAGTGCTGA TGCAACACCT GATACAATT AAAACACAA	1550
msa123961.2{80_A909}	ATACCGGTT ATAGTGCTGA TGCAACACCT GATACAATT AAAACACAA	
msa123961.2{80_M732}	ATACCGGTT ATAGTGCTGA TGCAACACCT GATACAATT AAAACACAA	
msa123961.2{80_090}	ATACCGGTT ATAGTGCTGA TGCAACACCT GATACAATT AAAACACAA	

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_COH1}	ATCACGGTTG ATAGTGCTGA TGCAACACCT GATACAATTAA AAAACAACAA
msa123961.2{80_M781}	ATCACGGTTG ATAGTGCTGA TGCAACACCT GATACAATTAA AAAACAACAA
msa123961.2{801_JM9130013}	ATCACGGTTG ATAGTGCTGA TGCAACACCT GATACAATTAA AAAACAACAA
msa123961.2{80_18RS21}	ATCACGGTTG ATAGTGCTGA TGCAACACCT GATACAATTAA AAAACAACAA
msa123961.2{80h_CJB110}	ATCACGGTTG ATAGTGCTGA TGCAACACCT GATACAATTAA AAAACAACAA
Consensus	***** * ***** * ***** * ***** * *****
1551	1600
msa123961.2{80_2603}	acgtccttca atccctaata ctgggttat tggtaggcgt atctttgtcg
msa123961.2{80_A909}	----- ----- ----- ----- ----- -----
msa123961.2{80_M732}	acgtccttca ----- ----- ----- ----- -----
msa123961.2{80_090}	acgtccttca ----- ----- ----- ----- -----
msa123961.2{80_COH1}	acgtccttca ----- ----- ----- ----- -----
msa123961.2{80_M781}	acgt ----- ----- ----- ----- -----
msa123961.2{801_JM9130013}	acgtccttca ----- ----- ----- ----- -----
msa123961.2{80_18RS21}	acgtccttca ----- ----- ----- ----- -----
msa123961.2{80h_CJB110}	acgtccttca ----- ----- ----- ----- -----
Consensus	----- ----- ----- ----- -----
1601	1650
msa123961.2{80_2603}	cstatecggtgc tgccgtgatg gctttgtcg ttaagggtat gaagcgctgt
msa123961.2{80_A909}	----- ----- ----- ----- -----
msa123961.2{80_M732}	----- ----- ----- ----- -----
msa123961.2{80_090}	----- ----- ----- ----- -----
msa123961.2{80_COH1}	----- ----- ----- ----- -----
msa123961.2{80_M781}	----- ----- ----- ----- -----
msa123961.2{801_JM9130013}	----- ----- ----- ----- -----
msa123961.2{80_18RS21}	----- ----- ----- ----- -----
msa123961.2{80h_CJB110}	----- ----- ----- ----- -----
Consensus	----- ----- ----- ----- -----
1651 1662	
msa123961.2{80_2603}	acaaaaagata ac
msa123961.2{80_A909}	----- --
msa123961.2{80_M732}	----- --
msa123961.2{80_090}	----- --
msa123961.2{80_COH1}	----- --
msa123961.2{80_M781}	----- --
msa123961.2{801_JM9130013}	----- --
msa123961.2{80_18RS21}	----- --
msa123961.2{80h_CJB110}	----- --
Consensus	----- --

SEQ ID NO. 8710

STRAIN 2603 frame: 1

MKLSKLLFSAVLTMVAGSTVEPVQAQFATGMSIVRAAEVSQERPAKTTVNIYKLQADSY
 KSEITSNGGIENKDGEVISNYAKLGDNVKGQLGVQFKRYVKTDISVDELKKLTTEVAAD
 AKVGTILEEGVSLPKQTKNAQGLVVLDSDSKSNVRYLVEDLKNSPSNITKAYAVPFL
 PVANSTGTGFLEINIPKVNVTDEPKTDKDVKKLGQDDAGTYIGEEFKWFLKSTIPANL
 GDYEKFEITDKFADGLTQKLVNQDALDKATANTDDAAFLEIPVASTINEKAVLGKA
 EIAELLKGMTLVKNQDALDKATANTDDAAFLEIPVASTINEKAVLGKAENTFELQDHT
 PDKADNPKPNSNPPRKPEVHTGGKRFVKKDSTETQTLGGAEDFDLLASDGTA
 NTKNYIAGEAVIGQPIKLKSHTDGTFEIKGLAYAVDANAEGTAVTYKLKETKA
 PEGYVI
 PDKEIEFTVQSQTSYNTKPTDITVDSADATPDTIKNNKRPSIPNTGGIGTA
 FVAIGAAM
 AFAVKGMKRRTKDN

SEQ ID NO. 8711

STRAIN 090 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGQLGVQFK
 RYVKTDISVDELKKLTTEVAADAKVGTILEEGVSLPKQTKNAQGLVVLDSDSKSNVRYL
 VEDLKNSPSNITKAYAVPFLPVA
 NSTGTGFLEINIPKVNVTDEPKTDKDVKKLGQ
 DDAGTYIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTQKLVNQDALDKATANTDDAAFLEIPV
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPV
 TINEKAVLGKAENTFELQDHTPDKADNPKPNSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTA
 VWTDALIKANTNKYIAGEAVIGQPIKLKSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVI
 PDKEIEFTVQSQTSYNTKPTDITVDSADATPDTIKNN
 RPS

SEQ ID NO. 8712

STRAIN 18RS21 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGQLGVQFK
 RYVKTDISVDELKKLTTEVAADAKVGTILEEGVSLPKQTKNAQGLVVLDSDSKSNVRYL
 VEDLKNSPSNITKAYAVPFLPVA
 NSTGTGFLEINIPKVNVTDEPKTDKDVKKLGQ
 DDAGTYIGEEFKWFLKSTIPANLGDYEKFEITDKFADGLTQKLVNQDALDKATANTDDAAFLEIPV
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMTLVKNQDALDKATANTDDAAFLEIPV
 TINEKAVLGKAENTFELQDHTPDKADNPKPNSNPPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTA
 VWTDALIKANTNKYIAGEAVIGQPIKLKSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVI
 PDKEIEFTVQSQTSYNTKPTDITVDSADATPDTIKNN
 RPS

SEQ ID NO. 8713

STRAIN M732 frame: 1

AEVSQERPAKTAVNIYKLQADSYKSEITSNGGIENKDGEVISNYAKLGDNVKGQLGVQFK

Table 87: Comparative Sequences relating to SAG0645

RYKVKTIDSVDELKLLTTVEAADAKVGTILEEGVSLPQKTNQAQLVVVDALDSKSNSVRYLY
 VEDLKNSPSNITKAYAVPFLPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLQG
 DDAGYTIGEEFKWFLKSTIPANLGDYKEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMLTVKNQDALDKATANTDDAAFLIEPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPKPNSNPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAWKWTDALIKANTNKNYIAGEAVTGQPICKLSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8714

STRAIN M781 frame: 1

AEVSQERPAKTAVNIIYKLQADSYKSEITSNGGIENKDGEVISNYAKLDNVKGLQGVQFK
 RYKVKTIDSVDELKLLTTVEAADAKVGTILEEGVSLPQKTNQAQLVVVDALDSKSNSVRYLY
 VEDLKNSPSNITKAYAVPFLPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLQG
 DDAGYTIGEEFKWFLKSTIPANLGDYKEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMLTVKNQDALDKATANTDDAAFLIEPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPKPNSNPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAWKWTDALIKANTNKNYIAGEAVTGQPICKLSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 R

SEQ ID NO. 8715

STRAIN COH1 frame: 1

AEVSQERPAKTAVNIIYKLQADSYKSEITSNGGIENKDGEVISNYAKLDNVKGLQGVQFK
 RYKVKTIDSVDELKLLTTVEAADAKVGTILEEGVSLPQKTNQAQLVVVDALDSKSNSVRYLY
 VEDLKNSPSNITKAYAVPFLPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLQG
 DDAGYTIGEEFKWFLKSTIPANLGDYKEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMLTVKNQDALDKATANTDDAAFLIEPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPKPNSNPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAWKWTDALIKANTNKNYIAGEAVTGQPICKLSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8716

STRAIN CJB110 frame: 1

AEVSQERPAKTAVNIIYKLQADSYKSEITSNGGIENKDGEVISNYAKLDNVKGLQGVQFK
 RYKVKTIDSVDELKLLTTVEAADAKVGTILEEGVSLPQKTNQAQLVVVDALDSKSNSVRYLY
 VEDLKNSPSNITKAYAVPFLPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLQG
 DDAGYTIGEEFKWFLKSTIPANLGDYKEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMLTVKNQDALDKATANTDDAAFLIEPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPKPNSNPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAWKWTDALIKANTNKNYIAGEAVTGQPICKLSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8717

STRAIN JM9130013 frame: 1

AEVSQERPAKTAVNIIYKLQADSYKSEITSNGGIENKDGEVISNYAKLDNVKGLQGVQFK
 RYKVKTIDSVDELKLLTTVEAADAKVGTILEEGVSLPQKTNQAQLVVVDALDSKSNSVRYLY
 VEDLKNSPSNITKAYAVPFLPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLQG
 DDAGYTIGEEFKWFLKSTIPANLGDYKEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMLTVKNQDALDKATANTDDAAFLIEPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPKPNSNPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAWKWTDALIKANTNKNYIAGEAVTGQPICKLSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

SEQ ID NO. 8718

STRAIN A909 frame: 1

AEVSQERPAKTAVNIIYKLQADSYKSEITSNGGIENKDGEVISNYAKLDNVKGLQGVQFK
 RYKVKTIDSVDELKLLTTVEAADAKVGTILEEGVSLPQKTNQAQLVVVDALDSKSNSVRYLY
 VEDLKNSPSNITKAYAVPFLPVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLQG
 DDAGYTIGEEFKWFLKSTIPANLGDYKEKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
 TIDEPTVDNQNTLKITFKPEKFKEIAELLKGMLTVKNQDALDKATANTDDAAFLIEPVAS
 TINEKAVLGKAIENTFELQYDHTPDKADNPKPNSNPRKPEVHTGGKRFVKKDSTETQTLG
 GAEFDLLASDGTAWKWTDALIKANTNKNYIAGEAVTGQPICKLSHTDGTFEIKGLAYAVD
 ANAEGTAVTYKLKETKAPEGYVIPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
 RPS

PRETTY of: /biotmp/msa124060.2{*} April 30, 2003 07:19 ..

	1	50
msa124060.2{80_2603}	mklskllfs aavltmvags tvepvaqfat gmsivraAEV	SQERPAKTTv
msa124060.2{80_M732}	-----	-----AEV
msa124060.2{80_A909}	-----	-----AEV
msa124060.2{80_090}	-----	-----AEV
msa124060.2{80_M781}	-----	-----AEV
msa124060.2{80_COH1}	-----	-----AEV
msa124060.2{801_JM9130013}	-----	-----AEV
msa124060.2{80_18RS21}	-----	-----AEV
msa124060.2{80h_CJB110}	-----	-----AEV
Consensus	-----	***** ***** -*

Table 87: Comparative Sequences relating to SAG0645

msa124060.2{80_2603}	51	NIYKLQADSY	KsEITsNGGI	ENKDGEVISN	YAKLGDNVKKG	LQGVQFKRYK	100
msa124060.2{80_M732}		NIYKLQADSY	KsEITsNGGI	ENKDGEVISN	YAKLGDNVKKG	LQGVQFKRYK	
msa124060.2{80_A909}		NIYKLQADSY	KsEITsNGGI	ENKDGEVISN	YAKLGDNVKKG	LQGVQFKRYK	
msa124060.2{80_090}		NIYKLQADSY	KsEITsNGGI	ENKDGEVISN	YAKLGDNVKKG	LQGVQFKRYK	
msa124060.2{80_M781}		NIYKLQADSY	KsEITsNGGI	ENKDGEVISN	YAKLGDNVKKG	LQGVQFKRYK	
msa124060.2{80_COH1}		NIYKLQADSY	KsEITsNGGI	ENKDGEVISN	YAKLGDNVKKG	LQGVQFKRYK	
msa124060.2{801_JM9130013}		NIYKLQADSY	KsEITsNGGI	ENKDGEVISN	YAKLGDNVKKG	LQGVQFKRYK	
msa124060.2{80_18RS21}		NIYKLQADSY	KsEITsNGGI	ENKDGEVISN	YAKLGDNVKKG	LQGVQFKRYK	
msa124060.2{80h_CJB110}		NIYKLQADSY	KsEITsNGGI	ENKDGEVISN	YAKLGDNVKKG	LQGVQFKRYK	
Consensus	*****	*****	*****	*****	*****	*****	*****
msa124060.2{80_2603}	101	VKTDISVDEL'	KKLTTVEAAD	AKVGTLILEEG	VSLPKTNAQ	GLVVDALESK	150
msa124060.2{80_M732}		VKTDISVDEL	KKLTTVEAAD	AKVGTLILEEG	VSLPKTNAQ	GLVVDALESK	
msa124060.2{80_A909}		VKTDISVDEL	KKLTTVEAAD	AKVGTLILEEG	VSLPKTNAQ	GLVVDALESK	
msa124060.2{80_090}		VKTDISVDEL	KKLTTVEAAD	AKVGTLILEEG	VSLPKTNAQ	GLVVDALESK	
msa124060.2{80_M781}		VKTDISVDEL	KKLTTVEAAD	AKVGTLILEEG	VSLPKTNAQ	GLVVDALESK	
msa124060.2{80_COH1}		VKTDISVDEL	KKLTTVEAAD	AKVGTLILEEG	VSLPKTNAQ	GLVVDALESK	
msa124060.2{801_JM9130013}		VKTDISVDEL	KKLTTVEAAD	AKVGTLILEEG	VSLPKTNAQ	GLVVDALESK	
msa124060.2{80_18RS21}		VKTDISVDEL	KKLTTVEAAD	AKVGTLILEEG	VSLPKTNAQ	GLVVDALESK	
msa124060.2{80h_CJB110}		VKTDISVDEL	KKLTTVEAAD	AKVGTLILEEG	VSLPKTNAQ	GLVVDALESK	
Consensus	*****	*****	*****	*****	*****	*****	*****
msa124060.2{80_2603}	151	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN	200
msa124060.2{80_M732}		SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN	
msa124060.2{80_A909}		SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN	
msa124060.2{80_090}		SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN	
msa124060.2{80_M781}		SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN	
msa124060.2{80_COH1}		SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN	
msa124060.2{801_JM9130013}		SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN	
msa124060.2{80_18RS21}		SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN	
msa124060.2{80h_CJB110}		SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF	LSEINIYPKN	
Consensus	*****	*****	*****	*****	*****	*****	*****
msa124060.2{80_2603}	201	VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD	250
msa124060.2{80_M732}		VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD	
msa124060.2{80_A909}		VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD	
msa124060.2{80_090}		VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD	
msa124060.2{80_M781}		VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD	
msa124060.2{80_COH1}		VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD	
msa124060.2{801_JM9130013}		VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD	
msa124060.2{80_18RS21}		VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD	
msa124060.2{80h_CJB110}		VVTDEPKTDK	DVKkLGQDDA	GYTIGEEFKW	FLKSTIPANL	GDYEKFEITD	
Consensus	*****	*****	*****	*****	*****	*****	*****
msa124060.2{80_2603}	251	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK	300
msa124060.2{80_M732}		KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK	
msa124060.2{80_A909}		KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK	
msa124060.2{80_090}		KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK	
msa124060.2{80_M781}		KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK	
msa124060.2{80_COH1}		KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK	
msa124060.2{801_JM9130013}		KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK	
msa124060.2{80_18RS21}		KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK	
msa124060.2{80h_CJB110}		KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL	KITFKPEKFK	
Consensus	*****	*****	*****	*****	*****	*****	*****
msa124060.2{80_2603}	301	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVALGKAE	350
msa124060.2{80_M732}		EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVALGKAE	
msa124060.2{80_A909}		EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVALGKAE	
msa124060.2{80_090}		EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVALGKAE	
msa124060.2{80_M781}		EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVALGKAE	
msa124060.2{80_COH1}		EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVALGKAE	
msa124060.2{801_JM9130013}		EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVALGKAE	
msa124060.2{80_18RS21}		EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVALGKAE	
msa124060.2{80h_CJB110}		EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN	EKAVALGKAE	
Consensus	*****	*****	*****	*****	*****	*****	*****
msa124060.2{80_2603}	351	NTFELQYDHT	PDKADNPKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE	400
msa124060.2{80_M732}		NTFELQYDHT	PDKADNPKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE	
msa124060.2{80_A909}		NTFELQYDHT	PDKADNPKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE	
msa124060.2{80_090}		NTFELQYDHT	PDKADNPKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE	
msa124060.2{80_M781}		NTFELQYDHT	PDKADNPKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE	
msa124060.2{80_COH1}		NTFELQYDHT	PDKADNPKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE	
msa124060.2{801_JM9130013}		NTFELQYDHT	PDKADNPKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE	
msa124060.2{80_18RS21}		NTFELQYDHT	PDKADNPKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE	
msa124060.2{80h_CJB110}		NTFELQYDHT	PDKADNPKPS	NPPRKPEVHT	GGKRFVKKDS	TETQTLGGAE	
Consensus	*****	*****	*****	*****	*****	*****	*****

Table 87: Comparative Sequences relating to SAG0645

msa124060.2{80_2603}	F DLLASDGTA	V KWTDALIKA	N TNKNYIAGE	A VTGQPIKLK	S HTDGTFEIK	401
msa124060.2{80_M732}	F DLLASDGTA	V KWTDALIKA	N TNKNYIAGE	A VTGQPIKLK	S HTDGTFEIK	
msa124060.2{80_A909}	F DLLASDGTA	V KWTDALIKA	N TNKNYIAGE	A VTGQPIKLK	S HTDGTFEIK	
msa124060.2{80_090}	F DLLASDGTA	V KWTDALIKA	N TNKNYIAGE	A VTGQPIKLK	S HTDGTFEIK	
msa124060.2{80_M781}	F DLLASDGTA	V KWTDALIKA	N TNKNYIAGE	A VTGQPIKLK	S HTDGTFEIK	
msa124060.2{80_COH1}	F DLLASDGTA	V KWTDALIKA	N TNKNYIAGE	A VTGQPIKLK	S HTDGTFEIK	
msa124060.2{801_JM9130013}	F DLLASDGTA	V KWTDALIKA	N TNKNYIAGE	A VTGQPIKLK	S HTDGTFEIK	
msa124060.2{80_18RS21}	F DLLASDGTA	V KWTDALIKA	N TNKNYIAGE	A VTGQPIKLK	S HTDGTFEIK	
msa124060.2{80h_CJB110}	F DLLASDGTA	V KWTDALIKA	N TNKNYIAGE	A VTGQPIKLK	S HTDGTFEIK	
Consensus	*****	*****	*****	*****	*****	*****
msa124060.2{80_2603}	G LAYAVDANA	E GTAVTYKLK	E TKAPEGVVI	P DKEIEFTVS	Q TSYNtKPTD	450
msa124060.2{80_M732}	G LAYAVDANA	E GTAVTYKLK	E TKAPEGVVI	P DKEIEFTVS	Q TSYNtKPTD	
msa124060.2{80_A909}	G LAYAVDANA	E GTAVTYKLK	E TKAPEGVVI	P DKEIEFTVS	Q TSYNtKPTD	
msa124060.2{80_090}	G LAYAVDANA	E GTAVTYKLK	E TKAPEGVVI	P DKEIEFTVS	Q TSYNtKPTD	
msa124060.2{80_M781}	G LAYAVDANA	E GTAVTYKLK	E TKAPEGVVI	P DKEIEFTVS	Q TSYNtKPTD	
msa124060.2{80_COH1}	G LAYAVDANA	E GTAVTYKLK	E TKAPEGVVI	P DKEIEFTVS	Q TSYNtKPTD	
msa124060.2{801_JM9130013}	G LAYAVDANA	E GTAVTYKLK	E TKAPEGVVI	P DKEIEFTVS	Q TSYNtKPTD	
msa124060.2{80_18RS21}	G LAYAVDANA	E GTAVTYKLK	E TKAPEGVVI	P DKEIEFTVS	Q TSYNtKPTD	
msa124060.2{80h_CJB110}	G LAYAVDANA	E GTAVTYKLK	E TKAPEGVVI	P DKEIEFTVS	Q TSYNpKPTD	
Consensus	*****	*****	*****	*****	*****	*****
msa124060.2{80_2603}	I TVDSDADATP	D TIKNNkrps	i pntggigta	i fvaigaavm	a favkgmkrr	501
msa124060.2{80_M732}	I TVDSDADATP	D TIKNNkrps	-----	-----	-----	
msa124060.2{80_A909}	I TVDSDADATP	D TIKNN-----	-----	-----	-----	
msa124060.2{80_090}	I TVDSDADATP	D TIKNNkrps	-----	-----	-----	
msa124060.2{80_M781}	I TVDSDADATP	D TIKNNkr-----	-----	-----	-----	
msa124060.2{80_COH1}	I TVDSDADATP	D TIKNNkrps	-----	-----	-----	
msa124060.2{801_JM9130013}	I TVDSDADATP	D TIKNNkrps	-----	-----	-----	
msa124060.2{80_18RS21}	I TVDSDADATP	D TIKNNkrps	-----	-----	-----	
msa124060.2{80h_CJB110}	I TVDSDADATP	D TIKNNkrps	-----	-----	-----	
Consensus	*****	*****	-----	-----	-----	
msa124060.2{80_2603}	t kdn	-----	551			
msa124060.2{80_M732}	----	-----				
msa124060.2{80_A909}	----	-----				
msa124060.2{80_090}	----	-----				
msa124060.2{80_M781}	----	-----				
msa124060.2{80_COH1}	----	-----				
msa124060.2{801_JM9130013}	----	-----				
msa124060.2{80_18RS21}	----	-----				
msa124060.2{80h_CJB110}	----	-----				
Consensus	----	-----				

Table 88: Comparative Sequences relating to SAG0477**SEQ ID NO. 8801****STRAIN 2603**

ATGCCCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTTGTCCTAACGGATGGCAA
 AAGCGTAACCTGAATTTTAAAAACGCCAAGAAGATGAAGAAGAACAAAACGTATT
 AACGAAAATTACGCTTAGATAAAAAGAAGTAAATTAAATATTCTCTCCTAGAAGAACCT
 CAAAATACTACTAAATTAAAGAAGCTCATTTCCAAGATTTCAAGACCTAACGATTGAA
 AGAAAACAGAAAAAGAAAAATAGTCACAGCTTAGCCAAAACTAATCGCATTAGAAT
 GCACCTATATTGTAGTAGCATTCAGTCATTAGTTCCGTTTCTACTAACCT
 TTAGTAAGCAAAACAATAACAGTTAGGAAATCAGCATACACCTGATGATAATTG
 ATAGAGAAAAGAATATTCAAAAAACGATTATTCTTTCTTAATTAAACATAAA
 GCTATTGACAACCTTTAGTCAGAAGATGTTAGGGTAAAACAGCTCAGATGACTTAT
 CAATTCCCAAATACTTCTATTCAGTCAAGAAAATAAGATTATTGCATATGCACAT
 ACAAAAGCAAGGATATCAACCTGCTTGGAAACTGGAAAAAGGCTGATCCCTGAAATAGT
 TCAGAGCTACCAAAAGCACTCTTAAACATTAACTTGATAAGGAAGATAGTTAAGCTA
 TTAAGTAAAGGTTAAAGGCTTACGGCTGATTTAAAGTGGAGATTCAAGGTTAG
 TTAGCTGATTCTAAACGACACTGACCTCTGCTGTAGATATGCACGATGAAATAGT
 ATTAGAATACCAATTCTAAATTAAAGAAGACTCCTTTTACAAACAAATTAAAGAAG
 AACCTTAAAGGAACCTTCTATGTTAGTAGGAGTTTACACAACACAAATACC
 ATTGAATCAACCCCTGTTAAAGCAGAAGATACAAAATAATCACTGATAAAACACAA
 ACACAAAATGGTCAGGTTGGGAAAATAGTCAGGACAAACAAATACTCAAATACTAAT
 CAACAAGGACAACAGATAGCAACAGAGCAGGCACCTAACCCCTCAAATGTTAAT

SEQ ID NO. 8802**STRAIN H36B**

CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTT
 GTCTTAACGGATGGCAAACCGTAACCTGAATTTTAAAAACGCAA
 AGAAGATGAAGAAGAACAAAACGTATTACGAAAATTACGCTTAGATA
 AAAGAAGTAAATTAAATATTCTCTCCTAGAAGAACCTCAAATACTACT
 AAAATTAAAGAAGCTCATTTCCAAGATTTCAAGACCTAACGATTGAAAAA
 GAAACAGAAAAAGAAAAATAGTCACAGCTTAGCCAAAACTAATCGCA
 TTAGAATGCAACCTACTATTGTAGTAGAAGCAAAACAATAGTTAGTGG
 AAATCAGCATACACCTGATGATAATTGATAGAGAAAACGAAATTCAA
 AAAACGATTATTCTTTAAACATAAAAGCTTAAAGGTTAAAGGCTT
 CGTTAGCTGAGATGTTAAAGCTTAAAGGCTTAAAGGCTTAAAGGCTT
 TAGACCCCTGATTAAAGTGGAGATTCAAGGTGATAAGTTAGCTGATTCT
 AAAACGACACCTGACCTCTGCTGTAGATGACGATGGAAATAGTGT
 ATTGCAATTCAGTCAAGGATATTGATAGGAGTTACAGCTGAGTTACAA
 ATGGTACACAAAGCAGGATATTGATAGGAGTTACAGCTGAGTTACAA
 CTGTTAGCTGAGAGATGTAGGTTAAAGCAGCTCAGATGACTTATCA
 ATTCCCATAATTGCTGATGATAATTGATAGGAGTTACAGCTGAGTTACAA
 ATGGCACATACAAAGCAGGATATTGATAGGAGTTACAGCTGAGTTACAA
 CGTTAGCTGAGAGATGTAGGTTAAAGCAGCTGAGTTACAGCTGAGTTACAA
 ATTGCAATTCAGTCAAGGATATTGATAGGAGTTACAGCTGAGTTACAA
 ATGGTACACAAAGCAGGAGTTACAGCTGAGTTACAGCTGAGTTACAA
 CTGTTAGCTGAGAGATGTAGGTTAAAGCAGCTGAGTTACAGCTGAGTTACAA
 ATGGCACACCTGACCTCTGCTGTAGATGACGATGGAAATAGTGT
 TAGACCCCTGATTAAAGTGGAGATTCAAGGTGATAAGTTAGCTGATTCT
 AAAACGACACCTGACCTCTGCTGTAGATGACGATGGAAATAGTGT
 TAGAATACCAATTCTAAATTAAAGAAGACTCTTTTACAAACAA
 TTAAGAAGAACCTTAAAGGAACTTCTATGTTGATATGGAAGTGGGAGTT
 TACACAACAAACAAATACCTGATAAAACACAAACAAATGGTCAGGTTGGGG
 AAAATAGTCAGGACAAACAAATACTCAAATACTAATCAACAAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCCCTCAAATGTTAAT

SEQ ID NO. 8803**STRAIN 18RS21**

CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTT
 GTCTTAACGGATGGCAAACCGTAACCTGAATTTTAAAAACGCAA
 AGAAGATGAAGAAGAACAAAACGTATTACGAAAATTACGCTTAGATA
 AAAGAAGTAAATTAAATATTCTCTCCTAGAAGAACCTCAAATACTACT
 AAAATTAAAGAAGCTCATTTCCAAGATTTCAAGACCTAACGATTGAAAAA
 GAAACAGAAAAAGAAAAATAGTCACAGCTTAGCCAAAACTAATCGCA
 TTAGAATGCAACCTATATTGTAGTAGCATTCCTAGTCATTAGTTTCC
 GTTTCTCTACTAACTCTTTAGTAGAAGCAAAACAAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATAATTGATAGGAGAAAACGAAATTCAA
 AAAACGATTATTCTTTAAACATAAAAGCTTAAAGGCTTAAAGGCTT
 CGTTAGCTGAGAGATGTAGGTTAAAGCAGCTCAGATGACTTATCA
 ATTCCCATAATTGCTGATGATAATTGATAGGAGTTACAGCTGAGTTACAA
 ATGGCACATACAAAGCAGGATATTGATAGGAGTTACAGCTGAGTTACAA
 CGTTAGCTGAGAGATGTAGGTTAAAGCAGCTGAGTTACAGCTGAGTTACAA
 ATTGCAATTCAGTCAAGGATATTGATAGGAGTTACAGCTGAGTTACAA
 ATGGTACACAAAGCAGGAGTTACAGCTGAGTTACAGCTGAGTTACAA
 CTGTTAGCTGAGAGATGTAGGTTAAAGCAGCTGAGTTACAGCTGAGTTACAA
 ATGGCACACCTGACCTCTGCTGTAGATGACGATGGAAATAGTGT
 TAGAATACCAATTCTAAATTAAAGAAGACTCTTTTACAAACAA
 TTAAGAAGAACCTTAAAGGAACTTCTATGTTGATATGGAAGTGGGAGTT
 TACACAACAAACAAATACCTGATAAAACACAAACAAATGGTCAGGTTGGGG
 AAAATAGTCAGGACAAACAAATACTCAAATACTAATCAACAAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCCCTCAAATGTTAAT

SEQ ID NO. 8804**STRAIN M732**

CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAG
 TTGCTTAACGGATGGCAAACCGTAACCTGAAATTTTAAAAACG
 AAAGAAGATGAAGAAGAACAAAACGTATTACGAAAATTACGCTTAGA
 TAAAAGAAGTAAATTAAATATTCTCTCTGAAAGAACCTCAAATACTA
 CTAAAATTAAAGAAGCTCATTTCCAAGATTTCAAAACCTAACGATTGAA
 AGAAACAGAAAAAGAAAAATAGTCACAGCTTAGCCAAAACTAATCG
 CATTAGAATGCAACCTATATTGTAGTAGCATTCCTAGTCATTAGTT

Table 88: Comparative Sequences relating to SAG0477

CGTTTCTACTAACCTTTAGTAAGGAAAAACATAACAGTTAGT
 GGAATCAGCATACACCTGATGATAATTGATAGAAAAACGAATATTCA
 AAAAACGATTATTCTTTAATTAAACATAAGCTATTGAAC
 AACGTTAGCTGAGAAGATGTATGGTAAACAGCTAGATGACTTAT
 CAATTCCAACTAACCTGATTCAGTCAAGGAAATTAAGATTATTGC
 ATATGCACTACAAAGCAAGGATATCAGCTCTGAAACTGGAAAAA
 AGGCTGATCTGTAATAGTCAGAGCTACAAAGCACTCTTAAACATT
 AACCTTGATAAGGAAGATAGTATTAGCTTAAAGATTTAAAGGC
 TTAGACCTGATAAGGAGATTAGTGTAGATAAGTTAGCTGATT
 CTAAAACGCCACCTGACCTCTGCTTAGATATGATGGAAATAGT
 ATAGAATACCAATTCTAAATTAAAGAAAGACTCCCTTTACAAACA
 AATTAAGAAGAACCTTAAGGAACTCTATGTTGATAATGGAAGTGGAG
 TTACACAACAAAGCTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 ACAAAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAGGTTGC
 GAAAAATAGTCAGGACAAACAAATAACTCAAATCTAATCAACAGGAC
 AACAGATAGCAACAGCAGGCCACCCACCTCAAAATGTTAAT

SEQ ID NO. 8805**STRAIN COH1**

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAGTT
 GTCTTAACGGATGGCAAAGCTAACCTGAAATTAAACCGCAA
 AGAAGATGAAGAACAAACGTTAACGAAAAATTACGTTAGATA
 AAAGAAGTAAATTAAATATTCTCTGAGAACCTCAAATACTACT
 AAAATTAGAAGCTCAATTCTCAAAGATTCAAAACCTAAAGATTGAAA
 GAAACGAAAAAGAAAAATAGTCACAGCTTAGCCTAAACTAATCGCA
 TTGAACTGCACCTATATTGTTAGTCAGTCTAGTCATTAGTTCC
 GTTTCTCTACTAACCTTTAGTAAGCAAAAAAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATAATTGATAGAAAAACGAATATTCAA
 AAAACGATTATTCTTTAATTAAACATAAAAGCTATTGAACAA
 CGTTAGCTGAGAAGATGTATGGTAAACAGCTCAGATGACTTATCA
 ATTCCCAATAAGTTCATATCAAGTTCAAGGAAATAAGATTATTGAT
 ATGCACATACAAAGCAAGGATATCAGCTCTGGAAACTGGAAAAAAG
 GCTGATCTGTTAAAGTCAGAGCTACCAAGGCACITCTTAAACATTAA
 CCTTGATAAGGAAGATAGTATTAGCTTAAAGATTAAAGCTT
 TAGACCTGATTAAAGTGAAGATTCAAGGTGATAAGTTAGCTGATTCT
 AAAACGACACCTGACCTCTGTTAGATATGCTGATGGAAATAGTAT
 TAGAATACCATTTCTAAATTAAAGGAAGACTTCTTTTAAACACAAA
 TTAGAAGAACCTTAAGGAACCTCTATTGTTGATAATGGAAGTGGAGTT
 TACACAACAAAGCTACTATTGAATCAACCCCTGTGAAAGCGGAAGATAC
 AAAAATAAATCAACTGATAAAACACAAACAAAATGGTCAGGTTGCGG
 AAAATAGTCAGGACAAACAAATAACTCAAATACTAATCAACAGGACAA
 CAGATAGCAACAGCAGGCCACCCACCTCAAAATGTTAAT

SEQ ID NO. 8806**STRAIN M781**

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAG
 TTGCTTAACGGATGGCAAAGCTAACCTGAAATTAAACCGC
 AAAGAAGATGAAGAACAAACGTTAACGAAAAATTACGTTAGA
 TAAAAGAAGTAAATTAAATATTCTCTGAGAACACCTCAAATACTA
 CTAAAATTAGAAGCTCAATTCTCAAAGATTCAAAACCTAAAGATTGAA
 AGAAAACAGAAAAAGAAAAATAGTCACAGCTTAGCCTAAACTAATCG
 CATTAGAACTGCACCTATTTGTTAGTCAGTCTAGTCATTAGTT
 CGTTTCTCTACTAACCTTTAGTAAGCAAAAACAAATAACAGTTAGT
 GAAAATCAGCATACACCTGATGATAATTGATAGAAAAACGAATATTCA
 AAAAACGATTATTCTTTTAATTAAACATAAAAGCTTATTGAAAC
 AACCTGAGACAGGATATCAGCTCTGGAAACTGGAAAA
 AGCTGATCTGTTAAAGTTCAGAGCTACCAAGCACTTAAACAA
 AACCTGATAAGGAAGATAGTATTAGCTTAAAGATTAAAGGCT
 TTAGACCTGTTAAATAAGTGAAGATTAGCTGATAAGTTAGCTGATT
 CTAAAACGACACCTGACCTCTGCTGTTAGATATGCTGATGGAAATAGT
 ATTGAATACCATTTATCTAAATTAAAGGAAGACTTCTTTTACAAACA
 AATTAAGAAGAACCTTAAGGAACCTCTATTGTTGATAATGGAAGTGGAG
 TTACACAACAAAGCTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
 ACAAAAAATAAATCAACTGATAAAACACAAACAAAATGGTCAGGTTG
 GAAAAATAGTCAGGACAAACAAATACTCAAATACTAATCAACAGGAC
 AACAGATAGCAACAGCAGGCCACCCACCTCAAAATGTTAAT

SEQ ID NO. 8807**STRAIN CJB110**

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAAG
 TTGCTTAACGGATGGCAAAGCTAACCTGAAATTAAACCGC
 AAAGAAGATGAAGAACAAACGTTAACGAAAAATTACGTTAGA
 TAAAAGAAGTAAATTAAATATTCTCTGAGAACACCTCAAATACTA
 CTAAAATTAGAAGCTCAATTCTCAAAGATTCAAAACCTAAAGATTGAA
 AGAAAACAGAAAAAGAAAAATAGTCACAGCTTAGCCTAAACTAATCG
 CATTAGAACTGCACCTATTTGTTAGTCAGTCTAGTCATTAGTT
 CGTTTCTCTACTAACCTTTAGTAAGCAAAAACAAATAACAGTTAGT
 GAAAATCAGCATACACCTGATGATAATTGATAGAAAAACGAATATTCA
 AAAAACGATTATTCTTTCTTAATTAAACATAAAAGCTTATTGAAAC
 AACGTTAGCTGAGAAGATGTATGGTAAACAGCTCAGATGACTTAT
 CAATTCCCAATAAGTTCATATTCAAGTTCAAGAAAATAAGATTATTG

Table 88: Comparative Sequences relating to SAG0477

ATATGCACATAAAAGCAAGGATATCAGCCTGTCTGGAAACTGGAAAAA
 AGCTGATCCCTGAAATAGTCAGAGCTACCAAAGCACTTCTAACAAATT
 AACCTTGATAAGGAAGATAGTATTAAGCTTAAATTAAGATTTAAAGGC
 TTAGACCCGTATTAAACTGAGATTCAGGTGATAAGTTAGCTGATT
 CTTAAAACGACACCTGACCTCTGCTTAGATGATGATGAAATAGT
 ATTAGAACCTTAAATTAAGGAAGACTTCTTTACAAACA
 AATTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAAACAAGTACTATTGAATCAACCCCTGTGAAGCGGAAGAT
 ACAAAACAAACTAAGTACTATTGAATCAACCCCTGTGAAGCGGAAGAT
 GAAAATAGTCAGGACAAACAAATACTCAAATACTAATCAACAGGAC
 AACAGATAGCAACAGAGCAGGCACCCACCCCTCAAATGTTAAT

SEQ ID NO. 8808**STRAIN 1169NT**

CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGT
 TGCTTAAACGGAAATGGCAAAGCGTAACCTGAAATTAAAAACGCA
 AAGAAGATGAAAGAACAAAAGCTTAAACGAAAATTACGCTTAGAT
 AAAAGAAGTAAATTAAATATTCTCTCTGAAGAACCTCAAATACTAC
 TAAAATTAAGAAGCTTCATTTCACAAAGATTCAAACCTAACGATTGAA
 AGAACACGAAAAAAAGAAAAAATAGTCACAGCTTAGCCAAAACAAATCGC
 ATTAGAACCTGCACTTATTTAGTAGCTGATTCTAGTCATTAGTTG
 CGTTTCTCTACTAACTCCCTTGTAGTCAGGAAACAAATAACAGTTAGTG
 GAAATCAGCACACCTGATGATATTGTTGATAGGAAAAGCAAAATTCAA
 AAAAACGATTATTCTCTTCTTAAATTAACATAAGCTTATTGAA
 ACGTTTAGCTGAGAAGATGTTGGGAAAAACAGCTCAGATGACTTATC
 ATTAGCTCAAGGAACTTCAAGGAACTTCAAGGAACTTCAAGGAACTTCA
 ATTTCCAATTAAGCTTCAAGGAACTTCAAGGAACTTCAAGGAACTTCA
 TTAGAACCTGACCTTATTTGTTAGTAGCTGATTCTAGTCATTAGTTG
 GTTTCTCTACTAACTCCCTTGTAGTCAGGAAACAAATAACAGTTAGTG
 AAATCAGCATACACCTGATGATATTGTTGATAGGAAAACGAAATATTCAA
 AAAACGATTATTCTCTTAAATTAACATAAGCTTATTGAA
 CGTTAGCTGAGAAGATGTTGGGAAAAACAGCTCAGATGACTTATC
 ATTCCCAATAAGCTTCAAGGAACTTCAAGGAACTTCAAGGAACTTCA
 ATGACACATACAAAGCAAGGATATCAACCTGCTTGGGAAAACGAAAG
 GCTGATCTGTAAATAGTCAGAGCTACCAAGCAGCTTCAACAAATTA
 CCTGATAAGGAAGATAGTATTAAGCTTAAATTAAGATTTAAAGGCTT
 TAGACCTGATTTAAATAACTGAGATTTCAGGTGATAAGTTAGCTGATTCT
 AAAACGACACCTGACCTCTGCTTGTAGATATGACGATGGAAATAGTAT
 TAGAATACCACTTATCTAAATTAAAGAAAGACTTCTTTTACAAACAA
 TTAGAAGAAGAACCTTAAGGAACCTTCAATTGTTGATATGGAAGTGGGAGTT
 TACACAAACAACAAATACCTGAAATCAACCCCTGTAAAGCAGAAGATAC
 AAAAATAAAATCAACTGATAAAACACAAACAAATGGTCAGGTTGCCG
 AAAATAGTCAGGACAAACAAATACTCAAATACTAATCAACAAAGGACAA
 ACAACAGATAGCAACGGAGCAGGCACCCACCCCTCAAATGTTAAT

SEQ ID NO. 8809**STRAIN JM9130013**

CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGT
 GTCTTAAACGGAAATGGCAAAGCGTAACCTGAAATTAAAAACGCA
 AGAACATGAAAGAACAAAACGTTAAACGAAAATTACGCTTAGATA
 AAAAGAAGTAAATTAAATATTCTCTCTGAAGAACCTCAAATACTAC
 AAAATTAAAGAAGCTTCATTTCACAAAGATTCAAGACCTAACGATTGAAA
 GAAACAGAAAAAAAGAAAAAATAGTCACACGCTTAGCCAAAACAAATCGCA
 TTAGAACCTGACCTTATTTGTTAGTAGCTGATTCTAGTCATTAGTTG
 GTTTCTCTACTAACTCCCTTGTAGTCAGGAAACAAATAACAGTTAGTG
 AAATCAGCATACACCTGATGATATTGTTGATAGGAAAACGAAATATTCAA
 AAAACGATTATTCTCTTAAATTAACATAAGCTTATTGAA
 CGTTAGCTGAGAAGATGTTGGGAAAAACAGCTCAGATGACTTATC
 ATTCCCAATAAGCTTCAAGGAACTTCAAGGAACTTCAAGGAACTTCA
 ATGACACATACAAAGCAAGGATATCAACCTGCTTGGGAAAACGAAAG
 GCTGATCTGTAAATAGTCAGAGCTACCAAGCAGCTTCAACAAATTA
 CCTGATAAGGAAGATAGTATTAAGCTTAAATTAAGATTTAAAGGCTT
 TAGACCTGATTTAAATAACTGAGATTTCAGGTGATAAGTTAGCTGATTCT
 AAAACGACACCTGACCTCTGCTTGTAGATATGACGATGGAAATAGTAT
 TAGAATACCACTTATCTAAATTAAAGAAAGACTTCTTTTACAAACAA
 TTAGAAGAAGAACCTTAAGGAACCTTCAATTGTTGATATGGAAGTGGGAGTT
 TACACAAACAACAAATACCTGAAATCAACCCCTGTAAAGCAGAAGATAC
 AAAAATAAAATCAACTGATAAAACACAAACAAATGGTCAGGTTGCCG
 AAAATAGTCAGGACAAACAAATACTCAAATACTAATCAACAAAGGACAA
 CAGATAGCAACAGAGCAGGCACCTAACCCCTCAAATGTTAAT

SEQ ID NO. 8810**STRAIN A909**

CCTAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTGTG
 TTAACGGAAATGGCAAAGCGTAACCTGAAATTAAAGAACGCAAAGA
 AGTAGAAGAAGAAACAAACGTTAAACGAAAATTACGCTTAGATAAAA
 GAAGTAAATTAAATATTCTCTCTGAAGAACCTCAAATACTACAAA
 ATTAAAGAAGCTTCATTTCACAAAGATTCAAGACCTAACGATTGAAAAGAA
 ACAGAAAAAAAGAAAAAATAGTCACAGCTTAGCCAAAACAAATCGCATTA
 GAACTGACCTTATTTGTTAGTAGCTGATTCTAGTCATTAGTTAGTTCCGT
 TTCTACTAACTCCCTTGTAGTCAGGAAACAAATAACAGTTAGTGAAA
 TCAGCATACACCTGATGATATTGTTAGAGGAAAACGAAATATTCAA
 ACGATTATTCTCTTAAATTTAAACATAAGCTTATGAAACAAACGTT
 TTAGCTGAGAAGATGTTGAGGAAAACAGCTCAGATGACTTATCAATT
 TCCCAATAAGCTTCAATTCAAGTCAAGGAAAATAAGATTATTGCTATG
 CACATACAAAGCAAGGATATCAACCTGCTTGGAAACTGGAAAAAGGCT
 GATCTGTAAATAGTCAGAGCTACCAAAAGCAGCTTCAACAAATTAAACCT
 TGATAAGGAAGATAGTATTAAGCTTAAATTAAGATTTAAAGGCTT
 ACCCTGATTTAAATAGTCAGGATTCAGGTGATAAGTTAGCTGATTCTAA
 ACGACACCTGACCTCTGCTGTTAGATATGCAAGATGGAAGATAGTATTAS

Table 88: Comparative Sequences relating to SAG0477

AATACCATTATCTAAATTAAAGAAAGACTTCCITTTACAAACAAATTAA
 AGAAGAACCTTAAGGAACCTCTATTGTTGATATGGAAAGTGGGAGTTTAC
 ACAACAACAAATACCATGAAATCAACCCCTGTTAAAGCAGAAGATAACAA
 AAATAAATCAACTGATAAAACAAACAAACAAACAAACAGTCAGGTTGCCGAAA
 ATAGTCAGGACAAACAAATACTCAAATCAATCAACAGGACAAACAG
 ATAGCAACAGAGCAGGCACCTAACCCCTCAAAATGTTAAT

SEQ ID NO. 8811

STRAIN 090

TAAGAAGAAATCAGATACCCCAGAAAAAGAAGAAGTTGTCTTAACCGAAT
 GGCAAAAGCGTAACCTTGAATTAAAAGCAGAAAGAAGATGAAGAA
 GAACAAAAACGTTAAGCAGAAACCTAAAGCTTAGATAAAAAGAAGTaaaTT
 AAATATTCTCTCTGAAGAACCTCAAATTAAGCTACTAAATTAAGAAGC
 TTCACTTTCTCAAAGATTCTAAACCTAAGATGAAAAGAACAGAAAAAA
 GAAAAAAATAGTCACACGCTTAGCCAAACTAAATCGCATTAGAACTGCACC
 TATATTGTTAGCTAGCATTTCTGTTAGCTTCCGTTTCTACTAA
 CTCTTTTCTAGAAGAAAACAAATAACAGTTAGTGGAAATCAGCATACA
 CCTGATGATTTGATAGAAAAACGAATTACAAAACGATTATTCAAAAAACGATTATT
 CTTTCTTAAATTTAAACATAAGCTTATGAAACAACGTTAGCTGCAAG
 AAGATGTTATGGTAAACAGCTCAGATGACTTATCAATTCTCAAATAG
 TTTCATATTCAAGTTCAAGAAAATAAGATTATTGCAATATGCACATACAA
 GCAAGGATATCAGCCCTGCTGGAAACTGGAAAAAGGCTGATCTGTAA
 ATAGTCAGAGCTACCAAAAGCACTTCAACAAATTAAACCTTGATAAGGA
 GATAGTATTAAAGCTTAAATTAAGGCTTATGACCTGATT
 AATAAGTGAGATTCAGGTGATAAGTTAGCTGATTCTAAACGACACCTG
 ACCTCTGCTGTAGATGATGATGAAATAGTATTGAATACCCATTA
 TCTAAATTAAAGAAAAGACTTCTTTTACAAACAAATTAAAGAACACT
 TAAGGAACCTCTATTGTTGATATGAAAGTGGGAGTTACACAAACAA
 GTACTATTGAAATCAACCCCTGTAAAGCAGAAGATAACAAAAAAATAATCA
 ACTGATAAAACAAACAAATAATGTCAGGTTGCGGAAATAGTCAGG
 ACAACAAATAACTCAAATCAACAAAGGACAACAGATAGCAACAG
 AGCAGGCACCCACCCCTCAAAATGTTAAT

PRETTY of: /biotmp/msa24691.2(*) August 5, 2002 05:14 ..

msa252409.2{85_090.con}	1	--TAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACCGGA	50
msa252409.2{85_CJB110}		CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACCGGA	
msa252409.2{85_COH1}		CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACCGGA	
msa252409.2{85_M732}		CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACCGGA	
msa252409.2{85_M781}		CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACCGGA	
msa252409.2{85_18RS21}		CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACCGGA	
msa252409.2{85_2603}		CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACCGGA	
msa252409.2{85_A909}		CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACCGGA	
msa252409.2{85_H36B}		CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACCGGA	
msa252409.2{85_JM9130013}		CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACCGGA	
msa252409.2{85_1169NT}		CCTAAGAAGA AATCAGATAC CCCAGAAAAA GAAGAAGTTG TCTTAACCGGA	
Consensus		*****	
msa252409.2{85_090.con}	51	ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAA GAAGATGAAG	100
msa252409.2{85_CJB110}		ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAA GAAGATGAAG	
msa252409.2{85_COH1}		ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAA GAAGATGAAG	
msa252409.2{85_M732}		ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAA GAAGATGAAG	
msa252409.2{85_M781}		ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAA GAAGATGAAG	
msa252409.2{85_18RS21}		ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAA GAAGATGAAG	
msa252409.2{85_2603}		ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAA GAAGATGAAG	
msa252409.2{85_A909}		ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAA GAAGATGAAG	
msa252409.2{85_H36B}		ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAA GAAGATGAAG	
msa252409.2{85_JM9130013}		ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAA GAAGATGAAG	
msa252409.2{85_1169NT}		ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAA GAAGATGAAG	
Consensus		*****	
msa252409.2{85_090.con}	101	AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	150
msa252409.2{85_CJB110}		AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_COH1}		AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_M732}		AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_M781}		AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_18RS21}		AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_2603}		AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_A909}		AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_H36B}		AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_JM9130013}		AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
msa252409.2{85_1169NT}		AAGAACAAAA ACGTATTAAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA	
Consensus		*****	
msa252409.2{85_090.con}	151	TTAAATATTT CTTCTCCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA	200
msa252409.2{85_CJB110}		TTAAATATTT CTTCTCCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA	
msa252409.2{85_COH1}		TTAAATATTT CTTCTCCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA	
msa252409.2{85_M732}		TTAAATATTT CTTCTCCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA	

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_M781}	TTAAATATTT	CTTCCTCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_18RS21}	TTAAATATTT	CTTCTCTCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_2603}	TTAAATATTT	CTTCTCTCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_A909}	TTAAATATTT	CTTCTCTCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_H36B}	TTAAATATTT	CTTCTCTCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_JM9130013}	TTAAATATTT	CTTCTCTCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_1169NT}	TTAAATATTT	CTTCTCTCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
Consensus	*****	*****	*****	*****	*****
	201				250
msa252409.2{85_090.con_}	GCTTCATTTT	CCAAAGATT	CAAAACCTAA	GATTGAAAAAG	AAACAGAAAA
msa252409.2{85_CJB110}	GCTTCATTTT	CCAAAGATT	CAAAACCTAA	GATTGAAAAAG	AAACAGAAAA
msa252409.2{85_COH1}	GCTTCATTTT	CCAAAGATT	CAAAACCTAA	GATTGAAAAAG	AAACAGAAAA
msa252409.2{85_M732}	GCTTCATTTT	CCAAAGATT	CAAAACCTAA	GATTGAAAAAG	AAACAGAAAA
msa252409.2{85_M781}	GCTTCATTTT	CCAAAGATT	CAAAACCTAA	GATTGAAAAAG	AAACAGAAAA
msa252409.2{85_18RS21}	GCTTCATTTT	CCAAAGATT	CAAgACCTAA	GATTGAAAAAG	AAACAGAAAA
msa252409.2{85_2603}	GCTTCATTTT	CCAAAGATT	CAAgACCTAA	GATTGAAAAAG	AAACAGAAAA
msa252409.2{85_A909}	GCTTCATTTT	CCAAAGATT	CAAgACCTAA	GATTGAAAAAG	AAACAGAAAA
msa252409.2{85_H36B}	GCTTCATTTT	CCAAAGATT	CAAgACCTAA	GATTGAAAAAG	AAACAGAAAA
msa252409.2{85_JM9130013}	GCTTCATTTT	CCAAAGATT	CAAgACCTAA	GATTGAAAAAG	AAACAGAAAA
msa252409.2{85_1169NT}	GCTTCATTTT	CCAAAGATT	CAAAACCTAA	GATTGAAAAAG	AAACAGAAAA
Consensus	*****	*****	**-	*****	*****
	251				300
msa252409.2{85_090.con_}	AAGAAAAAAAT	AGTCAACAGC	TTAGCCAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_CJB110}	AAGAAAAAAAT	AGTCAACAGC	TTAGCCAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_COH1}	AAGAAAAAAAT	AGTCAACAGC	TTAGCCAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_M732}	AAGAAAAAAAT	AGTCAACAGC	TTAGCCAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_M781}	AAGAAAAAAAT	AGTCAACAGC	TTAGCCAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_18RS21}	AAGAAAAAAAT	AGTCAACAGC	TTAGCCAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_2603}	AAGAAAAAAAT	AGTCAACAGC	TTAGCCAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_A909}	AAGAAAAAAAT	AGTCAACAGC	TTAGCCAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_H36B}	AAGAAAAAAAT	AGTCAACAGC	TTAGCCAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_JM9130013}	AAGAAAAAAAT	AGTCAACAGC	TTAGCCAAA	CTAATCGCAT	TAGAACTGCA
msa252409.2{85_1169NT}	AAGAAAAAAAT	AGTCAACAGC	TTAGCCAAA	CTAATCGCAT	TAGAACTGCA
Consensus	*****	*****	*****	*****	*****
	301				350
msa252409.2{85_090.con_}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTCCG	TTTTCTACT
msa252409.2{85_CJB110}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTCCG	TTTTCTACT
msa252409.2{85_COH1}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTCCG	TTTTCTACT
msa252409.2{85_M732}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTCCG	TTTTCTACT
msa252409.2{85_M781}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTCCG	TTTTCTACT
msa252409.2{85_18RS21}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTCCG	TTTTCTACT
msa252409.2{85_2603}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTCCG	TTTTCTACT
msa252409.2{85_A909}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTCCG	TTTTCTACT
msa252409.2{85_H36B}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTCCG	TTTTCTACT
msa252409.2{85_JM9130013}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTCCG	TTTTCTACT
msa252409.2{85_1169NT}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTCCG	TTTTCTACT
Consensus	*****	*****	*****	*****	*****
	351				400
msa252409.2{85_090.con_}	AACTCCTTTT	AGTAAGCAA	AAACAATAAC	AGTTAGTGG	AATCAGCATA
msa252409.2{85_CJB110}	AACTCCTTTT	AGTAAGCAA	AAACAATAAC	AGTTAGTGG	AATCAGCATA
msa252409.2{85_COH1}	AACTCCTTTT	AGTAAGCAA	AAACAATAAC	AGTTAGTGG	AATCAGCATA
msa252409.2{85_M732}	AACTCCTTTT	AGTAAGCAA	AAACAATAAC	AGTTAGTGG	AATCAGCATA
msa252409.2{85_M781}	AACTCCTTTT	AGTAAGCAA	AAACAATAAC	AGTTAGTGG	AATCAGCATA
msa252409.2{85_18RS21}	AACTCCTTTT	AGTAAGCAA	AAACAATAAC	AGTTAGTGG	AATCAGCATA
msa252409.2{85_2603}	AACTCCTTTT	AGTAAGCAA	AAACAATAAC	AGTTAGTGG	AATCAGCATA
msa252409.2{85_A909}	AACTCCTTTT	AGTAAGCAA	AAACAATAAC	AGTTAGTGG	AATCAGCATA
msa252409.2{85_H36B}	AACTCCTTTT	AGTAAGCAA	AAACAATAAC	AGTTAGTGG	AATCAGCATA
msa252409.2{85_JM9130013}	AACTCCTTTT	AGTAAGCAA	AAACAATAAC	AGTTAGTGG	AATCAGCATA
msa252409.2{85_1169NT}	AACTCCTTTT	AGTAAGCAA	AAACAATAAC	AGTTAGTGG	AATCAGCATA
Consensus	*****	*****	*****	*****	*****
	401				450
msa252409.2{85_090.con_}	CACCTGATGA	TATTTTGATA	GaaaaaacgA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_CJB110}	CACCTGATGA	TATTTTGATA	GaaaaaacgA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_COH1}	CACCTGATGA	TATTTTGATA	GaaaaaacgA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_M732}	CACCTGATGA	TATTTTGATA	GaaaaaacgA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_M781}	CACCTGATGA	TATTTTGATA	GaaaaaacgA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_18RS21}	CACCTGATGA	TATTTTGATA	GAGaaaaacgA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_2603}	CACCTGATGA	TATTTTGATA	GAGaaaaacgA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_A909}	CACCTGATGA	TATTTTGATA	GAGaaaaacgA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_H36B}	CACCTGATGA	TATTTTGATA	GAGaaaaacgA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_JM9130013}	CACCTGATGA	TATTTTGATA	GAGaaaaacgA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_1169NT}	CACCTGATGA	TATTTTGATA	GAGaaaaacgA	ATATTCAAAA	AAACGATTAT
Consensus	*****	*****	**-	*****	*****
	451				500
msa252409.2{85_090.con_}	TTCTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_CJB110}	TTCTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_COH1}	TTCTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_M732}	TTCTTTTCIT	TAATTTTAA	ACATAAAAGCT	ATTGAACAAC	GTTTAGCTGC	
msa252409.2{85_M781}	TTCTTTTCIT	TAATTTTAA	ACATAAAAGCT	ATTGAACAAC	GTTTAGCTGC	
msa252409.2{85_18RS21}	TTCTTTTCIT	TAATTTTAA	ACATAAAAGCT	ATTGAACAAC	GTTTAGCTGC	
msa252409.2{85_M732}	TTCTTTTCIT	TAATTTTAA	ACATAAAAGCT	ATTGAACAAC	GTTTAGCTGC	
msa252409.2{85_A909}	TTCTTTTCIT	TAATTTTAA	ACATAAAAGCT	ATTGAACAAC	GTTTAGCTGC	
msa252409.2{85_H36B}	TTCTTTTCIT	TAATTTTAA	ACATAAAAGCT	ATTGAACAAC	GTTTAGCTGC	
msa252409.2{85_JM9130013}	TTCTTTTCIT	TAATTTTAA	ACATAAAAGCT	ATTGAACAAC	GTTTAGCTGC	
msa252409.2{85_1169NT}	TTCTTTTCIT	TAATTTTAA	ACATAAAAGCT	ATTGAACAAC	GTTTAGCTGC	
Consensus	*****	*****	*****	*****	*****	
						501
msa252409.2{85_090.con_}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAatA	550
msa252409.2{85_CJB110}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAatA	
msa252409.2{85_COH1}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAatA	
msa252409.2{85_M732}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAatA	
msa252409.2{85_M781}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAatA	
msa252409.2{85_18RS21}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAatA	
msa252409.2{85_M732}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAatA	
msa252409.2{85_A909}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAatA	
msa252409.2{85_H36B}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAatA	
msa252409.2{85_JM9130013}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAatA	
msa252409.2{85_1169NT}	AGAAGATGTA	TGGGTAAAAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAAcA	
Consensus	*****	*****	*****	*****	*****	*****
						551
msa252409.2{85_090.con_}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCAAA	TGCACATACAA	600
msa252409.2{85_CJB110}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCAAA	TGCACATACAA	
msa252409.2{85_COH1}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCAAA	TGCACATACAA	
msa252409.2{85_M732}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCAAA	TGCACATACAA	
msa252409.2{85_M781}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCAAA	TGCACATACAA	
msa252409.2{85_18RS21}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCAAA	TGCACATACAA	
msa252409.2{85_M732}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCAAA	TGCACATACAA	
msa252409.2{85_A909}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCAAA	TGCACATACAA	
msa252409.2{85_H36B}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCAAA	TGCACATACAA	
msa252409.2{85_JM9130013}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCAAA	TGCACATACAA	
msa252409.2{85_1169NT}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCAAA	TGCACATACAA	
Consensus	*****	*****	*****	*****	*****	*****
						601
msa252409.2{85_090.con_}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAAGG	CTGATCCTGT	650
msa252409.2{85_CJB110}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAAGG	CTGATCCTGT	
msa252409.2{85_COH1}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAAGG	CTGATCCTGT	
msa252409.2{85_M732}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAAGG	CTGATCCTGT	
msa252409.2{85_M781}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAAGG	CTGATCCTGT	
msa252409.2{85_18RS21}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAAGG	CTGATCCTGT	
msa252409.2{85_M732}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAAGG	CTGATCCTGT	
msa252409.2{85_A909}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAAGG	CTGATCCTGT	
msa252409.2{85_H36B}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAAGG	CTGATCCTGT	
msa252409.2{85_JM9130013}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAAGG	CTGATCCTGT	
msa252409.2{85_1169NT}	AAGCAAGGAT	ATCAGCCTGT	CTTGGAAACT	GGAAAAAAAGG	CTGATCCTGT	
Consensus	*****	*****	*****	*****	*****	*****
						651
msa252409.2{85_090.con_}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAAGG	700
msa252409.2{85_CJB110}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAAGG	
msa252409.2{85_COH1}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAAGG	
msa252409.2{85_M732}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAAGG	
msa252409.2{85_M781}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAAGG	
msa252409.2{85_18RS21}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAAGG	
msa252409.2{85_M732}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAAGG	
msa252409.2{85_A909}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAAGG	
msa252409.2{85_H36B}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAAGG	
msa252409.2{85_JM9130013}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAAGG	
msa252409.2{85_1169NT}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAAGG	
Consensus	*****	*****	*****	*****	*****	*****
						701
msa252409.2{85_090.con_}	AAGATAGTAT	TAAGCTATTA	ATTTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	750
msa252409.2{85_CJB110}	AAGATAGTAT	TAAGCTATTA	ATTTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	
msa252409.2{85_COH1}	AAGATAGTAT	TAAGCTATTA	ATTTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	
msa252409.2{85_M732}	AAGATAGTAT	TAAGCTATTA	ATTTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	
msa252409.2{85_M781}	AAGATAGTAT	TAAGCTATTA	ATTTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	
msa252409.2{85_18RS21}	AAGATAGTAT	TAAGCTATTA	ATTTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	
msa252409.2{85_M732}	AAGATAGTAT	TAAGCTATTA	ATTTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	
msa252409.2{85_A909}	AAGATAGTAT	TAAGCTATTA	ATTTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	
msa252409.2{85_H36B}	AAGATAGTAT	TAAGCTATTA	ATTTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	
msa252409.2{85_JM9130013}	AAGATAGTAT	TAAGCTATTA	ATTTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	
msa252409.2{85_1169NT}	AAGATAGTAT	TAAGCTATTA	ATTTAAAGATT	TAAAGGCTTT	AGACCCCTGAT	
Consensus	*****	*****	*****	*****	*****	*****
						751
msa252409.2{85_090.con_}	TTAATAAGTG	AGATTCAAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC	800
msa252409.2{85_CJB110}	TTAATAAGTG	AGATTCAAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC	

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_COH1}	TTAATAAAGTG AGATTCAAGGT	GATAAGTTTA GCTGATTCTA AAACGACACC		
msa252409.2{85_M732}	TTAATAAAGTG AGATTCAAGGT	GATAAGTTTA GCTGATTCTA AAACGACACC		
msa252409.2{85_M781}	TTAATAAAGTG AGATTCAAGGT	GATAAGTTTA GCTGATTCTA AAACGACACC		
msa252409.2{85_18RS21}	TTAATAAAGTG AGATTCAAGGT	GATAAGTTTA GCTGATTCTA AAACGACACC		
msa252409.2{85_2603}	TTAATAAAGTG AGATTCAAGGT	GATAAGTTTA GCTGATTCTA AAACGACACC		
msa252409.2{85_A909}	TTAATAAAGTG AGATTCAAGGT	GATAAGTTTA GCTGATTCTA AAACGACACC		
msa252409.2{85_H36B}	TTAATAAAGTG AGATTCAAGGT	GATAAGTTTA GCTGATTCTA AAACGACACC		
msa252409.2{85_JM9130013}	TTAATAAAGTG AGATTCAAGGT	GATAAGTTTA GCTGATTCTA AAACGACACC		
msa252409.2{85_1169NT}	TTAATAAAGTG AGATTCAAGGT	GATAAGTTTA GCTGATTCTA AAACGACACC		
Consensus	*****	*****	*****	*****
	801		850	
msa252409.2{85_090.con_}	TGACCTCCCTG CTGTTAGATA	TGCATGATGG AAATAGTATT AgAATACCAT		
msa252409.2{85_CJB110}	TGACCTCCCTG CTGTTAGATA	TGCATGATGG AAATAGTATT AgAATACCAT		
msa252409.2{85_COH1}	TGACCTCCCTG CTGTTAGATA	TGCATGATGG AAATAGTATT AgAATACCAT		
msa252409.2{85_M732}	TGACCTCCCTG CTGTTAGATA	TGCATGATGG AAATAGTATT AgAATACCAT		
msa252409.2{85_M781}	TGACCTCCCTG CTGTTAGATA	TGCATGATGG AAATAGTATT AgAATACCAT		
msa252409.2{85_18RS21}	TGACCTCCCTG CTGTTAGATA	TGCACGATGG AAATAGTATT AgAATACCAT		
msa252409.2{85_2603}	TGACCTCCCTG CTGTTAGATA	TGCACGATGG AAATAGTATT AgAATACCAT		
msa252409.2{85_A909}	TGACCTCCCTG CTGTTAGATA	TGCACGATGG AAATAGTATT AgAATACCAT		
msa252409.2{85_H36B}	TGACCTCCCTG CTGTTAGATA	TGCACGATGG AAATAGTATT AgAATACCAT		
msa252409.2{85_JM9130013}	TGACCTCCCTG CTGTTAGATA	TGCACGATGG AAATAGTATT AgAATACCAT		
msa252409.2{85_1169NT}	TGACCTCCCTG CTGTTAGATA	TGCACGATGG AAATAGTATT AgAATACCAT		
Consensus	*****	*****	*****	*****
	851		900	
msa252409.2{85_090.con_}	TATCTAAATT TAAAGAAAAGA	CTTCCTTTTT ACAAAACAAT TAAGAAGAAC		
msa252409.2{85_CJB110}	TATCTAAATT TAAAGAAAAGA	CTTCCTTTTT ACAAAACAAT TAAGAAGAAC		
msa252409.2{85_COH1}	TATCTAAATT TAAAGAAAAGA	CTTCCTTTTT ACAAAACAAT TAAGAAGAAC		
msa252409.2{85_M732}	TATCTAAATT TAAAGAAAAGA	CTTCCTTTTT ACAAAACAAT TAAGAAGAAC		
msa252409.2{85_M781}	TATCTAAATT TAAAGAAAAGA	CTTCCTTTTT ACAAAACAAT TAAGAAGAAC		
msa252409.2{85_18RS21}	TATCTAAATT TAAAGAAAAGA	CTTCCTTTTT ACAAAACAAT TAAGAAGAAC		
msa252409.2{85_2603}	TATCTAAATT TAAAGAAAAGA	CTTCCTTTTT ACAAAACAAT TAAGAAGAAC		
msa252409.2{85_A909}	TATCTAAATT TAAAGAAAAGA	CTTCCTTTTT ACAAAACAAT TAAGAAGAAC		
msa252409.2{85_H36B}	TATCTAAATT TAAAGAAAAGA	CTTCCTTTTT ACAAAACAAT TAAGAAGAAC		
msa252409.2{85_JM9130013}	TATCTAAATT TAAAGAAAAGA	CTTCCTTTTT ACAAAACAAT TAAGAAGAAC		
msa252409.2{85_1169NT}	TATCTAAATT TAAAGAAAAGA	CTTCCTTTTT ACAAAACAAT TAAGAAGAAC		
Consensus	*****	*****	*****	*****
	901		950	
msa252409.2{85_090.con_}	CTTAAGGAAC CTTCTATTGT	TGATATGGAA GTGGGAGTTT ACACAAAC		
msa252409.2{85_CJB110}	CTTAAGGAAC CTTCTATTGT	TGATATGGAA GTGGGAGTTT ACACAAAC		
msa252409.2{85_COH1}	CTTAAGGAAC CTTCTATTGT	TGATATGGAA GTGGGAGTTT ACACAAAC		
msa252409.2{85_M732}	CTTAAGGAAC CTTCTATTGT	TGATATGGAA GTGGGAGTTT ACACAAAC		
msa252409.2{85_M781}	CTTAAGGAAC CTTCTATTGT	TGATATGGAA GTGGGAGTTT ACACAAAC		
msa252409.2{85_18RS21}	CTTAAGGAAC CTTCTATTGT	TGATATGGAA GTGGGAGTTT ACACAAAC		
msa252409.2{85_2603}	CTTAAGGAAC CTTCTATTGT	TGATATGGAA GTGGGAGTTT ACACAAAC		
msa252409.2{85_A909}	CTTAAGGAAC CTTCTATTGT	TGATATGGAA GTGGGAGTTT ACACAAAC		
msa252409.2{85_H36B}	CTTAAGGAAC CTTCTATTGT	TGATATGGAA GTGGGAGTTT ACACAAAC		
msa252409.2{85_JM9130013}	CTTAAGGAAC CTTCTATTGT	TGATATGGAA GTGGGAGTTT ACACAAAC		
msa252409.2{85_1169NT}	CTTAAGGAAC CTTCTATTGT	TGATATGGAA GTGGGAGTTT ACACAAAC		
Consensus	*****	*****	*****	*****
	951		1000	
msa252409.2{85_090.con_}	AAGTACTATT GAATCAACCC	CTGTgAAAGC gGAAGATACA AAAAATAAAT		
msa252409.2{85_CJB110}	AAGTACTATT GAATCAACCC	CTGTgAAAGC gGAAGATACA AAAAATAAAT		
msa252409.2{85_COH1}	AAGTACTATT GAATCAACCC	CTGTgAAAGC gGAAGATACA AAAAATAAAT		
msa252409.2{85_M732}	AAGTACTATT GAATCAACCC	CTGTgAAAGC gGAAGATACA AAAAATAAAT		
msa252409.2{85_M781}	AAGTACTATT GAATCAACCC	CTGTgAAAGC gGAAGATACA AAAAATAAAT		
msa252409.2{85_18RS21}	AAatACcATT GAATCAACCC	CTGTCAAAGC gGAAGATACA AAAAATAAAT		
msa252409.2{85_2603}	AAatACcATT GAATCAACCC	CTGTCAAAGC gGAAGATACA AAAAATAAAT		
msa252409.2{85_A909}	AAatACcATT GAATCAACCC	CTGTCAAAGC gGAAGATACA AAAAATAAAT		
msa252409.2{85_H36B}	AAatACcATT GAATCAACCC	CTGTCAAAGC gGAAGATACA AAAAATAAAT		
msa252409.2{85_JM9130013}	AAatACcATT GAATCAACCC	CTGTCAAAGC gGAAGATACA AAAAATAAAT		
msa252409.2{85_1169NT}	AAatACcATT GAATCAACCC	CTGTCAAAGC gGAAGATACA AAAAATAAAT		
Consensus	*****	*****	*****	*****
	1001		1050	
msa252409.2{85_090.con_}	CAACTGATAA AACACAAaCa	CAAAATGGTC AGGTTGCCGA AAATAGTC		
msa252409.2{85_CJB110}	CAACTGATAA AACACAAaCa	CAAAATGGTC AGGTTGCCGA AAATAGTC		
msa252409.2{85_COH1}	CAACTGATAA AACACAAaCa	CAAAATGGTC AGGTTGCCGA AAATAGTC		
msa252409.2{85_M732}	CAACTGATAA AACACAAaCa	CAAAATGGTC AGGTTGCCGA AAATAGTC		
msa252409.2{85_M781}	CAACTGATAA AACACAAaCa	CAAAATGGTC AGGTTGCCGA AAATAGTC		
msa252409.2{85_18RS21}	CAACTGATAA AACACAAaCa	CAAAATGGTC AGGTTGCCGA AAATAGTC		
msa252409.2{85_2603}	CAACTGATAA AACACAAaCa	CAAAATGGTC AGGTTGCCGA AAATAGTC		
msa252409.2{85_A909}	CAACTGATAA AACACAAaCa	CAAAATGGTC AGGTTGCCGA AAATAGTC		
msa252409.2{85_H36B}	CAACTGATAA AACACAAaCa	CAAAATGGTC AGGTTGCCGA AAATAGTC		
msa252409.2{85_JM9130013}	CAACTGATAA AACACAAaCa	CAAAATGGTC AGGTTGCCGA AAATAGTC		
msa252409.2{85_1169NT}	CAACTGATAA AACACAAaCc	CAAAATGGTC AGGTTGCCGA AAATAGTC		
Consensus	*****	*****	*****	*****
	1051		1100	
msa252409.2{85_090.con_}	GGACAAACAA ATAACCTCAA TACTAATCAA CAAGG...AC AACAGATAGC			

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_CJB110}	GGACAAACAA ATAACTCAA TACTAATCAA CAAGG...AC AACAGATAGC
msa252409.2{85_COH1}	GGACAAACAA ATAACTCAA TACTAATCAA CAAGG...AC AACAGATAGC
msa252409.2{85_M732}	GGACAAACAA ATAACTCAA TACTAATCAA CAAGG...AC AACAGATAGC
msa252409.2{85_M781}	GGACAAACAA ATAACTCAA TACTAATCAA CAAGG...AC AACAGATAGC
msa252409.2{85_18RS21}	GGACAAACAA ATAACTCAA TACTAATCAA CAAGG...AC AACAGATAGC
msa252409.2{85_2603}	GGACAAACAA ATAACTCAA TACTAATCAA CAAGG...AC AACAGATAGC
msa252409.2{85_A909}	GGACAAACAA ATAACTCAA TACTAATCAA CAAGG...AC AACAGATAGC
msa252409.2{85_H36B}	GGACAAACAA ATAACTCAA TACTAATCAA CAAGG...AC AACAGATAGC
msa252409.2{85_JM9130013}	GGACAAACAA ATAACTCAA TACTAATCAA CAAGG...AC AACAGATAGC
msa252409.2{85_1169NT}	GGACAAACAA ATAACTCAA TACTAATCAA CAAGG...AC AACAGATAGC
Consensus	***** * ***** * ***** * ***** - * *****
	1101
msa252409.2{85_090.con_}	AACaGAGCAG GCACCCAAACC CTCAAAATGT TAAT
msa252409.2{85_CJB110}	AACaGAGCAG GCACCCAAACC CTCAAAATGT TAAT
msa252409.2{85_COH1}	AACaGAGCAG GCACCCAAACC CTCAAAATGT TAAT
msa252409.2{85_M732}	AACaGAGCAG GCACCCAAACC CTCAAAATGT TAAT
msa252409.2{85_M781}	AACaGAGCAG GCACCCAAACC CTCAAAATGT TAAT
msa252409.2{85_18RS21}	AACaGAGCAG GCACCCAAACC CTCAAAATGT TAAT
msa252409.2{85_2603}	AACaGAGCAG GCACCCAAACC CTCAAAATGT TAAT
msa252409.2{85_A909}	AACaGAGCAG GCACCCAAACC CTCAAAATGT TAAT
msa252409.2{85_H36B}	AACaGAGCAG GCACCCAAACC CTCAAAATGT TAAT
msa252409.2{85_JM9130013}	AACaGAGCAG GCACCCAAACC CTCAAAATGT TAAT
msa252409.2{85_1169NT}	AACaGAGCAG GCACCCAAACC CTCAAAATGT TAAT
Consensus	*** - * ***** * ***** - * ***** * *****

SEQ ID NO. 8812**STRAIN 2603 frame: 1**

PKKKSDTPEKEEVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSEPEPQ
 NTTKIKKLHFPKISRPKIEKKQKKEKIVNSLAKTNRIRTA^PI FVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQR^LAAEDVWWVKT^AQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVL^ETGKKADPVNSSEL^PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEI^IQVISLADS^KITTPDLLLDMHDGNS^IR^IPLSKFKERLPFYQ^IKKN
 LKEPSIVDMEVGVT^TTNTIESTPVKAEDTKNKSTD^DKTQTQNGQVAENSQGQTNNNSNTNQ
 QQQIATEQAPNPQNVN

SEQ ID NO. 8813**STRAIN H36B frame: 1**

PKKKSDTPEKEEVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSEPEPQ
 NTTKIKKLHFPKISR^IPKIEKKQKKEKIVNSLAKTNRIRTA^PI FVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQR^LAAEDVWWVKT^AQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVL^ETGKKADPVNSSEL^PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEI^IQVISLADS^KITTPDLLLDMHDGNS^IR^IPLSKFKERLPFYQ^IKKN
 LKEPSIVDMEVGVT^TTNTIESTPVKAEDTKNKSTD^DKTQTQNGQVAENSQGQTNNNSNTNQ
 QQQIATEQAPNPQNVN

SEQ ID NO. 8814**STRAIN 18RS21 frame: 1**

PKKKSDTPEKEEVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSEPEPQ
 NTTKIKKLHFPKISR^IPKIEKKQKKEKIVNSLAKTNRIRTA^PI FVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQR^LAAEDVWWVKT^AQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVL^ETGKKADPVNSSEL^PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEI^IQVISLADS^KITTPDLLLDMHDGNS^IR^IPLSKFKERLPFYQ^IKKN
 LKEPSIVDMEVGVT^TTNTIESTPVKAEDTKNKSTD^DKTQTQNGQVAENSQGQTNNNSNTNQ
 QQQIATEQAPNPQNVN

SEQ ID NO. 8815**STRAIN M732 frame: 1**

PKKKSDTPEKEEVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSEPEPQ
 NTTKIKKLHFPKISR^IPKIEKKQKKEKIVNSLAKTNRIRTA^PI FVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQR^LAAEDVWWVKT^AQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVL^ETGKKADPVNSSEL^PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEI^IQVISLADS^KITTPDLLLDMHDGNS^IR^IPLSKFKERLPFYQ^IKKN
 LKEPSIVDMEVGVT^TTNTIESTPVKAEDTKNKSTD^DKTQTQNGQVAENSQGQTNNNSNTNQ
 QQQIATEQAPNPQNVN

SEQ ID NO. 8816**STRAIN COH1 frame: 1**

PKKKSDTPEKEEVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSEPEPQ
 NTTKIKKLHFPKISR^IPKIEKKQKKEKIVNSLAKTNRIRTA^PI FVVAFLVILVSVFLLTPF
 SKQKTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQR^LAAEDVWWVKT^AQMTYQ
 FPNKFHIQVQENKI IAYAHTKQGYQPVL^ETGKKADPVNSSEL^PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEI^IQVISLADS^KITTPDLLLDMHDGNS^IR^IPLSKFKERLPFYQ^IKKN
 LKEPSIVDMEVGVT^TTNTIESTPVKAEDTKNKSTD^DKTQTQNGQVAENSQGQTNNNSNTNQ
 QQQIATEQAPNPQNVN

SEQ ID NO. 8817**STRAIN M781 frame: 1**

PKKKSDTPEKEEVLTEWQKRNLFLKKRKEDEEEQKRINEKLRLDKRSKLNISSEPEPQ

Table 88: Comparative Sequences relating to SAG0477

NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPEFVVAFLVILVSVFLLTPF
 SKQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLLAAEDVVWVTKAQMTYQ
 FPNKFHIVQOENKIIAYAHTKQGYQPVLETGKCADPVNSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQLVSLADSCKTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTITSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNNSNTNQ
 QQQIATEQAPNPQNVN

SEQ ID NO. 8818

STRAIN CJB110 frame: 1

PKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRD KR SKLN ISSPEEPQ
 NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPEFVVAFLVILVSVFLLTPF
 SKQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLLAAEDVVWVTKAQMTYQ
 FPNKFHIVQOENKIIAYAHTKQGYQPVLETGKCADPVNSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQLVSLADSCKTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTITSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNNSNTNQ
 QQQIATEQAPNPQNVN

SEQ ID NO. 8819

STRAIN 1169NT frame: 1

PKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRD KR SKLN ISSPEEPQ
 NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPEFVVAFLVILVSVFLLTPF
 SKQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLLAAEDVVWVTKAQMTYQ
 FPNKFHIVQOENKIIAYAHTKQGYQPVLETGKCADPVNSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQLVSLADSCKTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTITSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNNSNTNQ
 QQQIATEQAPNPQNVN

SEQ ID NO. 8820

STRAIN JM9130013 frame: 1

PKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRD KR SKLN ISSPEEPQ
 NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPEFVVAFLVILVSVFLLTPF
 SKQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLLAAEDVVWVTKAQMTYQ
 FPNKFHIVQOENKIIAYAHTKQGYQPVLETGKCADPVNSELPKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQLVSLADSCKTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTITSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNNSNTNQ
 QQQIATEQAPNPQNVN

SEQ ID NO. 8821

STRAIN A909 frame: 1

PKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRD KR SKLN ISSPEEPQ
 NTTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPEFVVAFLVILVSVFLLTPF
 SKQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLLAAEDVVWVTKAQMTYQ
 FPNKFHIVQOENKIIAYAHTKQGYQPVLETGKCADPVNSEL PKHFLTINLDKEDSIKLL
 IKDLKALDPDLISEIQLVSLADSCKTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKKN
 LKEPSIVDMEVGVTITSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNNSNTNQ
 QQQIATEQAPNPQNVN

SEQ ID NO. 8822

STRAIN 090 frame: 2

KKKSDTPEKEEVVLTEWQKRNLFLKKRKEDEEEQKRINEKLRD KR SKLN ISSPEEPQ
 TTKIKKLHFPKISKPKIEKKQKKEKIVNSLAKTNRIRTAPEFVVAFLVILVSVFLLTPF
 KQKTTITVSGNQHTPDDILIEKTNIQKNDYFFSLIFKHKAIEQRLLAAEDVVWVTKAQMTYQF
 FPNKFHIVQOENKIIAYAHTKQGYQPVLETGKCADPVNSEL PKHFLTINLDKEDSIKLL
 KDLKALDPDLISEIQLVSLADSCKTPDLLLLDMHDGNSIRIPLSKFKERLPFYKQIKNL
 KEPSPIVDMEVGVTITSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGQTNNNSNTNQ
 QQQIATEQAPNPQNVN

PRETTY of: /biotmp/msa252337.2(*) January 31, 2003 03:32 ..

	1		50
msa252337.2{85_090}	-KKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRD KR SKLN		
msa252337.2{85_18RS21}	PKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRD KR SKLN		
msa252337.2{85_2603}	PKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRD KR SKLN		
msa252337.2{85_A909}	PKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRD KR SKLN		
msa252337.2{85_CJB110}	PKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRD KR SKLN		
msa252337.2{85_COH1}	PKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRD KR SKLN		
msa252337.2{85_H36B}	PKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRD KR SKLN		
msa252337.2{85_JM9130013}	PKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRD KR SKLN		
msa252337.2{85_M732}	PKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRD KR SKLN		
msa252337.2{85_M781}	PKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRD KR SKLN		
msa252337.2{85_1169NT}	PKKSDTPEK EEVVLTEWQK RNLEFLKKRK EDEEEQKRIN EKLRD KR SKLN		
Consensus	*****	*****	*****
	51		100
msa252337.2{85_090}	LNISSPEEPQ NTTKIKKLHF PKISPKIEK KQKKEKIVNS LAKTNRIRTA		
msa252337.2{85_18RS21}	LNISSPEEPQ NTTKIKKLHF PKISrPKIEK KQKKEKIVNS LAKTNRIRTA		
msa252337.2{85_2603}	LNISSPEEPQ NTTKIKKLHF PKISrPKIEK KQKKEKIVNS LAKTNRIRTA		
msa252337.2{85_A909}	LNISSPEEPQ NTTKIKKLHF PKISrPKIEK KQKKEKIVNS LAKTNRIRTA		
msa252337.2{85_CJB110}	LNISSPEEPQ NTTKIKKLHF PKISPKIEK KQKKEKIVNS LAKTNRIRTA		

Table 88: Comparative Sequences relating to SAG0477

msa252337.2{85_COH1}	LNISSPEEPQ	NTTKIKKLHF	PKISPKIEK	KQKKEKIVNS	LAKTNRIRTA	
msa252337.2{85_H36B}	LNISSPEEPQ	NTTKIKKLHF	PKISrPKIEK	KQKKEKIVNS	LAKTNRIRTA	
msa252337.2{85_JM9130013}	LNISSPEEPQ	NTTKIKKLHF	PKISrPKIEK	KQKKEKIVNS	LAKTNRIRTA	
msa252337.2{85_M732}	LNISSPEEPQ	NTTKIKKLHF	PKISPKIEK	KQKKEKIVNS	LAKTNRIRTA	
msa252337.2{85_M781}	LNISSPEEPQ	NTTKIKKLHF	PKISPKIEK	KQKKEKIVNS	LAKTNRIRTA	
msa252337.2{85_1169NT}	LNISSPEEPQ	NTTKIKKLHF	PKISPKIEK	KQKKEKIVNS	LAKTNRIRTA	
Consensus	*****	*****	*****	*****	*****	
msa252337.2{85_090}	101	PIFVVAFLVI	LVSVFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_18RS21}	PIFVVAFLVI	LVSVFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY	
msa252337.2{85_2603}	PIFVVAFLVI	LVSVFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY	
msa252337.2{85_A909}	PIFVVAFLVI	LVSVFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY	
msa252337.2{85_CJB110}	PIFVVAFLVI	LVSVFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY	
msa252337.2{85_COH1}	PIFVVAFLVI	LVSVFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY	
msa252337.2{85_H36B}	PIFVVAFLVI	LVSVFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY	
msa252337.2{85_JM9130013}	PIFVVAFLVI	LVSVFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY	
msa252337.2{85_M732}	PIFVVAFLVI	LVSVFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY	
msa252337.2{85_M781}	PIFVVAFLVI	LVSVFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY	
msa252337.2{85_1169NT}	PIFVVAFLVI	LVSVFLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY	
Consensus	*****	*****	*****	*****	*****	
msa252337.2{85_090}	151	FFSLIFKHKA	IEQRLLAEDV	WVKTAQMTRYQ	FPNKFHIQVQ	ENKIIAYAHT
msa252337.2{85_18RS21}	FFSLIFKHKA	IEQRLLAEDV	WVKTAQMTRYQ	FPNKFHIQVQ	ENKIIAYAHT	
msa252337.2{85_2603}	FFSLIFKHKA	IEQRLLAEDV	WVKTAQMTRYQ	FPNKFHIQVQ	ENKIIAYAHT	
msa252337.2{85_A909}	FFSLIFKHKA	IEQRLLAEDV	WVKTAQMTRYQ	FPNKFHIQVQ	ENKIIAYAHT	
msa252337.2{85_CJB110}	FFSLIFKHKA	IEQRLLAEDV	WVKTAQMTRYQ	FPNKFHIQVQ	ENKIIAYAHT	
msa252337.2{85_COH1}	FFSLIFKHKA	IEQRLLAEDV	WVKTAQMTRYQ	FPNKFHIQVQ	ENKIIAYAHT	
msa252337.2{85_H36B}	FFSLIFKHKA	IEQRLLAEDV	WVKTAQMTRYQ	FPNKFHIQVQ	ENKIIAYAHT	
msa252337.2{85_JM9130013}	FFSLIFKHKA	IEQRLLAEDV	WVKTAQMTRYQ	FPNKFHIQVQ	ENKIIAYAHT	
msa252337.2{85_M732}	FFSLIFKHKA	IEQRLLAEDV	WVKTAQMTRYQ	FPNKFHIQVQ	ENKIIAYAHT	
msa252337.2{85_M781}	FFSLIFKHKA	IEQRLLAEDV	WVKTAQMTRYQ	FPNKFHIQVQ	ENKIIAYAHT	
msa252337.2{85_1169NT}	FFSLIFKHKA	IEQRLLAEDV	WVKTAQMTRYQ	FPNKFHIQVQ	ENKIIAYAHT	
Consensus	*****	*****	*****	*****	*****	
msa252337.2{85_090}	201	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_18RS21}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD	
msa252337.2{85_2603}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD	
msa252337.2{85_A909}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD	
msa252337.2{85_CJB110}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD	
msa252337.2{85_COH1}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD	
msa252337.2{85_H36B}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD	
msa252337.2{85_JM9130013}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD	
msa252337.2{85_M732}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD	
msa252337.2{85_M781}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD	
msa252337.2{85_1169NT}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD	
Consensus	*****	*****	*****	*****	*****	
msa252337.2{85_090}	251	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSLPKKER	LPFYKQIKNN
msa252337.2{85_18RS21}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSLPKKER	LPFYKQIKNN	
msa252337.2{85_2603}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSLPKKER	LPFYKQIKNN	
msa252337.2{85_A909}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSLPKKER	LPFYKQIKNN	
msa252337.2{85_CJB110}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSLPKKER	LPFYKQIKNN	
msa252337.2{85_COH1}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSLPKKER	LPFYKQIKNN	
msa252337.2{85_H36B}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSLPKKER	LPFYKQIKNN	
msa252337.2{85_JM9130013}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSLPKKER	LPFYKQIKNN	
msa252337.2{85_M732}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSLPKKER	LPFYKQIKNN	
msa252337.2{85_M781}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSLPKKER	LPFYKQIKNN	
msa252337.2{85_1169NT}	LISEIQVISL	ADSKITPDLL	LLDMHDGNSI	rIPLSLPKKER	LPFYKQIKNN	
Consensus	*****	*****	*****	*****	*****	
msa252337.2{85_090}	301	LKEPSIVDME	VGVYTTTSTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ
msa252337.2{85_18RS21}	LKEPSIVDME	VGVYTTTSTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ	
msa252337.2{85_2603}	LKEPSIVDME	VGVYTTTSTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ	
msa252337.2{85_A909}	LKEPSIVDME	VGVYTTTSTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ	
msa252337.2{85_CJB110}	LKEPSIVDME	VGVYTTTSTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ	
msa252337.2{85_COH1}	LKEPSIVDME	VGVYTTTSTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ	
msa252337.2{85_H36B}	LKEPSIVDME	VGVYTTTSTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ	
msa252337.2{85_JM9130013}	LKEPSIVDME	VGVYTTTSTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ	
msa252337.2{85_M732}	LKEPSIVDME	VGVYTTTSTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ	
msa252337.2{85_M781}	LKEPSIVDME	VGVYTTTSTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ	
msa252337.2{85_1169NT}	LKEPSIVDME	VGVYTTTSTI	ESTPVKAEDT	KNKSTDKTQ	QNGQVAENSQ	
Consensus	*****	*****	*****	*****	*****	
msa252337.2{85_090}	351	GQTNNNSNTNQ	QQQQiateqa	pnpqnv-		
msa252337.2{85_18RS21}	GQTNNNSNTNQ	QQQQiateqa	pnpqnv-			
msa252337.2{85_2603}	GQTNNNSNTNQ	QQQQiateqa	pnpqnv-			
msa252337.2{85_A909}	GQTNNNSNTNQ	QQQQiateqa	pnpqnv-			

Table 88: Comparative Sequences relating to SAG0477

msa252337.2{85_CJB110}	GQTNNNSNTNQ	QGQQiateqa	pnpqnvvn-
msa252337.2{85_COH1}	GQTNNNSNTNQ	QGQQiateqa	pnpqnvvn-
msa252337.2{85_H36B}	GQTNNNSNTNQ	QGQQiateqa	pnpqnvvn-
msa252337.2{85_JM9130013}	GQTNNNSNTNQ	QGQQiateqa	pnpqnvvn-
msa252337.2{85_M732}	GQTNNNSNTNQ	QGQQiateqa	pnpqnvvn-
msa252337.2{85_M781}	GQTNNNSNTNQ	QGQQiateqa	pnpqnvvn-
msa252337.2{85_1169NT}	GQTNNNSNTNQ	QGQQiateq	apnpqnvvn
Consensus	*****	*****-----	-----*

Table 89: Comparative Sequences relating to SAG1350

SEQ ID NO. 8901

STRAIN 2603

ATGAAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTCTACGTAAA
 TATAAAATTGGTTAGCATCACTAAATTTCAGGTCAATTCTATAATGGTCACAGTCCCGTT
 TTTCGGATCAAACATCGGTCAGTTAATAATCAGACAGGCAGTAGTGATGCT
 AATAATTCTCCAATGAGACAAGTGCCTGAAGTGATTACTTCAATAATGATAGTGT
 CAAGCGTCTGATAAAAGTCAAATAGTCAAATAACCCGAAACAAAGGACATTACTCCT
 TTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACTGAAACAGGGAAATTATGTTTAT
 AGCAAAGAAACCGAGGTGAAAAAATACACCTTCAAATCAGCCCCAGTAGCTTCTATGCA
 AAGAAAGGTGATAAAGTTTCTATGACCAAGTATTAAATAAAGATAATGTGAAATGGATT
 TCATAAAGTCTTTGCGGTCAGCTCGATACGCAGCTATTGAGTCAGTACATGCCATCA
 GGAGGTTAGAGACTAAAGCACCTACTCTGTAACAAATTAGGAACAGCAATAATCAAGAG
 AAAATAGCAACGCAAGGAAATTACATTTACATAAGTAAAGTAGAAGTAAAAATGAAGCT
 AAGTAGGAGTCCAACTCAAGTCAATTACATTGACAAAGGAGACAGAATTTTTACGACCAA
 ATACTAATCTTGAAGGAAATCACTGGTTATCTTATAATCATTCAATGGTGTCTCGTCT
 TTGTTTGTAGGTAAGCATCTCAGTAGAAAAAACTGAAGATAAAAGAAAAAGTGTCT
 CCTCAACACAAAGCCGTTAACTAAACTGGTAGACTGACTATTCTAACGAAACAAACT
 ACAGGTTTGTATTTAAATACGAATATTAAAGATGATAACGGTATCGCTGCTGTTAAG
 GTACCGGTTGGACTGAACAAGGAGGGCAAGGTGATAATTAAATGGTATACAGCTGTAAC
 ACTGGGGATGGCAACTACAAAGTAGCTGATCTCATTGCTGACCATAGAATGAGAAGGGT
 CTTATAATATTCAATTACCAAGAAGTACTGGGACACTTGTAGGTGAAACAGGA
 ACTTAAAGTGGACTGACTGGAACATTACTTCTCAAGAACACTATTGAAATGTTAGCA
 AAGACTGGTGTATAATATTATCGGAAGTACTGAAGTAAAAAAATGAAGCTAAAATATCA
 AGTCAGACCCAAAGGTCACAAAATAATTATGATCAAGTATTGACA
 GTAGGTTTGTACAGTGGATTCTTCTACAAATCTTATAGTGGTTCTGCTGCTATAATTCT
 GTGAAAAGCTAATCACAAGTAGTGGAAAAGCTGAGATGAGGCAACTAACCGACTAGT
 TATCCCACCTACCTAACAGGTACCTACATTACTAAACTGTAGATGTGAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTAAATTCTCAAAGGGTGAAAAAAATACATTAT
 GATCAAGTGTAGTAGTGTAGATGGTCACTACAGAGTTATTCCGGTATT
 CGTCGCTATATTGAAATT

SEQ ID NO. 8902

STRAIN 090

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
 CTCACGTAATATAATTGGTTAGCATCACTAAATTTCAGGTCAATT
 ATAATGGTCAACAGTCTGTTTGCCTGATCAAACATCGGTCAGT
 TAATAATCAGACAGGCACTAGTGTGGATGCTAATAATTCTCCAATGAGA
 CAAGTGCCTGATGTTAGCTTCAAAATAATGATAGTGTCAAGCGTCT
 GATAAAGTGTAAATACTCCTAAATACGGCAACAAAGGACATTACTACTCC
 TTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAAGGG
 ATTATGTTTATAGCAGGAAACCCGAGGTGAAAAAAATACACCTTCAAATATCA
 GCCCCAGTAGCTTCTATGCAAAAGGGTACATAAGTTTCTATGACCA
 AGTATTAAATAAAGATAATGTGAAATGGATTCTATATAAGTCTTTTG
 GCCTACGTCGATACGCGCTATTGAGTCAGTACATCAGGAGCTTC
 GAGACTAAGCACCTACTCTGTAACCAAATTACGGCAAGCAATAATCAAGA
 GAAAATAGCAACGCAAGGAAATTATACATTTCACATAAAAGTAGAAGTAA
 AAAATGAAGCTAAGGTGAGTCCAACTCAATTACATTGGACAAAGGA
 GACAGAATTTTTACCGACCAAAACTAAACTTACATTGAGGAAATCAGTGGTT
 ATCTTATAATCATTCAATGGTGTCTGTTGTTGTCTGCTAGGTTAAAG
 CATCTTCAGTAGAAAAAACTGAAGATAAAAGAAAAAGTGTCTCTCAACCA
 CAAGCCGTTAACTAAACTGGTAGACTGACTATTCTAACGAAACAAAC
 TACAGGTTTGTATTTAAATTACGAATATTAAAGATGATAACGGTATCG
 CTGCTGTTAGGTACCGGTTGGACTGAACAAGGAGGGCAAGATGATATT
 AAATGGTATACAGCTGTAACTACTGGGATGCGCAACTCAAAGTAGCTGT
 ATCATTGCTGACCATAGAATGGTGTCTTATAATATTCTATTTAT
 ACTACCAAGAAGCTAGTGGACACTTGTAGGTGTAACGAAACTAAAGTG
 ACAGTAGCTGGAACAACTCTCTCAAGAACCTATTGAAAATGGTTAGC
 AAAGACTGGTTTATAATATTCGGAAGTACTGAAGTAAAAAAATGAAG
 CTTAAATATCAAGTCAGACCCAAATTACTTACATTGAAAAGCTGACAAAATA
 AATTATGATCAAGTATTGACAGCAGATGGTACCCAGTGGATTCTTACAA
 ATCTTATAGTGTGTTCTGCTATATTCTGTTGAAAAGCTAACACTACAA
 GTAGTGGAAAAGCGAAAGTGGACTAAACCGACTAGTTATCCCAAC
 TTACCTAAACAGGTACCTATACATTACTAAACTGTAGATGTGAAGAG
 TCAACCTAAAGTATCAAGTCCAGTGGAAATTAAATTCTCAAAGGGTGAAA
 AAATACATTATGATCAAGTGTAGTAGTGTACAGTGGATTTC
 TACAAAGAGTTATCCGGTATTGCTGCTATATTGAAATT

SEQ ID NO. 8903

STRAIN A909

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTAC
 TCTCTACGTAATATAATTGGTTAGCATCACTAAATTTCAGGTCAATT
 CATAATGGTCAACAGTCTGTTGCCTGATCAAACATCGGTCAG
 TTAATAATCAGACAGGCACTAGTGTGGATGCTAATAATTCTCCAATGAG
 ACAAGTGCCTGATGTTAGCTTCAAAATAATGATAGTGTCAAGCGTC
 TGATAAAAGTGTAAATAGTCAAACCCGCAACAAAGGACATTACTACTC
 CTTGTAGAGACAAAGCCAATGGTGGAAAAAAACATTACCTGAACAGGG
 AATTATGTTATAGCAAAGAACCGAGGTGAAAAATACACCTTCAAATC
 AGCCCCAGTAGCTTCTATGCAAAGGAAGGTGATAAAAGTTCTATGACC
 AAGTATTAAATAAGATAATGTGAAATGGATTCTCATATAAGTCTTTGT
 GGGCTACGTCGATACGCGACTATTGAGTCAGTACATCCATCAGGAGGTC
 AGAGACTAAAGCACCTACTCTGTAACAAATTACGGAAAGCAATAATCAAG
 AGAAAATAGCAACGCAAGGAAATTATACATTTCACATAAAAGTAGAAGTA
 AAAATGAAGCTAAGGTAGCGACTCAATTACATTGACAAAG

Table 89: Comparative Sequences relating to SAG1350

AGACAGAATTTCGACCAAATACTAACTATTAAGGAAATCAGTGGT
 TATCTTATAAAATCATTCAATGGTGTGCGTTTGTTTGCTAGGTAAA
 GCATCTTCAGTAGAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAACC
 ACAACCCGTTATTACTAAACCTGGTAGACTGACTATTCTAACGAAACAA
 CTACAGGTTTGATATTAAATACGAATATTAAAGATGATAACGGTATC
 GCTGCTGTTAAGGTAACGGGTTGGACTGAACAAGGAGGGCAAGATGATAT
 TAAATGTTACAGCTGTAACACTGGGGATGGCAACTAACAAAGTAGCTG
 TATCATTTGCTGACCATAAAGATGAGAACGGTCTTTATAATATTCAATTAA
 TACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACAAAGT
 GACAGTAGCTGAACTAATTCTCTCAAGAACCTATTGAAAATGGTTTAG
 CAAAGACTGGTGTATAATATTATCGGAAGTACTGAAGTAAAAAATGAA
 GCTAAATATCAAGTCAGACCCATTACTTAGAAAAGGTGACAAACAA
 AAATTATGATCAAGTATTGACAGCAGATGTTACCAAGTGGGATTTCTTACA
 AATCTTATAGTGGTGTGCTGCTATAATTCTGTGAAAAGGCTAAACTACA
 AGTAGTGAAGGAAAGATGAGGCGACTAACCGACTAGTATCCTCAA
 CTTACCTAAACAGGTACCTATACATTACTAAACTGTAGATGTGAAGA
 GTCAACCTAAAGTATCAAGTCAGTGGGAAATTAAATTTCAAAAGGGTGAA
 AAAATACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTC
 ATACAAGAGTTATTCCGGTATTGCTGCTATAATTGAAATT

SEQ ID NO. 8904

STRAIN H36B

AAAAAAGGACAAGTAAATGATACAAAGCAATCTTACT
 CTCACCTAAATAAATTTGGTTAGCATCAGTAATTAGGTCAATT
 ATAATGGTCACAAGTCTGTTTGCAGATCAAACATACATCGGTCAAGT
 TAATAATCAGACAGGCACTAGTGTGGATGATAATAATTCTCCAATGAGA
 CAAGTGGCTCAAGGTGATTACTCTCAAAATAATGATAGTGTCAAGCGTCT
 GATAAGTTGTAATAGTCAAACATCGGAACAAAGGACATTACTACTCC
 TTAGTAGAGACAAAGCCAATGGGAAAAAACATTACCTGAACAAGGG
 ATTATGTTATAGCAAGGAAACCCAGGTGAAAATACACCTTCAAATCA
 GCCCAGTAGCTATGCAAGAACGGTATAAGTTCTATGACCA
 AGTATTAATAAGATAATGTAATGGATTCTATATAAGTCTTTGTG
 GCGTAGCTGATAACGAGCTATTGAGTCAGTACATGATCCATCAGGAGGTTCA
 GAGACTAAAGCCTACTCTGTAACAAATTCAAGGAACAAATAATCAAGA
 GAAAATAGCAACGCAAGGAAATTATACATTTCACATAAAGTAGAAAGTAA
 AAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTACATGGACAAAGGA
 GACAGAATTTCACGGACCAAAACTAACTACTTGTAGAGTGTGAAG
 ATCTTATAATCAATTCAATGGTGTGCTGTTTGTTTGTTTGCTAGTAAAG
 CATCTTCACTAGAAAAAAACTGAAGATAAAGAAAAGTGTCTCTCAACCA
 CAAGCCCGTATTACTAAACTGGTAGACTGACTATTCTCAACGAAACAC
 TACAGGTATTGATATTAAATACGAATATAAAGATGATAACGGTATCG
 CTGCTGTTAAGGTACCGGTTGGACTGAACAGGAGGGCAAGATGATATT
 AAATGGTATACAGCTGTAACACTGGGGATGCCAACTAACAAAGTAGCTGT
 ATCATTTCTGTCACCAAGAAGAGAAAGGGCTTTATAATATTCAATTAT
 ACTACCAAGAAGCTAGTGGACACTTGTAGGTGTAACAGAAACTAAAGTG
 ACAGTAGCTGGAACATAATTCTCTCAAGAACCTATTGAAAATGGTTAGC
 AAAGACTGGTTATAATATTGGAAGTACTGAAGTAAAAAAATGAAG
 CTAAAATATCAAGTCAGACCCATTACTTGTAGAAAAGGTGACAAATA
 AATTATGATCAAGTATGACAGCAGATGGTACCAAGTGGATTCTTACA
 ATCTTATAATGTTGCTGCTGTTATAATTCCCTGTGAAAAGCTAACTACAA
 GTAGTGAAGGAAAGGAAAGATGAGGCGACTAACCGGACTAGTTATCCCAAC
 TTACCTTAAACAGGTACCTATACATTACTAAACTGTAGATGTGAAGAG
 TCACACCTAAAGTATCAAGTCAGTGGAAATTAAATTCTAAAGGGTGAA
 AAATACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTCA
 TACAAAGAGTTATTCCGGTATTGCTGCTATAATTGAAATT

SEQ ID NO. 8905

STRAIN 18RS21

AAAAAAGGACAAGTAAATGATACAAAGCAATCTTACTC
 TCTACGTTAAATAAATTTGGTTAGCATCAGTAATTAGGTCAATT
 TAATGGTCAACAGTCCCTGGGATCAAACATACATCGGTCAAGT
 AATAATCAGACAGGCACTAGTGTGGATGTAATAATTCTCCAATGAGAC
 AAGTGGCTCAAGTGTGATTACTTCAATAATGATAGTGTCAAGCGTCTG
 ATAAGTTGTAATAGTCAAACAGGCAACAAAGGACATTACTACTCC
 TTAGTAGAGACAAAGCCAATGGGAAAAAACATTACCTGAACAAGGGAA
 TTATGTTATAGCAAGAACCGAGGTGAAAATACACCTTCAAATCA
 CCCAGTAGCTTCTATGCAAGAACGGTGTAAAGGTTCTATGACCAA
 GTATTTAAAGATAATGTAAGGAAATGGGATTTCATATAAGTCTTTGTGG
 CGTAGCTGATACGCGACTATTGAGTCAGTACATCCATCAGGAGGTTGAG
 AGACTAAAGCCTACTCTGTAACAAATTCAAGGAACAAATCAAGAG
 AAAATAGCAACCCAAAGGAATTATACATTTCACATAAAAGTAGAAGTAA
 AAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTACATTGACAAAGGAG
 ACAGAATTTCACGACAAATAACTAACTATTGAAGGAAATCAGTGGTTA
 TCTTATAATCATTCAATGTTGCTGTTGGCTAGGTAAAGC
 ATCTTCAGTAGAAAAAAACTGAAGATAAAGAAAAGTGTCTCTCAACCC
 AACGCCGTATTACTAAACTGGTAGACTGACTATTCTCAAGAACAAACT
 ACAGGTTTGTGATATTAAATACGAATTAAAGATGATAACGGTATCGC
 TGCTGTTAAGGTACCGGTTGGACTGAACAGGAGGGCAAGATGATATT
 AATGGTATACAGCTGTAACACTGGGGATGGCAACTACAAAGTAGCTGTA
 TCATTGCTGACCATAGAATGAGAACGGGCTTTATAATATTCAATTATA
 CTACCAAGAAGCTAGTGGGACACTTGTAGGTGAAACAGGAACAAAGTGA
 CAGTAGCTGGAACCTATTCTCTCAAGAACCTATTGAAAATGGTTGACCA
 AAGACTGGTGTATAATTATCGGAAGTACTGAAGTAAAAAAATGAAGC

Table 89: Comparative Sequences relating to SAG1350

TAAAAATCAAGTCAGACCCAATTACTTTAGAAAAGGTGACAAAATAA
ATTATGATCAAGTATTGACAGCAGATGGTACCGAGTGGATTCTACAA
TCTTAGTGTGTCTGCTATATTCCCTGTGAAAAGCTAACTACAAG
TAGTGAACAGGAAAGATGAGGCCACTAACCGACTAGTTATCCCAC
TACCTAAACAGGTACCTATACATTACTAAAGCTAGATGTGAAAAGT
CAACCTAAAGTATCAAGTCAGTGAATTAAATTTCAAAAGGGTGAAA
AATACATTATGATCAAGTGTAGTAGTAGATGGTCATCACTGGATTTC
ACAAGAGTTTCCGTATCGCTATATTGAAATT

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STRAIN M732

CAAGTAATGATcaCTAACATCTTACTCTCACGTAATATAAATTGG
TTAGCATCAGTAATTAGGGTCAATTCTAACATGGTCACAAGTCCTGTT
TGCCTGCTAACACTACATCGGTTCAAGTAAATAATCAGACAGGCACTAGT
GTGGATGCTAAATTAATTCTCAATGAGACAAGTGGCTCAAGTGTGATTAC
TTCAAAATGATGTGTTCAAGCGTCTGATAAAGTGTAAAATGTC
ATACGGCAACAAAGGACATTACTCTTGTAGTAGAGACAAGGCAATG
GTGGAAAAAAACATTACCTGAAACAAGGGATAATGTTATAGCAAGGAAAC
CGAGGTGAAAATACACCTTAAACAGCCCCAGTAGCTTCTATGCAA
AGAAAGGTGATAAAAGTTTCTATGACCAAGTATTAAATAAGATAATGTG
AAATGGATTCTATATAAGTCTTGGTGGCTACGTCGATACGGCAGCTAT
TGAGTCAGTACATGATCCATCAGGAGGTTCAAGGACTAAAGCACCTACTCTG
TAACAAATTCAAGGAAGCAATAATCAAGGAAAATAGCAACGCAAGGAAAT
TATACATTTCACATAAAAGTAGAGTAAATAATGAAAGCTAAGGTAGCGAG
TCCAACTCAATTACATTGGACAAGGAGCAGAAATTTTACGACCAAA
TACTAActTGAAGGAAATCAGTGGTTATCTTATAAAATCATTCAATGGT
GTTCGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
AGATAAAGAAAAAGTGTCTCCCAACCAAGGCCGTTACTAAAGACTG
GTAGACTGACTTCTAACGAAACAACACTACAGGTTGTTGATATTAAATT
ACGAATTTAAAGATGATAACGGTATCGCCTGTTAAGGTACCGGTTG
GACTGAACAAGGAGGCAAGATGATATTAAATGGTATACAGCTGTAACTA
CTGGGGATGGCAACTACAAAGTAGCTGTTATCTGACCATATAAGAAT
GAGAAGGGCTTTATAATAATTCTTATAACTACCAAGAACGCTAGTGGGAC
ACTTGTAGGTGTTACAGGAACTAAAGTGTACAGTGGAAACTAAATTCTT
CTCAAGAACCTATTGAAATGGTTTACCAAAGACTGTTGTTATAAATT
ATCGGAAGTACTGAAGTAAAAATGAAGCTAAATATCAAGTCAGACCCA
ATTACTTTAGCAAAAGGTGACAAAATAATTATGATCAAGTATTGACAG
CAGATGGTTACCTGGATTCTTACAAATCTTATAGTGGTGTCTGCG
TATATTCTGTGAAAAGCTAACACTAACGTTGTTATGACCAAGTAA
GGCGACTAACCGCACTAGTTATCCAACTTACCTAAACAGGTACCTATA
CATTTACTAAACGTTAGATGTGAAAGTCAACCTAAAGTATCAAGTC
CTGGGAAATTCTAAAGGGTGAAAATAACATTATGATCAAGTGT
AGTAGTAGATGGTCATCACTGGTTATCTACAGAGTTTCCGGTATT
GTCGCTATATTGAAATT

SEQ ID NO. 8907

STRAIN COH1

AAAAAGGACAAGTAAATGATACATCAAGAACATCTTACTCTCT
ACGTAATATAAATTGGTTAGCATCAGTAATTAGGGTCAATTCTAA
TGGTCACAAGTCTGTTTGCCTGATCAAAACTACATCGGTTCAAGTTA
AATCAGACAGGACTAGTGGATGCTAAATTAATTCTTCCAAATGAGACAAG
TGCCTGCTAACGTGTGATTACTCTAACATGATAGTGTGTTCAAGCGTCTGATA
AAAGTTGTAATAGTCAAATACCGCAACAAAGGACATTACTACTCTT
GTAGAGACAAAGGCAATGGGAAAAAAACATTACCTGAAACAAGGGAAATT
TGTGTTATAGCAAAAGGAGGTGAAAATACACCTTCAAATCAGCCC
CAGTAGCTTCTATGCAAAAGGAGGTGATAAGTTCTATGACCAAGTA
TTAATAAAGGATAATGTTAAATGGATTCTATATAACTCTTTGGTGGCGT
ACGTCGATACGCGAGCTATTGACTAGATCCATCAGGAGGGTTCAGGAGA
CTAAAGCACCTACTCTGTAAACAAATTCAAGGAAATAATCAAGAGAAA
ATAGCAACGCAAGGAAATTACATTTACATAAAGTAGAAGTAA
TGAAGCTAACGGTACGGAGTCCACTCAATTACATGGACAAGGAGACA
GAATTTTTACGACCAAATACTAACACTAACGAGGAAATCAGTGGTTATCT
TATAAACTTACATTCAATGGTGTCTGTTGTTGTTGTTGTTGTTGTTGTTG
TTCAGTAGAAAAAACTGAAGGATAAGGAAAGTGTCTCTCAACCCAAAG
CCGTATTACTAAACTGGTAGACTGACTTCTAACGAAACAACCTACA
GGTTTGATATTAAATTACGAATATTAAAGATGATAACGGTATCGTGC
TGTAAAGTACCGGTTGGACTGAAACAAGGGCAAGATGATTTAAAT
GGTACAGCTGAACTACTGGGAGTGGCAACTACAAAGTAGCTGATACA
TTGGCTGACCATATAAGATGAGAAGGGCTTTATAATTCTTACATTACTA
CCAAGGAAGCTAGTGGACACTTGTAGGTCTAACAGGAACCTAAAGTGACAG
TAGCTGGAAACTAACTCTCTCAAGAACCTATTGAAAATGGTTACCAAAG
ACTGGTGTATTAAATTATCGGAAGTAGCTGAAGTAAAAAATGAAGCTAA
AAATATCAAGTCAGACCCAATTACTTTAGAAAAGGTGACAAAATAATT
ATGATCAAGTATTGACAGCAGATGGTACCGAGTGGATTCTTACAAATCT
TATAGTGGTGTCTGCTATATTCTGTGAAAAGCTAACACTACAAGTAG
TGAAGGAGCAGGAAAGATGAGGCCACTAACCGACTAGTTATCCAACTTAC
CTAAACAGGTACCTATACATTACTAAACGTTAGATGTGAAAAGTCAA
CTTAAAGTCAAGTCCAGTGGAAATTAAATTCTCAAAGGGTGAAAAT
ACATTATGATCAAGTGTAGTAGTAGATGGTCATCACTGGATTTC
AGAGTTTCCGGTATTGCTGCTATATTGAAATT

SEQ ID NO. 8908

STRAIN M781

Table 89: Comparative Sequences relating to SAG1350

AAAAAAGGACAAGTAAATGATACTAAGCAATCTT
ACTCTCTACGTAAATATAAATTGGTTAGCATCAGTAATTAGGGTCA
TCATCATATGTCACAAGTCCGTGTTTGCGGATCAAACATACATCGGTC
AGTTAATATCAGACAGCAGTGTGATTACTTCATAATGATAGTGTCAAGCG
TCGTGATAAAGTGTAAATAGTCAAAATACGGCAACAAAGGACATTACTAC
TCCTTAGTAGAGACAAAGCCAATGGTGGAAAAAAACATTACCTGAACAG
GGAAATTATGTTATAGCAAAGAACCCGAGGTGAAAAAATACACCTTCAA
TCAGCCCCAGTAGCTTCTATGCAAAGAAGGTGATAAAGTTCTATGA
CCAAGTATTATAAGATAATGTAAGGATTTCATATAAGTCTTGTG
GTGCGGTACCTCGATACCGAGCTATTGAGTCAGTAGATCCATCAGGAGGT
TCAGAGACTAAAGCACCTACTCCGTGAAACAAATTCAAGGAAGCAATAATCA
AGAGAAAATAGCAACGCAAGGAAATTATACATTTCACATAAAGTAGAAG
TAAAAAATGAAGCTAAGGTAGCGAGTCAACTTACATTGAGACAAA
GGAGACAGAATTTCAGACCAAATACTAACTATTGAGGAAATCAGTG
GTATCTTATAATCATTCAATGGTGTCTCGTTTGTTTGTTTGTTTGTT
AAGCATCTCCAGTAAAGGAAACTAAAGGATAAAGGAAAAGTGTCTCTCAA
CCACAAGCGGTAACTCAACTGGTAGACTGACTATTCTTAACGAAAC
AACTACAGGTTTGTATTTAATTACGAATTAAAGATGATAACGGTA
TCGCTGTGTTAAGgTACCGGTTGGACTGAACAAGGAGGGCAAGATGAT
ATTAAATGTTATACAGCTGTAACACTGGGGATGGCACTACAAAGTAGC
TGATCTTGTGACCATAGAATGAGAAGGGTCTTATAATATTCTT
TATACTACCAAGAAGCTAGTGGGACACTGTAGGTGTAACAGGAACCTAA
GTGACAGTAGCTGGAACTAATTCTTCTCAAGAACCTATTGAAAATGGTT
ACCAAGACTGGTGTATAATATTATCGGAAGTACTGAAGTAAAATG
AGCTAAATATCAAGTCAGACCCAATTTCAGGAACTTACAGGAAAGGTGACAAA
ATAAAATGTTATGCAAGTATTGACAGCAGATGGTACACAGTGGATTCTTA
CAAAATCTTATAGTGGTGTCTCGCTTATATTCTGTGAAAAGCTAACTA
CAAGTAGTGAAGGAGGCAAGATGAGGGGCACTAACCGACTAGTTATCCC
ACTAAAGCCTACTCTGTAAACAAATTCAAGGAAGCAATAATCAAGAGAA
AATAGCAACGCAAGGAAATTATACATTTCACATAAAGTAGAAGTAAAAA
ATGAAGCTAAGGTAGCGAGTCAACTCAATTACATTGACAAAGGAGAC
AGAATTTTTACGACCAAATACTAACTATTGAAGGAAATCAGTGGTTATC
TTATAATCTTACGGTGTCTCGTTTGTGTTCTGTGAAAAGCAT
CTTCAGTAGAAAAAACTGAAGATAAAGGAAAAGTGTCTCTCAACCCCAA
GCCGCTTAACTTAAACTTAAACTGGTAGACTGACTATTCTAACGAAACACTAC
AGGTTTTGATATTAAATTCAGAATTAAAGATGATAACGGTATCGCTG
CTGTTAAGGTACCGGTTGGACTGAACAAGGAGGGCAAGATGATATTAA
TGGTATCAGCTGTAACACTGGGAGTGGCAACTACAAAGTAGCTGTATC
ATTGCTGACCATATAAGATGAGAGGGCTTTATAATATTCTTACT
ACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACAAAGTGACA
GTAGCTGGAACTAATTCTTCTCAAGAACCTATTGAAAATGGTTTAGC
GACTGGTTTATAATTATTCGGAAAGTACTGAAGTAAAAAATGAAGCTA
AAATATCAAGTCAGACCCAATTACTTAAAGGTTGACAAAATAAAT
TATGATCAAGTATTGACAGCAGATGGTACACAGTGGATTCTACAAATC
TATAGTGGTTCTCGCTTATATTCTGTGAAAAGCTAACTACAAGTA
GTGAAAAGCAGGAAAGATGAGGGGCACTAACCGACTAGTTATCCCAACTA
CCTAAACAGGTACCTATACTTACTAAACTGTAGATGTGAAGAGTC
ACTAAAGTATCAAGTGTAGTAGATGTCATCAGTGGATTCTAC
AAGAGTTATTCCGGTATTGTCGCTTATATTGAAATT

SEQ ID NO. 8909

STRAIN CJB110

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTCTC
TACGTAAATATAAATTGGTTAGCATCAGTAATTAGGGTCAATTCA
ATGGTCACAAGTCCGTGTTTGCGGATCAAACATACATCGGTTCAAGTTAA
TAATCAGACAGGCACTAGTGTGGATGCTAAATTCCTCAATGAGACAA
GTGCGGTACAGTGTGATTACTTCATAATGATAGTGTCAAGCGTCTGAT
AAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTCTT
ACTAGAGACAAGCCAATTGGGAAAAAAACATTACCTGAAACAAGGGAATT
ATGTTTATAGCAGGAAACCGAGGTGAAAATACACCTTCAAAATCAGCC
CCAGTAGCTTCTATGCAAGGAGGTGATAAAGGTTTCTATGACCAAGT
ATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTGTGGG
TACGTGATACGCTATTGAGTCAGTACGATCCATCAGGAGGGTTGAGAG
ACTAAAGCCTACTCTGTAAACAAATTCAAGGAAGCAATAATCAAGAGAA
AATAGCAACGCAAGGAAATTATACATTTCACATAAAGTAGAAGTAAAAA
ATGAAGCTAAGGTAGCGAGTCAACTCAATTACATTGACAAAGGAGAC
AGAATTTTTACGACCAAATACTAACTATTGAAGGAAATCAGTGGTTATC
TTATAATCTTACGGTGTCTCGTTTGTGTTCTGTGAAAAGCAT
CTTCAGTAGAAAAAACTGAAGATAAAGGAAAAGTGTCTCTCAACCCCAA
GCCGCTTAACTTAAACTTAAACTGGTAGACTGACTATTCTAACGAAACACTAC
AGGTTTTGATATTAAATTCAGAATTAAAGATGATAACGGTATCGCTG
CTGTTAAGGTACCGGTTGGACTGAACAAGGAGGGCAAGATGATATTAA
TGGTATCAGCTGTAACACTGGGAGTGGCAACTACAAAGTAGCTGTATC
ATTGCTGACCATATAAGATGAGAGGGCTTTATAATATTCTTACT
ACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACAAAGTGACA
GTAGCTGGAACTAATTCTTCTCAAGAACCTATTGAAAATGGTTTAGC
GACTGGTTTATAATTATTCGGAAAGTACTGAAGTAAAAAATGAAGCTA
AAATATCAAGTCAGACCCAATTACTTAAAGGTTGACAAAATAAAT
TATGATCAAGTATTGACAGCAGATGGTACACAGTGGATTCTACAAATC
TATAGTGGTTCTCGCTTATATTCTGTGAAAAGCTAACTACAAGTA
GTGAAAAGCAGGAAAGATGAGGGGCACTAACCGACTAGTTATCCCAACTA
CCTAAACAGGTACCTATACTTACTAAACTGTAGATGTGAAGAGTC
ACTAAAGTATCAAGTCCGAGTGGATTAAATTCTAACGAAAGGTGAAAAAA
TACATTATGATCAAGTGTAGTAGATGTCATCAGTGGATTCTAC
AAGAGTTATTCCGGTATTGTCGCTTATATTGAAATT

SEQ ID NO. 8910

STRAIN 1169NT

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTC
TCTACGTAAATATAAATTGGTTAGCATCAGTAATTAGGGTCAATTCA
TAATGGTCACAAGTCCGTGTTTGCGGATCAAACATACATCGGTTCAAGTT
ATAATCAGACAGGCACTAGTGTGGATGCTAAATTCCTCAATGAGAC
AAGTGCCTCAAGTGTGATTACTTCATAATGATAGTGTCAAGCGTCTG
AAAGTTGTAATAGTCAAAATACGGCAACAAAGGACATTACTCT
TTAGTAGAGACAAAGCCAATTGGTGGAAAAAAACATTACCTGAAACAGGGA
TTATGTTTATAGCAGGAAAGGAGGTGAAAATACACCTTCAAATCAG
CCCTAGTAGCTTCTATGCAAGAACAGGAGTAAAGTTTCTATGACCAA
GTATTAAATAAGATAATGTGAAATGGATTCTATATAAGTCTTTGGTGG
CGTACGTCGATACGCGCTATTGAGTCAGTAGATCCATCAGGAGGGTCA

Table 89: Comparative Sequences relating to SAG1350

AGACTAAAGCACCTACTCCGTAAACAAATTAGGAAGCAATAATCAAGAG
 AAAATAGCAACCGAAGGAAATTATAACATTTCACATAAAGTAGAAGTAA
 AAATGAAGCTAAGGTAGCGACTCCAACCTCAATTACATTGGACAAAGGGAG
 ACAGAATTTTACGACCAAATTAACTAATTGAGAAATCAGTGGTTA
 TCTTATAAATCATTCAATGGTTCGCGTTTGTGTTGCTAGGTAAAGC
 ATCTTCAGTAGAGAAAATCAGAAGATAAAGAAAAAGTGTCTCTCAACCCAC
 AAGCCGTTAATTAACTAACCTGGTAGACTATTCTAACGAAACAAACT
 ACAGGTTTGATATTAAACGAAATTTAGATGATAACCGGTATCGC
 TGCTGTTAAGGTACCGGTTGGACTGAACAAGGAGGGCAAGATGATATTAA
 AATGGTACAGCTGTAACACTGGGATGCAACTACAAAGTAGCTGTTA
 TCATTTGCTGACCATAAAGATGAGAAGGGTCTTTATAATATTCTTATA
 CTACCAAGAAGCTAGTGGGACACTGTAGGTGTAACAGGAACCTAAAGTGA
 CAGTAGCTGAACTAATTCTCAAGAACCTATTGAAAATGGTTAGCA
 AAGACTGGTGTATAATATTGAGTAACGAGTAAAGTGAAGC
 TAAAATATCAAGTCAGACCCAAATTACTTAAAGAAAAGGTGACAAAATAA
 ATTATGATCAAGTATTGACAGCAGATGGTACCTAGTGGATTCTTACAAA
 TCTTATAGTGGTTCGCGCTATATTCTGTGAAAAAAGCTAACACTAACAG
 TAGTGAAGGACGAAAGATGAGGCGACTAAACCGACTAGTTTACCCAACT
 TACCTAAAACAGTACCTATACTTAAACTAAACTGTAGATGTGAAAAGT
 CAACCTAAAGTACAGTCCAGTGGAAATTAACTTAAAGGGTGAAGA
 AATACATTATGATCAAGTGTAGTAGATGATGGTCACTAGTGGATTTCAT
 ACAAGAGTTTCCGGTATTGCTCGCTATATTGAAATT

SEQ ID NO. 8911

STRAIN JM9130013

AAAAAAGGACAAGTAAATGATACTAACGAACTCTTACT
 CTCACCTAAATATAATTGGTTAGCATCAGTAATTAGGGTCATT
 ATAATGGTCACAAAGTCCTGTTTTCGGATCAAACCTACATGGTTCAAGT
 TATAATCAGACAGGCACACTAGTGTGGATGCTAATAATTCTCAATGAGA
 CAAGTGGCTAGTGTGATTACTCCAAATAATGATAGTGTCAAGGGCTCT
 GATAAAGTGTAAATAGTCAAAATACGGCAACAAAGGGACATTACTACTCC
 TTAGTAGAGACAAGCCAATGGGAAAAAACATTACCTAACAGGAA
 ATTATGTTATAGCAGGAAAGGGAGGTGAAAAAATACACCTTCAAAATCA
 GCCCAGTAGCTTCTATGCAAGAAGGGTGTGAAAAAGTTCTATGACCA
 AGTATTAAATAAGATAATGTGAAATGGATTCTATATAAGTCTTTTGTG
 GCGTACGTCGATACGCGACTATTGAGTCAGTACATCAGGAGGGTCA
 GAGACTAAAGCCTACTCCTGTAACAAATTCAAGGAAGCAATAATCAAGA
 GAAAATAGCAACGCAAGGAAATTACATTTACATTTCACATAAAGTAGAAGTAA
 AAAATGAAGCTAAGGTAGCGAGTCAACTCAATTACATTGGACAAAGGA
 GACAGAATTTCAGGACCAAAACTAAACTATTGAGGAAATCACTGGTT
 ATCTTATAATCAATGGTGTGCTGTTTGTGTTTGTGCTAGGTAAAG
 CATCTTCAGTAGAAAAAAACTGAAGATAAAGAAAAAGTGTCTCCCAACCA
 CAAGCCCATTACTAAACTGGTAGACTGACTATTATAACGAAACAAAC
 TACAGGTTTGATATTAAATACGAATAATTAAAGATGATAACGGTATCG
 CTGCTGTTAAGGTACCGGTTGGACTGACAAGGAGGGCAAGATGATATT
 AAATGGTATACAGCTGTAACACTGGGATGCAACTACAAAGTAGCTGT
 ATCATTTGCTGACATAAGAATGAGAAGGGCTTTATAATATTCTTACATT
 ACTACCAAGACTACTGGGACACTTGTAGGTGTAACAGGAACCTAAAGTG
 ACAGTAGCTGGAACTAACTCTCAAGAACCTATTGAAAATGGTTAGC
 AAAGACTGGTGTATAATATAATGAGTACTGAAGTAAAGGAA
 CTAAAATATCAAGTCAGACCCAAATTACTTAAAGGGTGAACAAATAA
 AATTATGATCAAGTATTGACAGCAGATGGTACCACTGGGATTTCTTACAA
 ATCTTATAGTGGTGTGCTGCTATATTCTGTGAAAAGCTAACACAA
 GTAGTGAAGGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
 TACCTAAAACAGGTACCTACATTTACTAAACTGTAGATGTGAGAG
 TCAACCTAAAGTACAGTCCAGTGGAAATTAAATTTCAAAAGGGTGAAA
 AATACATTATGATCAAGTGTAGTAGATGGTCACTAGTGGATTTC
 TACAAGAGTTTCCGGTATTGCTCGCTATATTGAAATT

PRETTY of: /biotmp/msa255059.2{ *} February 11, 2003 08:41 ..

msa255059.2{91_M732}	-----	--CAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA	1
msa255059.2{91_M781}	~~AAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA	
msa255059.2{91_COH1}	~~AAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA	
msa255059.2{91_18RS21}	~~AAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA	
msa255059.2{91_2603}	atgAAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA	
msa255059.2{91_1169NT}	~~AAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA	
msa255059.2{91_090}	~~AAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA	
msa255059.2{91_A909}	~~AAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA	
msa255059.2{91_CJB110}	~~AAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA	
msa255059.2{91_H36B}	~~AAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA	
msa255059.2{91_JM9130013}	~~AAAAG	GACAAGTAAA	TGATACTAAG	CAATCTTACT	CTCTACGTAA	
Consensus	*****	*****	*****	*****	*****	
msa255059.2{91_M732}	ATATAAAATT	GGTTAGCAT	CAGTAATT	AGGGTCATT	ATAATGGTCA	50
msa255059.2{91_M781}	ATATAAAATT	GGTTAGCAT	CAGTAATT	AGGGTCATT	ATAATGGTCA	
msa255059.2{91_COH1}	ATATAAAATT	GGTTAGCAT	CAGTAATT	AGGGTCATT	ATAATGGTCA	
msa255059.2{91_18RS21}	ATATAAAATT	GGTTAGCAT	CAGTAATT	AGGGTCATT	ATAATGGTCA	
msa255059.2{91_2603}	ATATAAAATT	GGTTAGCAT	CAGTAATT	AGGGTCATT	ATAATGGTCA	
msa255059.2{91_1169NT}	ATATAAAATT	GGTTAGCAT	CAGTAATT	AGGGTCATT	ATAATGGTCA	
51						100
msa255059.2{91_M732}	ATATAAAATT	GGTTAGCAT	CAGTAATT	AGGGTCATT	ATAATGGTCA	
msa255059.2{91_M781}	ATATAAAATT	GGTTAGCAT	CAGTAATT	AGGGTCATT	ATAATGGTCA	
msa255059.2{91_COH1}	ATATAAAATT	GGTTAGCAT	CAGTAATT	AGGGTCATT	ATAATGGTCA	
msa255059.2{91_18RS21}	ATATAAAATT	GGTTAGCAT	CAGTAATT	AGGGTCATT	ATAATGGTCA	
msa255059.2{91_2603}	ATATAAAATT	GGTTAGCAT	CAGTAATT	AGGGTCATT	ATAATGGTCA	
msa255059.2{91_1169NT}	ATATAAAATT	GGTTAGCAT	CAGTAATT	AGGGTCATT	ATAATGGTCA	

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_090}	ATATAAATTG	GGTTTAGCAT	CAGTAATT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_A909}	ATATAAATTG	GGTTTAGCAT	CAGTAATT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_CJB110}	ATATAAATTG	GGTTTAGCAT	CAGTAATT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_H36B}	ATATAAATTG	GGTTTAGCAT	CAGTAATT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_JM9130013}	ATATAAATTG	GGTTTAGCAT	CAGTAATT	AGGGTCATTC	ATAATGGTCA
Consensus	*****	*****	*****	*****	*****
	101			150	
msa255059.2{91_M732}	CAAGTCCTGT	TTTGCGGAT	CAAACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_M781}	CAAGTCCTGT	TTTGCGGAT	CAAACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_COH1}	CAAGTCCTGT	TTTGCGGAT	CAAACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_18RS21}	CAAGTCCTGT	TTTGCGGAT	CAAACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_2603}	CAAGTCCTGT	TTTGCGGAT	CAAACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_1169NT}	CAAGTCCTGT	TTTGCGGAT	CAAACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_090}	CAAGTCCTGT	TTTGCGGAT	CAAACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_A909}	CAAGTCCTGT	TTTGCGGAT	CAAACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_CJB110}	CAAGTCCTGT	TTTGCGGAT	CAAACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_H36B}	CAAGTCCTGT	TTTGCGGAT	CAAACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_JM9130013}	CAAGTCCTGT	TTTGCGGAT	CAAACAT	CGGTTCAAGT	TAATAATCAG
Consensus	*****	*****	*****	*****	*****
	151			200	
msa255059.2{91_M732}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_M781}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_COH1}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_18RS21}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_2603}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_1169NT}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_090}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_A909}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_CJB110}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_H36B}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_JM9130013}	ACAGGCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
Consensus	*****	*****	*****	*****	*****
	201			250	
msa255059.2{91_M732}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAAGTTG
msa255059.2{91_M781}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAAGTTG
msa255059.2{91_COH1}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAAGTTG
msa255059.2{91_18RS21}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAAGTTG
msa255059.2{91_2603}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAAGTTG
msa255059.2{91_1169NT}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAAGTTG
msa255059.2{91_090}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAAGTTG
msa255059.2{91_A909}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAAGTTG
msa255059.2{91_CJB110}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAAGTTG
msa255059.2{91_H36B}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAAGTTG
msa255059.2{91_JM9130013}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAAGTTG
Consensus	*****	*****	*****	*****	*****
	251			300	
msa255059.2{91_M732}	TAAATAGTC	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_M781}	TAAATAGTC	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_COH1}	TAAATAGTC	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_18RS21}	TAAATAGTC	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_2603}	TAAATAGTC	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_1169NT}	TAAATAGTC	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_090}	TAAATAGTC	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_A909}	TAAATAGTC	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_CJB110}	TAAATAGTC	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_H36B}	TAAATAGTC	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_JM9130013}	TAAATAGTC	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
Consensus	*****	*****	*****	*****	*****
	301			350	
msa255059.2{91_M732}	ACAAAGCCAA	TGGTGGAAAAA	AACATTACCT	GAACAAGGGAA	ATTATGTTTA
msa255059.2{91_M781}	ACAAAGCCAA	TGGTGGAAAAA	AACATTACCT	GAACAAGGGAA	ATTATGTTTA
msa255059.2{91_COH1}	ACAAAGCCAA	TGGTGGAAAAA	AACATTACCT	GAACAAGGGAA	ATTATGTTTA
msa255059.2{91_18RS21}	ACAAAGCCAA	TGGTGGAAAAA	AACATTACCT	GAACAAGGGAA	ATTATGTTTA
msa255059.2{91_2603}	ACAAAGCCAA	TGGTGGAAAAA	AACATTACCT	GAACAAGGGAA	ATTATGTTTA
msa255059.2{91_1169NT}	ACAAAGCCAA	TGGTGGAAAAA	AACATTACCT	GAACAAGGGAA	ATTATGTTTA
msa255059.2{91_090}	ACAAAGCCAA	TGGTGGAAAAA	AACATTACCT	GAACAAGGGAA	ATTATGTTTA
msa255059.2{91_A909}	ACAAAGCCAA	TGGTGGAAAAA	AACATTACCT	GAACAAGGGAA	ATTATGTTTA
msa255059.2{91_CJB110}	ACAAAGCCAA	TGGTGGAAAAA	AACATTACCT	GAACAAGGGAA	ATTATGTTTA
msa255059.2{91_H36B}	ACAAAGCCAA	TGGTGGAAAAA	AACATTACCT	GAACAAGGGAA	ATTATGTTTA
msa255059.2{91_JM9130013}	ACAAAGCCAA	TGGTGGAAAAA	AACATTACCT	GAACAAGGGAA	ATTATGTTTA
Consensus	*****	*****	*****	*****	*****
	351			400	
msa255059.2{91_M732}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAAATCA	GCCCCAGTAG
msa255059.2{91_M781}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAAATCA	GCCCCAGTAG
msa255059.2{91_COH1}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAAATCA	GCCCCAGTAG
msa255059.2{91_18RS21}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAAATCA	GCCCCAGTAG
msa255059.2{91_2603}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAAATCA	GCCCCAGTAG

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_1169NT}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TCAAAATCA	GCCCCAGTAG
msa255059.2{91_090}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TCAAAATCA	GCCCCAGTAG
msa255059.2{91_A909}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TCAAAATCA	GCCCCAGTAG
msa255059.2{91_CJB110}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TCAAAATCA	GCCCCAGTAG
msa255059.2{91_H36B}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TCAAAATCA	GCCCCAGTAG
msa255059.2{91_JM9130013}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TCAAAATCA	GCCCCAGTAG
Consensus	*****	*****	*****	*****	*****
	401				450
msa255059.2{91_M732}	CTTTCTATGC	AAAGAAAAGCT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_M781}	CTTTCTATGC	AAAGAAAAGCT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_COH1}	CTTTCTATGC	AAAGAAAAGCT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_18RS21}	CTTTCTATGC	AAAGAAAAGCT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_2603}	CTTTCTATGC	AAAGAAAAGCT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_1169NT}	CTTTCTATGC	AAAGAAAAGCT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_090}	CTTTCTATGC	AAAGAAAAGCT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_A909}	CTTTCTATGC	AAAGAAAAGCT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_CJB110}	CTTTCTATGC	AAAGAAAAGCT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_H36B}	CTTTCTATGC	AAAGAAAAGCT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_JM9130013}	CTTTCTATGC	AAAGAAAAGCT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
Consensus	*****	*****	*****	*****	*****
	451				500
msa255059.2{91_M732}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_M781}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_COH1}	AAAGATAATG	TtAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_18RS21}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_2603}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_1169NT}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_090}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_A909}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_CJB110}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_H36B}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_JM9130013}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
Consensus	*****	*****	*****	*****	*****
	501				550
msa255059.2{91_M732}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_M781}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_COH1}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_18RS21}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_2603}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_1169NT}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_090}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_A909}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_CJB110}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_H36B}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
msa255059.2{91_JM9130013}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTCA	GAGACTAAAG
Consensus	*****	*****	*****	*****	*****
	551				600
msa255059.2{91_M732}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_M781}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_COH1}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_18RS21}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_2603}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_1169NT}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_090}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_A909}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_CJB110}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_H36B}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_JM9130013}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
Consensus	*****	*****	*****	*****	*****
	601				650
msa255059.2{91_M732}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_M781}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_COH1}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_18RS21}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_2603}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_1169NT}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_090}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_A909}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_CJB110}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_H36B}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_JM9130013}	ACGCAAGGAA	ATTATACATT	TTCACATAAA	GTAGAAGTAA	AAAATGAAGC
Consensus	*****	*****	*****	*****	*****
	651				700
msa255059.2{91_M732}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_M781}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_COH1}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_18RS21}	TAAGGTAGCG	AGTCCAACCTC	AATTTACATT	GGACAAAGGA	GACAGAATTT

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_M732}	TTAGGTAGCG	AGTCCAACTC	AATTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_M781}	TTAGGTAGCG	AGTCCAACTC	AATTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_COH1}	TTAGGTAGCG	AGTCCAACTC	AATTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_18RS21}	TTAGGTAGCG	AGTCCAACTC	AATTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_2603}	TTAGGTAGCG	AGTCCAACTC	AATTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_1169NT}	TTAGGTAGCG	AGTCCAACTC	AATTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_090}	TTAGGTAGCG	AGTCCAACTC	AATTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_A909}	TTAGGTAGCG	AGTCCAACTC	AATTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_CJB110}	TTAGGTAGCG	AGTCCAACTC	AATTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_H36B}	TTAGGTAGCG	AGTCCAACTC	AATTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_JM9130013}	TTAGGTAGCG	AGTCCAACTC	AATTACATT	GGACAAAGGA	GACAGAATTT
Consensus	*****	*****	*****	*****	*****
701	750				
msa255059.2{91_M732}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_M781}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_COH1}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_18RS21}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_2603}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_1169NT}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_090}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_A909}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_CJB110}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_H36B}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_JM9130013}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
Consensus	*****	*****	*****	*****	*****
751	800				
msa255059.2{91_M732}	TCATTCAATG	GTGTTCGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_M781}	TCATTCAATG	GTGTTCGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_COH1}	TCATTCAATG	GTGTTCGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_18RS21}	TCATTCAATG	GTGTTCGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_2603}	TCATTCAATG	GTGTTCGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_1169NT}	TCATTCAATG	GTGTTCGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_090}	TCATTCAATG	GTGTTCGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_A909}	TCATTCAATG	GTGTTCGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_CJB110}	TCATTCAATG	GTGTTCGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_H36B}	TCATTCAATG	GTGTTCGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_JM9130013}	TCATTCAATG	GTGTTCGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
Consensus	*****	*****	*****	*****	*****
801	850				
msa255059.2{91_M732}	AGAAAAAAACT	GAAGATAAAAG	AAAAAGTGTG	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_M781}	AGAAAAAAACT	GAAGATAAAAG	AAAAAGTGTG	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_COH1}	AGAAAAAAACT	GAAGATAAAAG	AAAAAGTGTG	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_18RS21}	AGAAAAAAACT	GAAGATAAAAG	AAAAAGTGTG	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_2603}	AGAAAAAAACT	GAAGATAAAAG	AAAAAGTGTG	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_1169NT}	AGAAAAAAACT	GAAGATAAAAG	AAAAAGTGTG	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_090}	AGAAAAAAACT	GAAGATAAAAG	AAAAAGTGTG	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_A909}	AGAAAAAAACT	GAAGATAAAAG	AAAAAGTGTG	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_CJB110}	AGAAAAAAACT	GAAGATAAAAG	AAAAAGTGTG	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_H36B}	AGAAAAAAACT	GAAGATAAAAG	AAAAAGTGTG	TCCTCAACCA	CAAGCCCGTA
msa255059.2{91_JM9130013}	AGAAAAAAACT	GAAGATAAAAG	AAAAAGTGTG	TCCTCAACCA	CAAGCCCGTA
Consensus	*****	*****	*****	*****	*****
851	900				
msa255059.2{91_M732}	TTACTAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAAACAA	TACAGGTTTT
msa255059.2{91_M781}	TTACTAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAAACAA	TACAGGTTTT
msa255059.2{91_COH1}	TTACTAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAAACAA	TACAGGTTTT
msa255059.2{91_18RS21}	TTACTAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAAACAA	TACAGGTTTT
msa255059.2{91_2603}	TTACTAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAAACAA	TACAGGTTTT
msa255059.2{91_1169NT}	TTACTAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAAACAA	TACAGGTTTT
msa255059.2{91_090}	TTACTAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAAACAA	TACAGGTTTT
msa255059.2{91_A909}	TTACTAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAAACAA	TACAGGTTTT
msa255059.2{91_CJB110}	TTACTAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAAACAA	TACAGGTTTT
msa255059.2{91_H36B}	TTACTAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAAACAA	TACAGGTTTT
msa255059.2{91_JM9130013}	TTACTAAAC	TGGTAGACTG	ACTATTTcTA	ACGAAAACAA	TACAGGTTTT
Consensus	*****	*****	*****	*****	*****
901	950				
msa255059.2{91_M732}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTAA
msa255059.2{91_M781}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTAA
msa255059.2{91_COH1}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTAA
msa255059.2{91_18RS21}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTAA
msa255059.2{91_2603}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTAA
msa255059.2{91_1169NT}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTAA
msa255059.2{91_090}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTAA
msa255059.2{91_A909}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTAA
msa255059.2{91_CJB110}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTAA
msa255059.2{91_H36B}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTAA
msa255059.2{91_JM9130013}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTAA
Consensus	*****	*****	*****	*****	*****
951	1000				
msa255059.2{91_M732}	GGTACCGGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_M781}	GGTACCGGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_COH1}	GGTACCGGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_18RS21}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA	
msa255059.2{91_2603}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA	
msa255059.2{91_1169NT}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA	
msa255059.2{91_090}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA	
msa255059.2{91_A909}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA	
msa255059.2{91_CJB110}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA	
msa255059.2{91_H36B}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA	
msa255059.2{91_JM9130013}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA	
Consensus	*****	*****	*****	*****	*****	
						1050
msa255059.2{91_M732}	CAGCTGTAAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT	
msa255059.2{91_M781}	CAGCTGTAAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT	
msa255059.2{91_COH1}	CAGCTGTAAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT	
msa255059.2{91_18RS21}	CAGCTGTAAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT	
msa255059.2{91_2603}	CAGCTGTAAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT	
msa255059.2{91_1169NT}	CAGCTGTAAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT	
msa255059.2{91_090}	CAGCTGTAAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT	
msa255059.2{91_A909}	CAGCTGTAAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT	
msa255059.2{91_CJB110}	CAGCTGTAAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT	
msa255059.2{91_H36B}	CAGCTGTAAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT	
msa255059.2{91_JM9130013}	CAGCTGTAAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT	
Consensus	*****	*****	*****	*****	*****	
						1100
msa255059.2{91_M732}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTAT	ACTACCAAGA	
msa255059.2{91_M781}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTAT	ACTACCAAGA	
msa255059.2{91_COH1}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTAT	ACTACCAAGA	
msa255059.2{91_18RS21}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTAT	ACTACCAAGA	
msa255059.2{91_2603}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTAT	ACTACCAAGA	
msa255059.2{91_1169NT}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTAT	ACTACCAAGA	
msa255059.2{91_090}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTAT	ACTACCAAGA	
msa255059.2{91_A909}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTAT	ACTACCAAGA	
msa255059.2{91_CJB110}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTAT	ACTACCAAGA	
msa255059.2{91_H36B}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTAT	ACTACCAAGA	
msa255059.2{91_JM9130013}	GACCATAAGA	ATGAGAAGGG	TCTTTATAAT	ATTCAATTAT	ACTACCAAGA	
Consensus	*****	*****	*****	*****	*****	
						1150
msa255059.2{91_M732}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_M781}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_COH1}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_18RS21}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_2603}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_1169NT}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_090}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_A909}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_CJB110}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_H36B}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_JM9130013}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
Consensus	*****	*****	*****	*****	*****	
						1151
msa255059.2{91_M732}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_M781}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_COH1}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_18RS21}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_2603}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_1169NT}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_090}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_A909}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_CJB110}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_H36B}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
msa255059.2{91_JM9130013}	AGCTAGTGGG	ACACTTGTAG	GITGTAACAGG	AACTAAAGTG	ACAGTAGCTG	
Consensus	*****	*****	*****	*****	*****	
						1200
msa255059.2{91_M732}	GAACTAATTTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTACCC	AAAGACTGGT	
msa255059.2{91_M781}	GAACTAATTTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTACCC	AAAGACTGGT	
msa255059.2{91_COH1}	GAACTAATTTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTACCC	AAAGACTGGT	
msa255059.2{91_18RS21}	GAACTAATTTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTACCC	AAAGACTGGT	
msa255059.2{91_2603}	GAACTAATTTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTACCC	AAAGACTGGT	
msa255059.2{91_1169NT}	GAACTAATTTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTACCC	AAAGACTGGT	
msa255059.2{91_090}	GAACTAATTTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTACCC	AAAGACTGGT	
msa255059.2{91_A909}	GAACTAATTTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTACCC	AAAGACTGGT	
msa255059.2{91_CJB110}	GAACTAATTTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTACCC	AAAGACTGGT	
msa255059.2{91_H36B}	GAACTAATTTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTACCC	AAAGACTGGT	
msa255059.2{91_JM9130013}	GAACTAATTTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTACCC	AAAGACTGGT	
Consensus	*****	*****	*****	*****	*****	
						1250
msa255059.2{91_M732}	GTTTATAATA	TTATCGGAAG	TACTGAACTA	AAAAATGAAG	CTAAAATATC	
msa255059.2{91_M781}	GTTTATAATA	TTATCGGAAG	TACTGAACTA	AAAAATGAAG	CTAAAATATC	
msa255059.2{91_COH1}	GTTTATAATA	TTATCGGAAG	TACTGAACTA	AAAAATGAAG	CTAAAATATC	
msa255059.2{91_18RS21}	GTTTATAATA	TTATCGGAAG	TACTGAACTA	AAAAATGAAG	CTAAAATATC	
msa255059.2{91_2603}	GTTTATAATA	TTATCGGAAG	TACTGAACTA	AAAAATGAAG	CTAAAATATC	
msa255059.2{91_1169NT}	GTTTATAATA	TTATCGGAAG	TACTGAACTA	AAAAATGAAG	CTAAAATATC	
msa255059.2{91_090}	GTTTATAATA	TTATCGGAAG	TACTGAACTA	AAAAATGAAG	CTAAAATATC	
msa255059.2{91_A909}	GTTTATAATA	TTATCGGAAG	TACTGAACTA	AAAAATGAAG	CTAAAATATC	
msa255059.2{91_CJB110}	GTTTATAATA	TTATCGGAAG	TACTGAACTA	AAAAATGAAG	CTAAAATATC	
msa255059.2{91_H36B}	GTTTATAATA	TTATCGGAAG	TACTGAACTA	AAAAATGAAG	CTAAAATATC	
msa255059.2{91_JM9130013}	GTTTATAATA	TTATCGGAAG	TACTGAACTA	AAAAATGAAG	CTAAAATATC	
Consensus	*****	*****	*****	*****	*****	
						1251
msa255059.2{91_M732}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC	
msa255059.2{91_M781}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC	

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_COH1}	AGTCAGACCC	CAATTTACTT	TAGAAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_18RS21}	AGTCAGACCC	CAATTTACTT	TAGAAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_2603}	AGTCAGACCC	CAATTTACTT	TAGAAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_1169NT}	AGTCAGACCC	CAATTTACTT	TAGAAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_090}	AGTCAGACCC	CAATTTACTT	TAGAAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_A909}	AGTCAGACCC	CAATTTACTT	TAGAAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_CJB110}	AGTCAGACCC	CAATTTACTT	TAGAAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_H36B}	AGTCAGACCC	CAATTTACTT	TAGAAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_JM9130013}	AGTCAGACCC	CAATTTACTT	TAGAAAAAAGG	TGACAAAATA	AATTATGATC
Consensus	*****	*****	*****	*****	*****
1301					1350
msa255059.2{91_M732}	AAGTATTGAC	AGCAGATGGT	TACCAGTGG	TTCTTACAA	ATCTTATAGT
msa255059.2{91_M781}	AAGTATTGAC	AGCAGATGGT	TACCAGTGG	TTCTTACAA	ATCTTATAGT
msa255059.2{91_COH1}	AAGTATTGAC	AGCAGATGGT	TACCAGTGG	TTCTTACAA	ATCTTATAGT
msa255059.2{91_18RS21}	AAGTATTGAC	AGCAGATGGT	TACCAGTGG	TTCTTACAA	ATCTTATAGT
msa255059.2{91_2603}	AAGTATTGAC	AGCAGATGGT	TACCAGTGG	TTCTTACAA	ATCTTATAGT
msa255059.2{91_1169NT}	AAGTATTGAC	AGCAGATGGT	TACCAGTGG	TTCTTACAA	ATCTTATAGT
msa255059.2{91_090}	AAGTATTGAC	AGCAGATGGT	TACCAGTGG	TTCTTACAA	ATCTTATAGT
msa255059.2{91_A909}	AAGTATTGAC	AGCAGATGGT	TACCAGTGG	TTCTTACAA	ATCTTATAGT
msa255059.2{91_CJB110}	AAGTATTGAC	AGCAGATGGT	TACCAGTGG	TTCTTACAA	ATCTTATAGT
msa255059.2{91_H36B}	AAGTATTGAC	AGCAGATGGT	TACCAGTGG	TTCTTACAA	ATCTTATAGT
msa255059.2{91_JM9130013}	AAGTATTGAC	AGCAGATGGT	TACCAGTGG	TTCTTACAA	ATCTTATAGT
Consensus	*****	*****	*****	*****	*****
1351					1400
msa255059.2{91_M732}	GGTGTTCGTC	GCTATATTC	TGTAAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_M781}	GGTGTTCGTC	GCTATATTC	TGTAAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_COH1}	GGTGTTCGTC	GCTATATTC	TGTAAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_18RS21}	GGTGTTCGTC	GCTATATTC	TGTAAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_2603}	GGTGTTCGTC	GCTATATTC	TGTAAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_1169NT}	GGTGTTCGTC	GCTATATTC	TGTAAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_090}	GGTGTTCGTC	GCTATATTC	TGTAAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_A909}	GGTGTTCGTC	GCTATATTC	TGTAAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_CJB110}	GGTGTTCGTC	GCTATATTC	TGTAAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_H36B}	GGTGTTCGTC	GCTATATTC	TGTAAAAAG	CTAACTACAA	GTAGTGAAA
msa255059.2{91_JM9130013}	GGTGTTCGTC	GCTATATTC	TGTAAAAAG	CTAACTACAA	GTAGTGAAA
Consensus	*****	*****	*****	*****	*****
1401					1450
msa255059.2{91_M732}	AGCGAAAGAT	GAGGCCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_M781}	AGCGAAAGAT	GAGGCCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_COH1}	AGCGAAAGAT	GAGGCCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_18RS21}	AGCGAAAGAT	GAGGCCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_2603}	AGCGAAAGAT	GAGGCCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_1169NT}	AGCGAAAGAT	GAGGCCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_090}	AGCGAAAGAT	GAGGCCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_A909}	AGCGAAAGAT	GAGGCCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_CJB110}	AGCGAAAGAT	GAGGCCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_H36B}	AGCGAAAGAT	GAGGCCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_JM9130013}	AGCGAAAGAT	GAGGCCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
Consensus	*****	*****	*****	*****	*****
1451					1500
msa255059.2{91_M732}	CAGGTACCTA	TACATTTACT	AAAACGTGAG	ATGTGAAAG	TCAACCTAAA
msa255059.2{91_M781}	CAGGTACCTA	TACATTTACT	AAAACGTGAG	ATGTGAAAG	TCAACCTAAA
msa255059.2{91_COH1}	CAGGTACCTA	TACATTTACT	AAAACGTGAG	ATGTGAAAG	TCAACCTAAA
msa255059.2{91_18RS21}	CAGGTACCTA	TACATTTACT	AAAACGTGAG	ATGTGAAAG	TCAACCTAAA
msa255059.2{91_2603}	CAGGTACCTA	TACATTTACT	AAAACGTGAG	ATGTGAAAG	TCAACCTAAA
msa255059.2{91_1169NT}	CAGGTACCTA	TACATTTACT	AAAACGTGAG	ATGTGAAAG	TCAACCTAAA
msa255059.2{91_090}	CAGGTACCTA	TACATTTACT	AAAACGTGAG	ATGTGAAAG	TCAACCTAAA
msa255059.2{91_A909}	CAGGTACCTA	TACATTTACT	AAAACGTGAG	ATGTGAAAG	TCAACCTAAA
msa255059.2{91_CJB110}	CAGGTACCTA	TACATTTACT	AAAACGTGAG	ATGTGAAAG	TCAACCTAAA
msa255059.2{91_H36B}	CAGGTACCTA	TACATTTACT	AAAACGTGAG	ATGTGAAAG	TCAACCTAAA
msa255059.2{91_JM9130013}	CAGGTACCTA	TACATTTACT	AAAACGTGAG	ATGTGAAAG	TCAACCTAAA
Consensus	*****	*****	*****	*****	*****
1501					1550
msa255059.2{91_M732}	GTATCAAGTC	CAGTGGAAATT	TAATTTCAA	AAGGGTAAAA	AAATACATTA
msa255059.2{91_M781}	GTATCAAGTC	CAGTGGAAATT	TAATTTCAA	AAGGGTAAAA	AAATACATTA
msa255059.2{91_COH1}	GTATCAAGTC	CAGTGGAAATT	TAATTTCAA	AAGGGTAAAA	AAATACATTA
msa255059.2{91_18RS21}	GTATCAAGTC	CAGTGGAAATT	TAATTTCAA	AAGGGTAAAA	AAATACATTA
msa255059.2{91_2603}	GTATCAAGTC	CAGTGGAAATT	TAATTTCAA	AAGGGTAAAA	AAATACATTA
msa255059.2{91_1169NT}	GTATCAAGTC	CAGTGGAAATT	TAATTTCAA	AAGGGTAAAA	AAATACATTA
msa255059.2{91_090}	GTATCAAGTC	CAGTGGAAATT	TAATTTCAA	AAGGGTAAAA	AAATACATTA
msa255059.2{91_A909}	GTATCAAGTC	CAGTGGAAATT	TAATTTCAA	AAGGGTAAAA	AAATACATTA
msa255059.2{91_CJB110}	GTATCAAGTC	CAGTGGAAATT	TAATTTCAA	AAGGGTAAAA	AAATACATTA
msa255059.2{91_H36B}	GTATCAAGTC	CAGTGGAAATT	TAATTTCAA	AAGGGTAAAA	AAATACATTA
msa255059.2{91_JM9130013}	GTATCAAGTC	CAGTGGAAATT	TAATTTCAA	AAGGGTAAAA	AAATACATTA
Consensus	*****	*****	*****	*****	*****
1551					1600
msa255059.2{91_M732}	GTATCAAGTC	TTAGTAGTAG	ATGGTCATCA	GTGGATITCA	TACAAGAGTT

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_M781}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_COH1}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_18RS21}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_2603}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_1169NT}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_090}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_A909}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_CJB110}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_H36B}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_JM9130013}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
Consensus	*****	*****	*****	*****	*****

1601	1629		
msa255059.2{91_M732}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_M781}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_COH1}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_18RS21}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_2603}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_1169NT}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_090}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_A909}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_CJB110}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_H36B}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
msa255059.2{91_JM9130013}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT
Consensus	*****	*****	*****

SEQ ID NO. 8912

STRAIN 2603 frame: 1

MKKGVNNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNQGTTSVDANNS
 NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNVYVSKET
 TEVKNTPSKSAPVAFYAKKGDKVYDQVFNKDNVKWISYKSFCKVRRYAAIESLDPSSGS
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILITI
 IEGNQWLISYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 DILITNIKDDNGIAAVKPVVTEQGGQDDIKWYTAVITGDNKYKAVSFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKTVAGTNSSQEPPIENGLAKTGVYNIIGSTEVKNEAKISSQTO
 QFTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKLTTSSSEKAKDEATKPTSYPNL
 PTKTGTYTFTKTVDVKSQPKVSSPVEFNFKGEKIHQDQLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8913

STRAIN 090 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNQGTTSVDANNS
 NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNVYVSKET
 EVKNTPSKSAPVAFYAKKGDKVYDQVFNKDNVKWISYKSFCKVRRYAAIESLDPSSGS
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILITI
 EGNQWLISYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 DILITNIKDDNGIAAVKPVVTEQGGQDDIKWYTAVITGDNKYKAVSFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKTVAGTNSSQEPPIENGLAKTGVYNIIGSTEVKNEAKISSQTO
 QFTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKLTTSSSEKAKDEATKPTSYPNL
 PTKTGTYTFTKTVDVKSQPKVSSPVEFNFKGEKIHQDQLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8914

STRAIN A909 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNQGTTSVDANNS
 NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNVYVSKET
 EVKNTPSKSAPVAFYAKKGDKVYDQVFNKDNVKWISYKSFCKVRRYAAIESLDPSSGS
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILITI
 EGNQWLISYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 DILITNIKDDNGIAAVKPVVTEQGGQDDIKWYTAVITGDNKYKAVSFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKTVAGTNSSQEPPIENGLAKTGVYNIIGSTEVKNEAKISSQTO
 QFTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKLTTSSSEKAKDEATKPTSYPNL
 PTKTGTYTFTKTVDVKSQPKVSSPVEFNFKGEKIHQDQLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8915

STRAIN H36B frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNQGTTSVDANNS
 NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNVYVSKET
 EVKNTPSKSAPVAFYAKKGDKVYDQVFNKDNVKWISYKSFCKVRRYAAIESLDPSSGS
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILITI
 EGNQWLISYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 DILITNIKDDNGIAAVKPVVTEQGGQDDIKWYTAVITGDNKYKAVSFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKTVAGTNSSQEPPIENGLAKTGVYNIIGSTEVKNEAKISSQTO
 QFTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKLTTSSSEKAKDEATKPTSYPNL
 PTKTGTYTFTKTVDVKSQPKVSSPVEFNFKGEKIHQDQLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8916

STRAIN 18RS21 frame: 1

KKGQVNDTKQSYSLRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNQGTTSVDANNS
 NETSASSVITSNNDSVQASDKVVNSQNTATKDITTPLVETKPMVEKTLPEQGNVYVSKET

Table 89: Comparative Sequences relating to SAG1350

EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCKGVRRYAAIESLDPSGGSE
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKPVWTEQGGQDDIKWYTAVTTGDNKYKVAASFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKTVAGTNSSQEPPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTAADGYQWISYKSYSGVRRYIPVKKLITSSEKADEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8917

STRAIN M732 frame: 1
 QVNDTKQSYSLSRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNTGTSVDANNSSNET
 SASSVITSNNDSVQASDKVVNSQNTATKDITTPVETKPMVEKTLPEQGNYVYSKET
 NTTPVNTSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 PTPVNTSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKPVWTEQGGQDDIKWYTAVTTGDNKYKVAASFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKTVAGTNSSQEPPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTAADGYQWISYKSYSGVRRYIPVKKLITSSEKADEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8918

STRAIN COH1 frame: 1
 KKGQVNDTKQSYSLSRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNTGTSVDANNSSNET
 SASSVITSNNDSVQASDKVVNSQNTATKDITTPVETKPMVEKTLPEQGNYVYSKET
 EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCKGVRRYAAIESLDPSGGSE
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKPVWTEQGGQDDIKWYTAVTTGDNKYKVAASFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKTVAGTNSSQEPPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTAADGYQWISYKSYSGVRRYIPVKKLITSSEKADEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8919

STRAIN M781 frame: 1
 KKGQVNDTKQSYSLSRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNTGTSVDANNSSNET
 SASSVITSNNDSVQASDKVVNSQNTATKDITTPVETKPMVEKTLPEQGNYVYSKET
 EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCKGVRRYAAIESLDPSGGSE
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKPVWTEQGGQDDIKWYTAVTTGDNKYKVAASFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKTVAGTNSSQEPPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTAADGYQWISYKSYSGVRRYIPVKKLITSSEKADEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8920

STRAIN CJB110 frame: 1
 KKGQVNDTKQSYSLSRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNTGTSVDANNSSNET
 SASSVITSNNDSVQASDKVVNSQNTATKDITTPVETKPMVEKTLPEQGNYVYSKET
 EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCKGVRRYAAIESLDPSGGSE
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKPVWTEQGGQDDIKWYTAVTTGDNKYKVAASFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKTVAGTNSSQEPPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTAADGYQWISYKSYSGVRRYIPVKKLITSSEKADEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8921

STRAIN 1169NT frame: 1
 KKGQVNDTKQSYSLSRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNTGTSVDANNSSNET
 SASSVITSNNDSVQASDKVVNSQNTATKDITTPVETKPMVEKTLPEQGNYVYSKET
 EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCKGVRRYAAIESLDPSGGSE
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKPVWTEQGGQDDIKWYTAVTTGDNKYKVAASFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKTVAGTNSSQEPPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ
 FTLEKGDKINYDQVLTAADGYQWISYKSYSGVRRYIPVKKLITSSEKADEATKPTSYPNL
 PKTGTYTFTKTVDVKSQPKVSSPVEFNQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
 EI

SEQ ID NO. 8922

STRAIN JM9130013 frame: 1
 KKGQVNDTKQSYSLSRKYKFGLASVILGSFIMVTSPVFADQTTSVQVNNTGTSVDANNSSNET
 SASSVITSNNDSVQASDKVVNSQNTATKDITTPVETKPMVEKTLPEQGNYVYSKET
 EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVKWISYKSFCKGVRRYAAIESLDPSGGSE
 TKAPTPVTNSGSNNQEKIATQGNYTFSHKVEVKNEAKVASPTQFTLDKGDRIFYDQILTI
 EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPQPQARITKTGRLTISNETTTGFD
 ILITNIKDDNGIAAVKPVWTEQGGQDDIKWYTAVTTGDNKYKVAASFADHKNEKGLYNI
 HLYYQEASGTLVGVGTGKTVAGTNSSQEPPIENGLAKTGVYNIIGSTEVKNEAKISSQTQ

Table 89: Comparative Sequences relating to SAG1350

FTLEKGDKINYDQVLTADGYOWISYKSYGVRYYIPVKKLTTSEKAKEATKPTSYPL
 PKTGTYTFTKTIVDKSOPKVSSPVEFNFKGEKIHYDQVLVVDGHQWISYKSYGIRRYI
 EI

PRETTY of: /biotmp/msa255178.2{*} February 11, 2003 08:51 ..

						50
msa255178.2{91_090}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNO	
msa255178.2{91_18RS21}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNO	
msa255178.2{91_2603}	mkkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNO	
msa255178.2{91_A909}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNO	
msa255178.2{91_CJB110}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNO	
msa255178.2{91_H36B}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNO	
msa255178.2{91_JM9130013}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNO	
msa255178.2{91_COH1}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNO	
msa255178.2{91_M781}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNO	
msa255178.2{91_M732}	---QVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNO	
msa255178.2{91_1169NT}	-kkgQVNDTK	QSYSLRKYKF	GLASVILGSF	IMVTSPVFAD	QTTSVQVNNO	
Consensus	*****	*****	*****	*****	*****	
						100
msa255178.2{91_090}	TGTSVDA NNS	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPLVE	
msa255178.2{91_18RS21}	TGTSVDA NNS	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPLVE	
msa255178.2{91_2603}	TGTSVDA NNS	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPLVE	
msa255178.2{91_A909}	TGTSVDA NNS	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPLVE	
msa255178.2{91_CJB110}	TGTSVDA NNS	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPLVE	
msa255178.2{91_H36B}	TGTSVDD NNS	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPLVE	
msa255178.2{91_JM9130013}	TGTSVDA NNS	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPLVE	
msa255178.2{91_COH1}	TGTSVDA NNS	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPLVE	
msa255178.2{91_M781}	TGTSVDA NNS	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPLVE	
msa255178.2{91_M732}	TGTSVDA NNS	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPLVE	
msa255178.2{91_1169NT}	TGTSVDA NNS	SNETSASSVI	TSNNDSVQAS	DKVVNSQNTA	TKDITTPLVE	
Consensus	*****	*****	*****	*****	*****	
						101
msa255178.2{91_090}	TKPMVEKTL P	EQGNVYYSKE	TEVKNTPSKS	APVAFYAKKG	DKFYDQVFN	
msa255178.2{91_18RS21}	TKPMVEKTL P	EQGNVYYSKE	TEVKNTPSKS	APVAFYAKKG	DKFYDQVFN	
msa255178.2{91_2603}	TKPMVEKTL P	EQGNVYYSKE	TEVKNTPSKS	APVAFYAKKG	DKFYDQVFN	
msa255178.2{91_A909}	TKPMVEKTL P	EQGNVYYSKE	TEVKNTPSKS	APVAFYAKKG	DKFYDQVFN	
msa255178.2{91_CJB110}	TKPMVEKTL P	EQGNVYYSKE	TEVKNTPSKS	APVAFYAKKG	DKFYDQVFN	
msa255178.2{91_H36B}	TKPMVEKTL P	EQGNVYYSKE	TEVKNTPSKS	APVAFYAKKG	DKFYDQVFN	
msa255178.2{91_JM9130013}	TKPMVEKTL P	EQGNVYYSKE	TEVKNTPSKS	APVAFYAKKG	DKFYDQVFN	
msa255178.2{91_COH1}	TKPMVEKTL P	EQGNVYYSKE	TEVKNTPSKS	APVAFYAKKG	DKFYDQVFN	
msa255178.2{91_M781}	TKPMVEKTL P	EQGNVYYSKE	TEVKNTPSKS	APVAFYAKKG	DKFYDQVFN	
msa255178.2{91_M732}	TKPMVEKTL P	EQGNVYYSKE	TEVKNTPSKS	APVAFYAKKG	DKFYDQVFN	
msa255178.2{91_1169NT}	TKPMVEKTL P	EQGNVYYSKE	TEVKNTPSKS	APVAFYAKKG	DKFYDQVFN	
Consensus	*****	*****	*****	*****	*****	
						150
msa255178.2{91_090}	KDNVKWISYK	SFCGVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNQEKIA	
msa255178.2{91_18RS21}	KDNVKWISYK	SFCGVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNQEKIA	
msa255178.2{91_2603}	KDNVKWISYK	SFCGVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNQEKIA	
msa255178.2{91_A909}	KDNVKWISYK	SFCGVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNQEKIA	
msa255178.2{91_CJB110}	KDNVKWISYK	SFCGVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNQEKIA	
msa255178.2{91_H36B}	KDNVKWISYK	SFCGVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNQEKIA	
msa255178.2{91_JM9130013}	KDNVKWISYK	SFCGVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNQEKIA	
msa255178.2{91_COH1}	KDNVKWISYK	SFCGVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNQEKIA	
msa255178.2{91_M781}	KDNVKWISYK	SFCGVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNQEKIA	
msa255178.2{91_M732}	KDNVKWISYK	SFCGVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNQEKIA	
msa255178.2{91_1169NT}	KDNVKWISYK	SFCGVRRYAA	IESLDPSGGS	ETKAPTPVTN	SGSNNQEKIA	
Consensus	*****	*****	*****	*****	*****	
						200
msa255178.2{91_090}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_18RS21}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_2603}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_A909}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_CJB110}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_H36B}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_JM9130013}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_COH1}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_M781}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_M732}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_1169NT}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
Consensus	*****	*****	*****	*****	*****	
						250
msa255178.2{91_090}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_18RS21}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_2603}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_A909}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_CJB110}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_H36B}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_JM9130013}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_COH1}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_M781}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_M732}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
msa255178.2{91_1169NT}	TQGNYTFSHK	VEVKNEAKVA	SPTQFTL DKG	DRIFYDQILT	IEGNQWL SYK	
Consensus	*****	*****	*****	*****	*****	
						251
msa255178.2{91_090}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	T1sNETTGF	
msa255178.2{91_18RS21}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	T1sNETTGF	
msa255178.2{91_2603}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	T1sNETTGF	
msa255178.2{91_A909}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	T1sNETTGF	
msa255178.2{91_CJB110}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	T1sNETTGF	

Table 89: Comparative Sequences relating to SAG1350

msa255178.2{91_H36B}	SFNGVRRFVL LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	T1sNETTTGF	
msa255178.2{91_JM9130013}	SFNGVRRFVL LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	T1yNETTTGF	
msa255178.2{91_COH1}	SFNGVRRFVL LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	T1sNETTTGF	
msa255178.2{91_M781}	SFNGVRRFVL LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	T1sNETTTGF	
msa255178.2{91_M732}	SFNGVRRFVL LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	T1sNETTTGF	
msa255178.2{91_1169NT}	SFNGVRRFVL LGKASSVEKT	EDKEKVSPQP	QARITKTGRL	T1sNETTTGF	
Consensus	*****	*****	*****	*****	*****
msa255178.2{91_090}	301 DILITNIKDD NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNYKVAVSFA	350
msa255178.2{91_18RS21}	DILITNIKDD NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNYKVAVSFA	
msa255178.2{91_2603}	DILITNIKDD NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNYKVAVSFA	
msa255178.2{91_A909}	DILITNIKDD NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNYKVAVSFA	
msa255178.2{91_CJB110}	DILITNIKDD NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNYKVAVSFA	
msa255178.2{91_H36B}	DILITNIKDD NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNYKVAVSFA	
msa255178.2{91_JM9130013}	DILITNIKDD NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNYKVAVSFA	
msa255178.2{91_COH1}	DILITNIKDD NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNYKVAVSFA	
msa255178.2{91_M781}	DILITNIKDD NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNYKVAVSFA	
msa255178.2{91_M732}	DILITNIKDD NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNYKVAVSFA	
msa255178.2{91_1169NT}	DILITNIKDD NGIAAVKVPV	WTEQGGQDDI	KWYTAVTGTD	GNYKVAVSFA	
Consensus	*****	*****	*****	*****	*****
msa255178.2{91_090}	351 DHKNEKGLYN IHLYYYQEASG	TLVGVGTGTVK	TVAGTNSSQE	PIENGLaKTG	400
msa255178.2{91_18RS21}	DHKNEKGLYN IHLYYYQEASG	TLVGVGTGTVK	TVAGTNSSQE	PIENGLaKTG	
msa255178.2{91_2603}	DHKNEKGLYN IHLYYYQEASG	TLVGVGTGTVK	TVAGTNSSQE	PIENGLaKTG	
msa255178.2{91_A909}	DHKNEKGLYN IHLYYYQEASG	TLVGVGTGTVK	TVAGTNSSQE	PIENGLaKTG	
msa255178.2{91_CJB110}	DHKNEKGLYN IHLYYYQEASG	TLVGVGTGTVK	TVAGTNSSQE	PIENGLaKTG	
msa255178.2{91_H36B}	DHKNEKGLYN IHLYYYQEASG	TLVGVGTGTVK	TVAGTNSSQE	PIENGLaKTG	
msa255178.2{91_JM9130013}	DHKNEKGLYN IHLYYYQEASG	TLVGVGTGTVK	TVAGTNSSQE	PIENGLaKTG	
msa255178.2{91_COH1}	DHKNEKGLYN IHLYYYQEASG	TLVGVGTGTVK	TVAGTNSSQE	PIENGLpKTG	
msa255178.2{91_M781}	DHKNEKGLYN IHLYYYQEASG	TLVGVGTGTVK	TVAGTNSSQE	PIENGLpKTG	
msa255178.2{91_M732}	DHKNEKGLYN IHLYYYQEASG	TLVGVGTGTVK	TVAGTNSSQE	PIENGLpKTG	
msa255178.2{91_1169NT}	DHKNEKGLYN IHLYYYQEASG	TLVGVGTGTVK	TVAGTNSSQE	PIENGLaKTG	
Consensus	*****	*****	*****	*****	*****
msa255178.2{91_090}	401 VYNIIGSTEV KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS	450
msa255178.2{91_18RS21}	VYNIIGSTEV KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS	
msa255178.2{91_2603}	VYNIIGSTEV KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS	
msa255178.2{91_A909}	VYNIIGSTEV KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS	
msa255178.2{91_CJB110}	VYNIIGSTEV KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS	
msa255178.2{91_H36B}	VYNIIGSTEV KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS	
msa255178.2{91_JM9130013}	VYNIIGSTEV KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS	
msa255178.2{91_COH1}	VYNIIGSTEV KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS	
msa255178.2{91_M781}	VYNIIGSTEV KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS	
msa255178.2{91_M732}	VYNIIGSTEV KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS	
msa255178.2{91_1169NT}	VYNIIGSTEV KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS	
Consensus	*****	*****	*****	*****	*****
msa255178.2{91_090}	451 GVRRYIPVKK LTSSEKAKD	EATKPTSYNP	LPKTGTYTFT	KTVDVKSQPK	500
msa255178.2{91_18RS21}	GVRRYIPVKK LTSSEKAKD	EATKPTSYNP	LPKTGTYTFT	KTVDVKSQPK	
msa255178.2{91_2603}	GVRRYIPVKK LTSSEKAKD	EATKPTSYNP	LPKTGTYTFT	KTVDVKSQPK	
msa255178.2{91_A909}	GVRRYIPVKK LTSSEKAKD	EATKPTSYNP	LPKTGTYTFT	KTVDVKSQPK	
msa255178.2{91_CJB110}	GVRRYIPVKK LTSSEKAKD	EATKPTSYNP	LPKTGTYTFT	KTVDVKSQPK	
msa255178.2{91_H36B}	GVRRYIPVKK LTSSEKAKD	EATKPTSYNP	LPKTGTYTFT	KTVDVKSQPK	
msa255178.2{91_JM9130013}	GVRRYIPVKK LTSSEKAKD	EATKPTSYNP	LPKTGTYTFT	KTVDVKSQPK	
msa255178.2{91_COH1}	GVRRYIPVKK LTSSEKAKD	EATKPTSYNP	LPKTGTYTFT	KTVDVKSQPK	
msa255178.2{91_M781}	GVRRYIPVKK LTSSEKAKD	EATKPTSYNP	LPKTGTYTFT	KTVDVKSQPK	
msa255178.2{91_M732}	GVRRYIPVKK LTSSEKAKD	EATKPTSYNP	LPKTGTYTFT	KTVDVKSQPK	
msa255178.2{91_1169NT}	GVRRYIPVKK LTSSEKAKD	EATKPTSYNP	LPKTGTYTFT	KTVDVKSQPK	
Consensus	*****	*****	*****	*****	*****
msa255178.2{91_090}	501 VSSPVBFNFQ KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRR	IEI	543
msa255178.2{91_18RS21}	VSSPVBFNFQ KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRR	IEI	
msa255178.2{91_2603}	VSSPVBFNFQ KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRR	IEI	
msa255178.2{91_A909}	VSSPVBFNFQ KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRR	IEI	
msa255178.2{91_CJB110}	VSSPVBFNFQ KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRR	IEI	
msa255178.2{91_H36B}	VSSPVBFNFQ KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRR	IEI	
msa255178.2{91_JM9130013}	VSSPVBFNFQ KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRR	IEI	
msa255178.2{91_COH1}	VSSPVBFNFQ KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRR	IEI	
msa255178.2{91_M781}	VSSPVBFNFQ KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRR	IEI	
msa255178.2{91_M732}	VSSPVBFNFQ KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRR	IEI	
msa255178.2{91_1169NT}	VSSPVBFNFQ KGEKIHYDQV	LVVDGHQWIS	YKSYSGIRR	IEI	
Consensus	*****	*****	*****	***	

CLAIMS:

1. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of both GAS and *Streptococcus pneumoniae*.
5
2. The immunogenic composition of claim 1, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 1.
3. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of GAS.
10
4. The immunogenic composition of claim 3, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 2.
5. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of *Streptococcus pneumoniae*.
15
6. The immunogenic composition of claim 5, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 3.
20
7. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS serotype polynucleotide sequence which is homologous to at least one other GBS serotype.
25
8. The immunogenic composition of claim 2, 4 or 6, wherein one or more of the GBS polypeptides are encoded by GBS serotype polynucleotide sequences which are homologous to at least one other GBS serotype.
9. An immunogenic composition comprising a fusion protein, wherein said fusion protein comprises a first polypeptide sequence which is encoded by a GBS serotype polynucleotide which is conserved across one or more GBS serotypes.
30
10. A polynucleotide sequence, or a fragment comprising at least 10 contiguous polynucleotides, selected from the sequences set forth on Tables 13 – 31 and 40 – 89.
11. The polynucleotide fragment of claim 10, wherein said fragment is derived from a GBS serotype polynucleotide sequence and is homologous to at least one additional GBS serotype polynucleotide sequence.
35

Figure 1

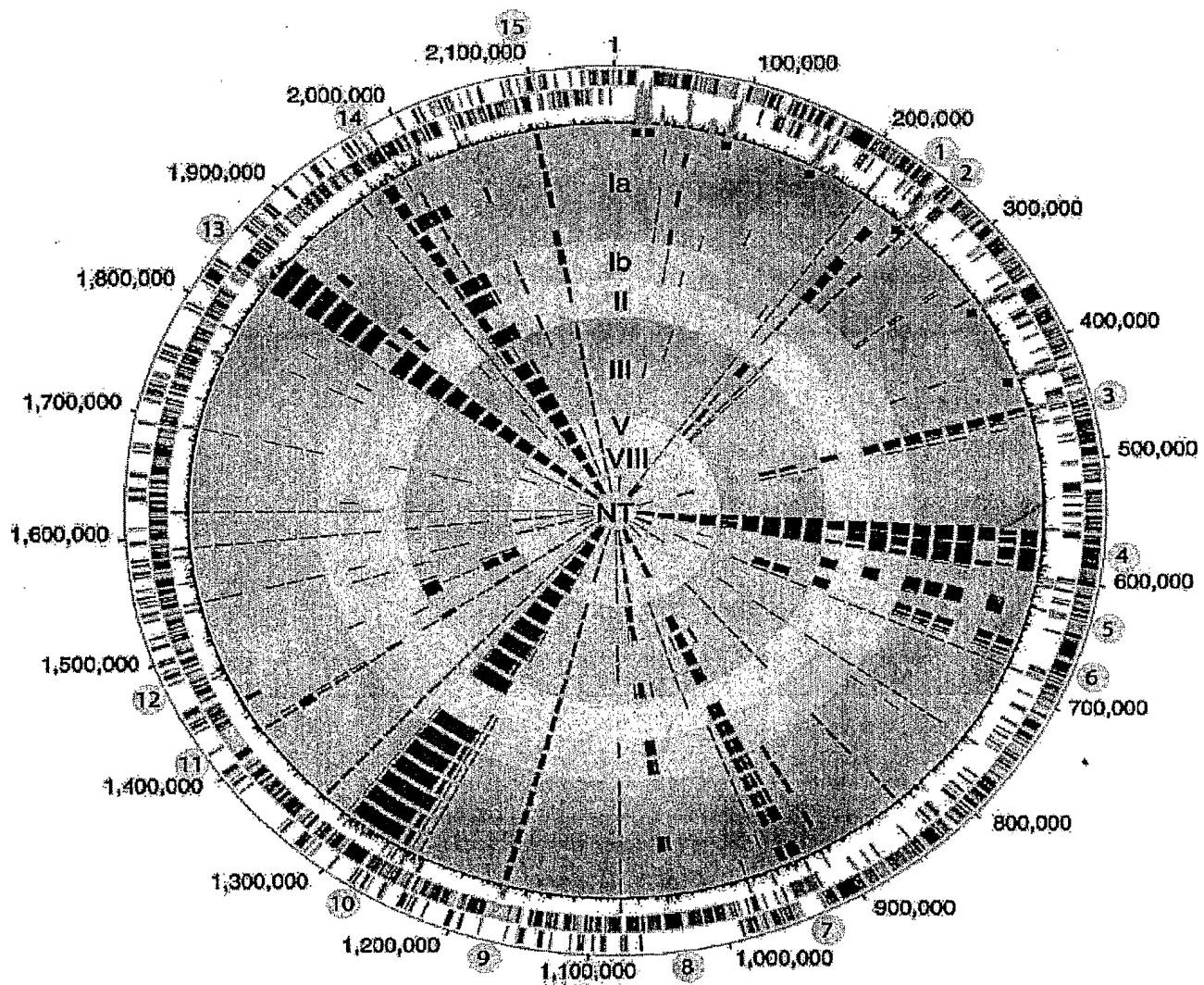


Figure 2

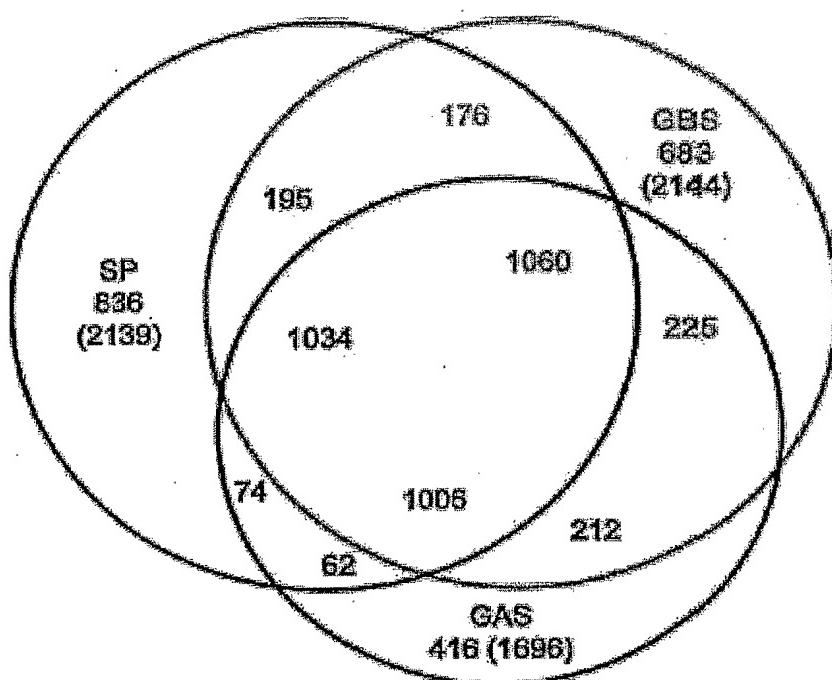
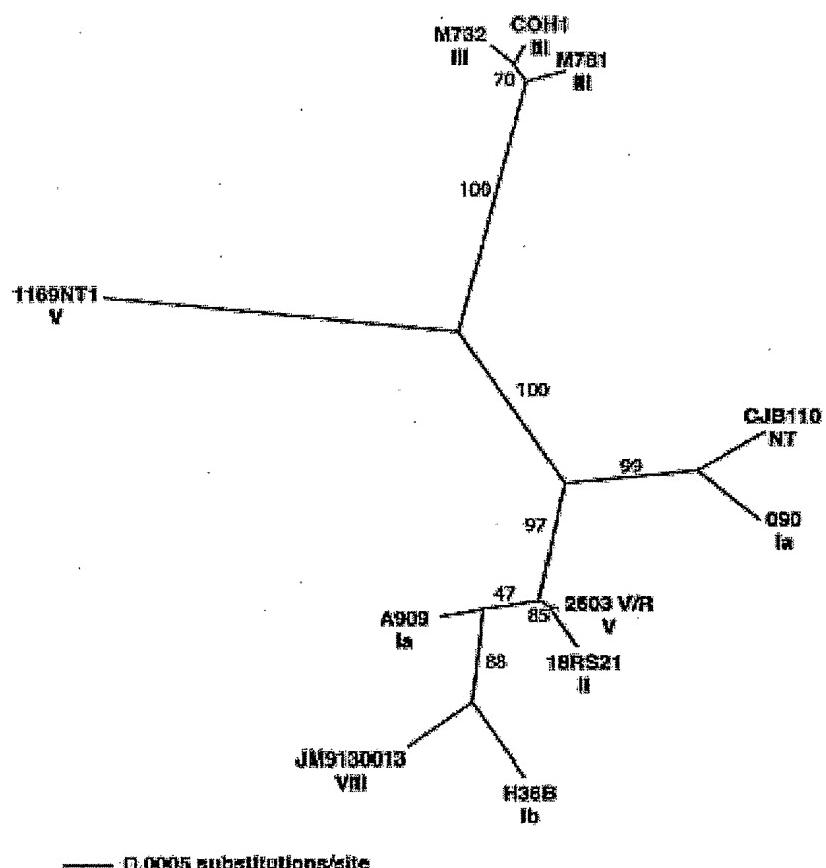


Figure 3



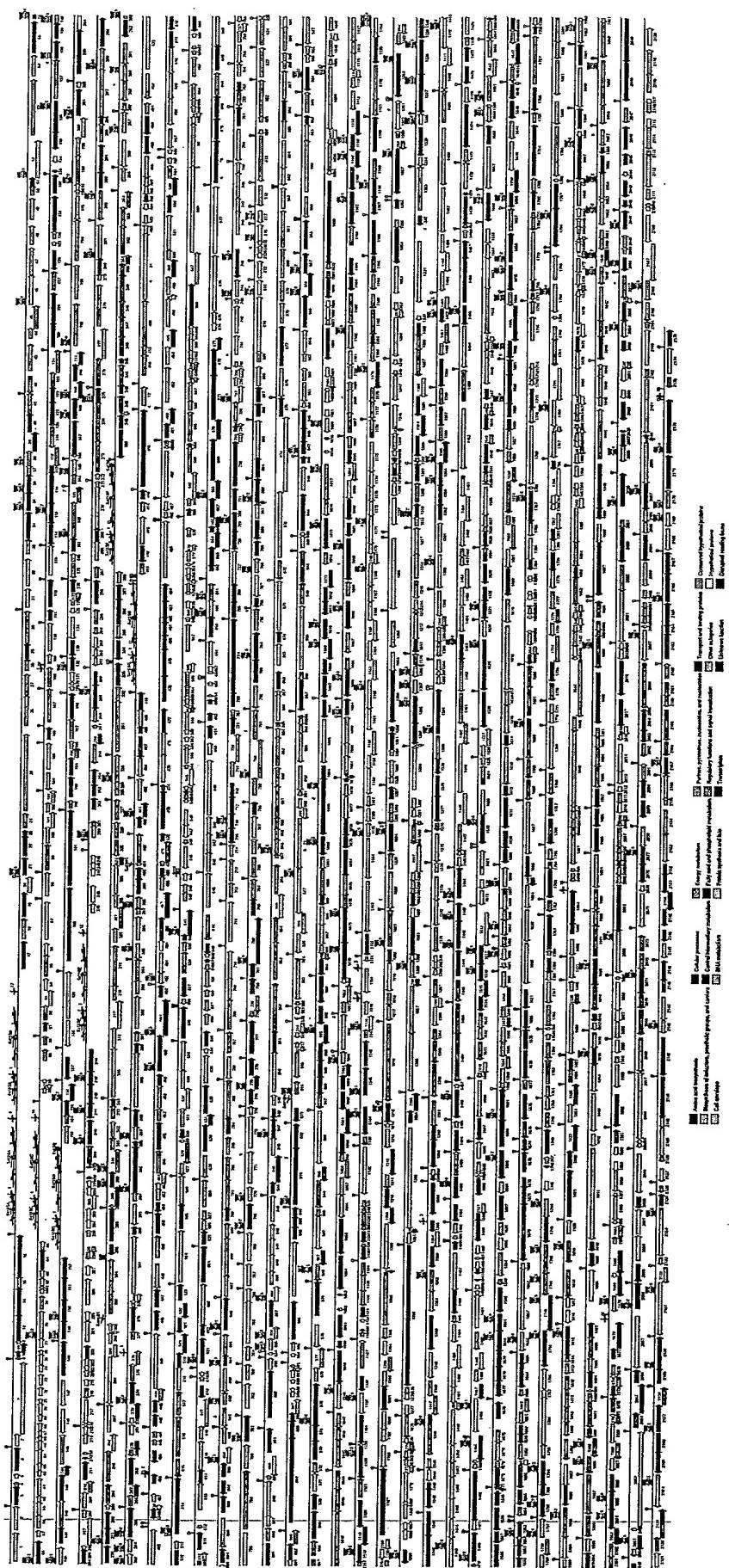


FIGURE 4

Strains:
Serotype:

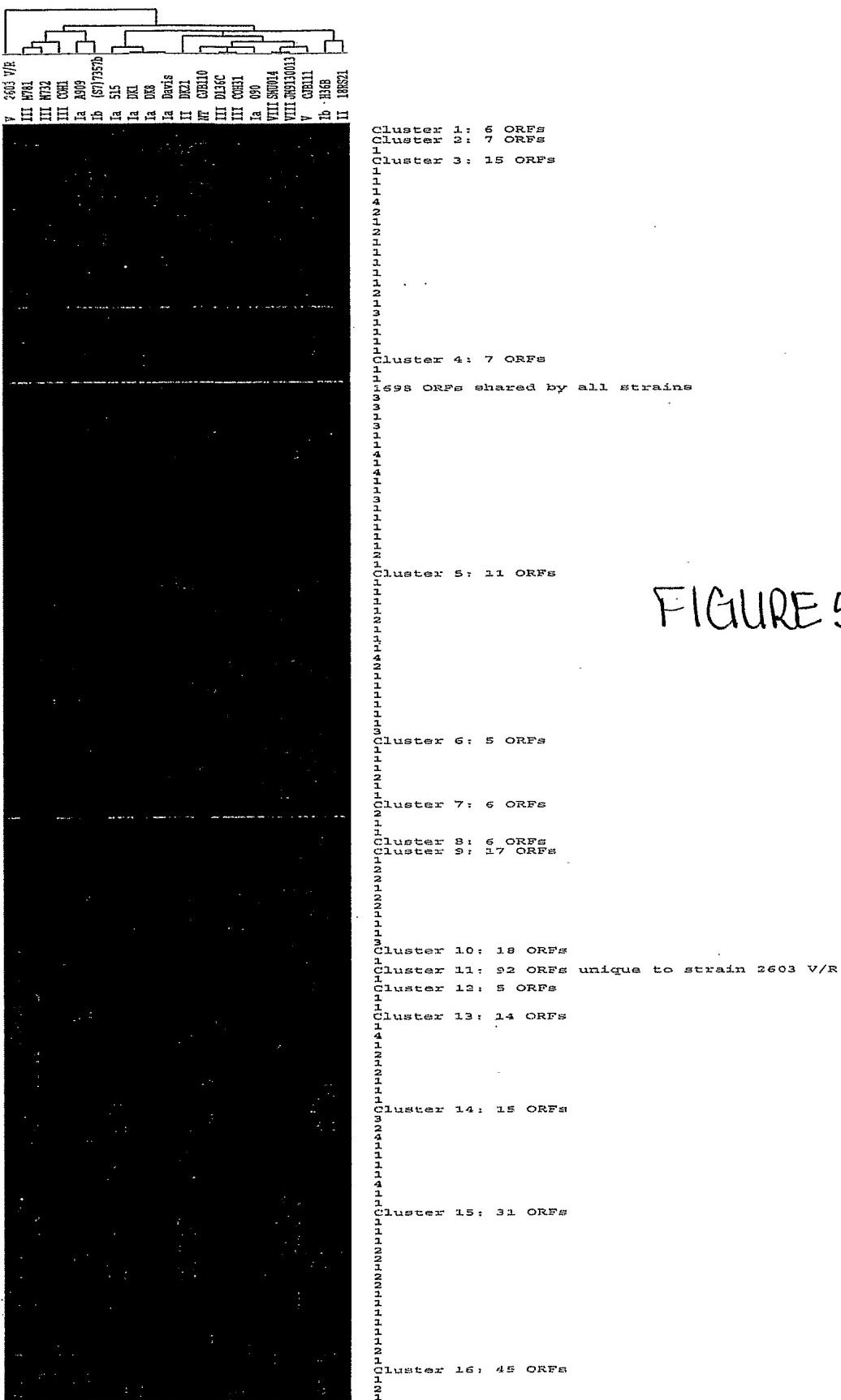


FIGURE 5